

Sun Mar 9 08:18:39 2003

us-08-982-272-2.rge

Page 1

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: March 8, 2003, 18:35:23 ; Search time 2040.79 Seconds
(without alignments)
1166.008 Million cell updates/sec

Title: US-08-982-272-2

Perfect score: 783
Sequence: 1 ATGATGAAACATACAGCCA.....TTGGCTTACTCAACTCTGGA 783

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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45: em_hcg_mus: *

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	783	100.0	818	6	AR044778	AR044778 Sequence
2	783	100.0	818	6	AR171646	AR171646 Sequence
3	783	100.0	1250	6	AX208160	AX208160 Sequence
4	781.4	99.8	783	6	AR076938	AR076938 Sequence
5	781.4	99.8	783	6	AR078308	AR078308 Sequence
6	781.4	99.8	783	6	AR085411	AR085411 Sequence
7	781.4	99.8	783	6	AR103367	AR103367 Sequence
8	781.4	99.8	783	6	AR169224	AR169224 Sequence
9	781.4	99.8	783	6	187865	187865 Sequence 5
10	781.4	99.8	1250	10	AP013985	X55453 M. musculus
11	701.4	89.6	783	10	AF116582	AF116582 Rattus no
12	698.2	89.2	783	10	AF116582	AF116582 Rattus no
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14	631.4	80.6	878	6	AR078323	AR078323 Sequence
15	631.4	80.6	878	6	AR085426	AR085426 Sequence
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17	631.4	80.6	878	6	AR169239	AR169239 Sequence
18	560.4	71.6	840	6	187864	187864 Sequence 3
19	560.4	71.6	840	6	AR044779	AR044779 Sequence
20	560.4	71.6	840	6	AR076926	AR076926 Sequence
21	560.4	71.6	840	6	AR078316	AR078316 Sequence
22	560.4	71.6	840	6	AR085419	AR085419 Sequence
23	560.4	71.6	840	6	AR103375	AR103375 Sequence
24	560.4	71.6	840	6	AR106246	AR106246 Sequence
25	560.4	71.6	840	6	AR169232	AR169232 Sequence
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28	560.4	71.6	840	6	127345	127345 Sequence 7
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ALIGNMENTS

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DEFINITION Sequence 1 from patent US 5817516.
ACCESSION AR044778
VERSION AR044778.1 GI:5966243
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 818)
AUTHORS Kehry, M. and Castle, B.
TITLE Methods for proliferating and differentiating B cells with high
density membrane CD40 ligand
JOURNAL Patent: US 5817516-A 1 06-Oct-1998;

Db 481 ACGGTTAAAGAGAGACTTATATGCTACACTCAAGTCACTCTGCTTAATCCG 540
 Qy 541 GAGCCTTCAGTCAACGCCCATTCATCTGTCGCTGCTGCTGAGCCAGCATGATCT 600
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 Db 781 TGA 783

RESULT 5
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 DEFINITION Sequence 1 from patent US 5962406.
 ACCESSION AR078308
 VERSION AR078308.1 GI:10005054
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 783)
 AUTHORS Armitage, R.J., Fanslow, W.C., Spriggs, M.K., Srinivasan, S.,
 Gibson, M.G., Morris, A.E. and McGrew, J.T.
 TITLE Recombinant soluble CD40 ligand polypeptide and pharmaceutical
 composition containing the same
 JOURNAL Patent: US 5962406-A 1 05-OCT-1999;
 FEATURES Location/Qualifiers
 source 1..783
 /organism="unknown"

BASE COUNT 243 a 159 c 178 g 203 t
 ORIGIN

Query Match 99.8%; Score 781.4; DB 6; Length 783;
 Best Local Similarity 99.9%; Pred. No. 2e-197;
 Matches 782; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGATAGAAACATACAGCCAACTTCCCAAGATCCGTGCAACTGCACTTCCAGGAGC 60
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 Qy 61 ATGAAGATTTTATGATTTTATCTTACTGTTTCTTATCAACCAATGATGATCTGTG 120
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 Qy 781 TGA 783
 Db 781 TGA 783

RESULT 6
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 LOCUS AR085411 783 bp DNA linear PAT 01-SEP-2000
 DEFINITION Sequence 1 from patent US 5981724.
 ACCESSION AR085411
 VERSION AR085411.1 GI:10012180
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 783)
 AUTHORS Armitage, R.J., Fanslow, W.C., Spriggs, M.K., Srinivasan, S.,
 Gibson, M.G., Morris, A.E. and McGrew, J.T.
 TITLE DNA encoding CD40 ligand, a cytokine that binds CD40
 JOURNAL Patent: US 5981724-A 1 09-NOV-1999;
 FEATURES Location/Qualifiers
 source 1..783
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BASE COUNT 243 a 159 c 178 g 203 t
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Query Match 99.8%; Score 781.4; DB 6; Length 783;
 Best Local Similarity 99.9%; Pred. No. 2e-197;
 Matches 782; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGATAGAAACATACAGCCAACTTCCCAAGATCCGTGCAACTGCACTTCCAGGAGC 60
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 Db 61 ATGAAGATTTTATGATTTTATCTTACTGTTTCTTATCAACCAATGATGATCTGTG 120
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Oy	301	AACAAGAAGAGAAAAAAGAAAACAGCTTTGAAATGCCAAGAAGTGATGAGATTCTCAA	360
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Db	541	GAGCTTTCAGATCAACGCCCATTCATCGTGGGCGCTGTGGCTGAAGCCCAAGATTGGATCT	600
Oy	601	GAGAGATCTTACTCAAGGCGGCAATACCAAGTTCCTCCAGCTTTGGCAGCACAG	660
Db	601	GAGAGATCTTACTCAAGGCGGCAATACCAAGTTCCTCCAGCTTTGGCAGCACAG	660
Oy	661	TCTGTTCACTTGGGGGAGGTGTGAATTAACAAGCTGTGCTTCTGTGTGTGCAACGTG	720
Db	661	TCTGTTCACTTGGGGGAGGTGTGAATTAACAAGCTGTGCTTCTGTGTGTGCAACGTG	720
Oy	721	ACTGAAACAAGCCAAGTGATCCACAGAGTTGGCTTCTCAATCTTTGGCTTCCAAATCC	780
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Oy	781	TGA 783	
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DEFINITION	Sequence 1 from patent US 6087329.		
ACCESSION	ARI03367		
VERSION	ARI03367.1 GI:12814955		
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclabified.		
AUTHORS	1 (bases 1 to 783)		
TITLE	Ar40e/R.J., Fanslow,W.C. and Spriggs,M.K.		
JOURNAL	CD4 ligand polypeptide		
FEATURES	Patent: US 6087329-A 1 11-JUL-2000;		
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	source	1..783	
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Db	61	ATGAGATTTTTATGATATTACTTACCTGTTTTCCCTTATCACCCAAATGATGGATCTGTG	120

Oy	121	CTTTTGTGCTGTATTCCTTAAGAAGTTGGATTAAAGCTCGAAGGAAGTAAACCTTCAT	180
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Db	241	TTCCTGAACCTGTAGAGATGTGAAGCAATTTGAAAGACTTGTCAAGATATAACGTTA	300
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Db	481	ACGGTTAAAGAGAGAGACTTATTATGTCTACACTGCAAGTCACTTGTCTTAATCGG	540
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Db	601	GAGAGATCTTACTCAGAGCGGCAATATCCACAGTTCCTCCACACTTGGAGACAGCG	660
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LOCUS	ARI69224	783 bp	linear PAT 17-DEC-2001
DEFINITION	Sequence 1 from patent US 6290972.		
VERSION	ARI69224.1 GI:17907035		
KEYWORDS	unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 783)		
AUTHORS	Amitshe R.J., Fanslow,W.C., Spriggs,M.K., Srinivasan,S. and Gibson,M.G.		
TITLE	Method of augmenting a vaccine response by administering CD40 ligand		
JOURNAL	Patent: US 6290972-A 1 18-SEP-2001;		
FEATURES	location/Qualifiers		
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BASE COUNT	243 a 159 c 178 g 203 t		
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Best Local Similarity 99.9%; Pred. No. 2e-197;
Matches 782; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1 ATGATGAAACATACAGCACTTCCCGAGATCCGTGCAACCTGACCTTCCAGCAGC 60
QY 61 ATGAGATTTTATGATTTTACTTACCTGTTTCCCTTATCAACCAATGATGATCTG 120
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QY 781 TGA 783
Db 781 TGA 783

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RESULT 9
187865
LOCUS 187865 783 bp DNA linear PAT 10-AUG-1998
DEFINITION Sequence 5 from patent US 5716805.
ACCESSION 187865
VERSION 187865.1 GI:3407805
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 783)
AUTHORS Srinivasan,S. and Spriggs,M.K.
TITLE Methods of preparing soluble, oligomeric proteins

JOURNAL Patent: US 5716805-A 5 10-FEB-1998;
FEATURES Location/Qualifiers
source 1..783
BASE COUNT 243 a 159 c 178 g 203 t
ORIGIN

Query Match 99.8%; Score 781.4; DB 6; Length 783;
Best Local Similarity 99.9%; Pred. No. 2e-197;
Matches 782; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1 ATGATGAAACATACAGCACTTCCCGAGATCCGTGCAACCTGACCTTCCAGCAGC 60
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QY 781 TGA 783
Db 781 TGA 783

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RESULT 10
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DEFINITION M. musculus mRNA for CD40 ligand.
ACCESSION X65453

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 EEKKEKSPMQGDEDPQIAHVSANSNASVLAQAKGYITKSNLVLNENGOL
 TVRBSGLYVTVQVFCSPNRPISQRPVLSLWMLKPSGSEIRLLRAANTHSSKICE
 QOSIHGSGFELQAGASVFNVTASQVTHIGIFSSIGLTKL"
 BASE COUNT 236 a 152 c 189 g 206 t
 ORIGIN

Query Match 89.6% Score 701.4; DB 10; Length 783;
 Best Local Similarity 93.5%; Pred. No. 4.3e-176;
 Matches 732; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 1 ATGATGAAACATACACCCACCTTCCCAAGATCCGTCGCAACTGACCTTCCAGGAC 60
 Db 1 ATGATGAAACATACACCCACCTTCCCAAGATCCGTCGCAACTGACCTTCCAGGAC 60
 QY 61 ATGAGATTTTATGATTTACTTACTGTTTCTTATACCCCAATGATGATGATG 120
 Db 61 ATGAGATTTTATGATTTACTTACTGTTTCTTATACCCCAATGATGATGATG 120
 QY 121 CTTTGGCTGTATCTTATGAAAGATGATGATGATGATGATGATGATGATGATG 180
 Db 121 CTTTGGCTGTATCTTATGAAAGATGATGATGATGATGATGATGATGATGATG 180
 QY 181 GAGATTTTGTATTTCAAAAAAGCTAAAGATGCAACAAAGAGAGATCTTATCC 240
 Db 181 GAGATTTTGTATTTCAAAAAAGCTAAAGATGCAACAAAGAGAGATCTTATCC 240
 QY 241 TTGCTGAACCTGTAGAGAGATGAGAGCAATTTGAAAGCTTGTCAAGATTAACGTTA 300
 Db 241 TTGCTGAACCTGTAGAGAGATGAGAGCAATTTGAAAGCTTGTCAAGATTAACGTTA 300
 QY 301 AACAAAGAGAAAAAAGAAAAAGCTTTGAAATGCAAGAGTGAATGATGATCTTCA 360
 Db 301 AACAAAGAGAAAAAAGAAAAAGCTTTGAAATGCAAGAGTGAATGATGATCTTCA 360
 QY 361 ATTGACAGACAGCTGTATGAGAGAGCAACAGTATGAGATCTTCTTCAAGTGGGCC 420
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 QY 421 AAGAAAGATATTTATCCATGAAAGCACTTGTATGCTTGAATGAGAAAGAGCTG 480
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 QY 481 ACGGTTAAAAAGAGAGACTTATTTATGCTACACTCAAGTCACTTGTCTTATGG 540
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 QY 541 GAGCTTCGATCAACGCCATTATGCTGGCTTGTGCTGAAAGCCAGCAATGATCT 600
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 QY 661 TCTGTTCACTGGGGGAGTGTGTTGAATTAAGTGTGCTTCTGTGTTGTCAAGTG 720
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 QY 721 ACTGAAGCAAGCAAGTATCAAGAGTGTGCTTCTTATGCTTGTGCTTCAAACTC 780
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 QY 781 TGA 783
 Db 781 TGA 783

RESULT 12
 AF116582 783 bp mRNA linear ROD 12-JUL-2000
 LOCUS AF116582

DEFINITION Rattus norvegicus CD40 ligand mRNA, complete cds.
 ACCESSION AF116582
 VERSION AF116582.1 GI:4545249
 KEYWORDS
 SOURCE
 ORGANISM

Rattus norvegicus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE 1 (bases 1 to 783)

AUTHORS Halleck, K.M. and Oaks, M.K.

TITLE Nucleotide sequence of the rat CD40 ligand

JOURNAL DNA Seq. 10 (6), 405-406 (2000)

MEDLINE 20284949

PUBMED 10826698

REFERENCE 2 (bases 1 to 783)

AUTHORS Halleck, K.M. and Oaks, M.K.

TITLE Direct Submission

JOURNAL Submitted (24-DEC-1998) Transplant Research, St. Luke's Medical
 Center, 2900 W. Oklahoma Ave., Milwaukee, WI 53215, USA

FEATURES

source

1..783

/organism="Rattus norvegicus"

/strain="Sprague Dawley"

/db_xref="taxon:10116"

/cell_type="splenocyte"

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/codon_start=1

/product="CD40 ligand"

/protein_id="AAD22460.1"

/db_xref="GI:4545250"

/translation="MIETVQSPSPSVATGCPASMKITPMYLLTVPLITOMIGSVLPAY
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BASE COUNT

237 a

153 c

189 g

204 t

ORIGIN

Query Match

Best Local Similarity 93.2%; Score 698.2; DB 10; Length 783;
 Matches 730; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 1 ATGATGAAACATACACCCACCTTCCCAAGATCCGTCGCAACTGACCTTCCAGGAC 60

Db 1 ATGATGAAACATACACCCACCTTCCCAAGATCCGTCGCAACTGACCTTCCAGGAC 60

QY 61 ATGAGATTTTATGATTTACTTACTGTTTCTTATACCCCAATGATGATGATGATG 120

Db 61 ATGAGATTTTATGATTTACTTACTGTTTCTTATACCCCAATGATGATGATGATG 120

QY 121 CTTTGGCTGTATCTTATGAAAGATGATGATGATGATGATGATGATGATGATG 180

Db 121 CTTTGGCTGTATCTTATGAAAGATGATGATGATGATGATGATGATGATGATG 180

QY 181 GAGATTTTGTATTTCAAAAAAGCTAAAGATGCAACAAAGAGAGATCTTATCC 240

Db 181 GAGATTTTGTATTTCAAAAAAGCTAAAGATGCAACAAAGAGAGATCTTATCC 240

QY 241 TTGCTGAACCTGTAGAGAGATGAGAGCAATTTGAAAGCTTGTCAAGATTAACGTTA 300

Db 241 TTGCTGAACCTGTAGAGAGATGAGAGCAATTTGAAAGCTTGTCAAGATTAACGTTA 300

QY 301 AACAAAGAGAAAAAAGAAAAAGCTTTGAAATGCAAGAGTGAATGATGATCTTCA 360

Db 301 AACAAAGAGAAAAAAGAAAAAGCTTTGAAATGCAAGAGTGAATGATGATCTTCA 360

QY 361 ATTGACAGACAGCTGTATGAGAGAGCAACAGTATGAGATCTTCTTCAAGTGGGCC 420

Db 361 ATTGACAGACAGCTGTATGAGAGAGCAACAGTATGAGATCTTCTTCAAGTGGGCC 420

QY 421 AAGAAAGATATTTATCCATGAAAGCACTTGTATGCTTGAATGAGAAAGAGCTG 480

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 Qy 481 ACGGTTAAAGAGAGAGACTTATATATGCTACATCAAGTCACTTCTGCTTATGCG 540
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 Qy 721 ACTGAAGCAAGCCAGATGATCCAGAGTGGCTTCTCATCTTTGGCTTACTCAACTC 780
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 Qy 781 TGA 783
 Db 781 TGA 783

RESULT 13
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 LOCUS
 DEFINITION Sequence 22 from patent US 5961974.
 ACCESSION AR076933
 VERSION AR076933.1 GI:10003679
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCES
 1 (bases 1 to 878)
 AUTHORS Armitage, R.J., Fanslow, W.C. and Spriggs, M.K.
 TITLE Monoclonal antibodies to CD40 ligand, pharmaceutical composition comprising the same and hybridomas producing the same
 JOURNAL Patent: US 5961974-A 22 05-OCT-1999;
 FEATURES
 source location/Qualifiers
 1..878 /organism="unknown"
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 ORIGIN

Query Match 80.6%; Score 631.4; DB 6; Length 878;
 Best Local Similarity 99.8%; Pred. No. 2e-157; 1; Indels 0; Gaps 0;
 Matches 632; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 151 GATPAGGTGAAAGAGAACTTCAATGAAATTTGTTATTCATTAATAAGCTTAAG 210
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 Qy 211 AGATGCAAGAAAGAGAGATCTTATCTTCTGCTGAAGCTGAGAGATGAGAGCA 270
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 Qy 331 GAAATGCAAGAGGTGATGAGATCTCAATTTGAGACACGTTTGAAGCAAGCCAC 390
 Db 405 GAAATGCAAGAGGTGATGAGATCTCAATTTGAGACACGTTTGAAGCAAGCCAC 464
 Qy 391 AGTAATGCAAGATCGTTCTCAAGTGGCCCAAGAAAGATTTATCACTGAAAGCAAC 450
 Db 465 AGTAATGCAAGATCGTTCTCAAGTGGCCCAAGAAAGATTTATCACTGAAAGCAAC 524
 Qy 451 TTGGTAATGCTTGAATAATGGGAAACAGCTGACGTTAAAGAGAAAGAACTTATATGTC 510

Db 525 TTGGTAATGCTTGAATAATGGGAAACAGCTGACGTTAAAGAGAAAGAACTTATATGTC 584
 Qy 511 TACACTCAAGTCACTTCTGCTTATATGGAGCTTCAAGTCAAGCCATTCATGTC 570
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 Qy 631 CACAGTTCTTCCAGCTTTGCGAGCAGAGCTGCTCACTTGGCGGAGTGTGAATTA 690
 Db 705 CACAGTTCTTCCAGCTTTGCGAGCAGAGCTGCTCACTTGGCGGAGTGTGAATTA 764
 Qy 691 CAACTGCTGCTTCTGCTTGTTCACAGTGAAGCAAGCAAGTATCCAGAGTT 750
 Db 765 CAACTGCTGCTTCTGCTTGTTCACAGTGAAGCAAGCAAGTATCCAGAGTT 824
 Qy 751 GGCCTTCAAGCTTTTGGCTTACTCAAACTCTGA 783
 Db 825 GGCCTTCAAGCTTTTGGCTTACTCAAACTCTGA 857

RESULT 14
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 LOCUS
 DEFINITION Sequence 22 from patent US 5962406.
 ACCESSION AR078323
 VERSION AR078323.1 GI:10005069
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCES
 1 (bases 1 to 878)
 AUTHORS Armitage, R.J., Fanslow, W.C., Spriggs, M.K., Stinivasan, S.,
 Gibson, M.G., Morris, A.B. and McGrew, J.T.
 TITLE Recombinant soluble CD40 ligand and polypeptide and pharmaceutical composition containing the same
 JOURNAL Patent: US 5962406-A 22 05-OCT-1999;
 FEATURES
 source location/Qualifiers
 1..878 /organism="unknown"
 BASE COUNT 277 a 178 c 203 g 220 t
 ORIGIN

Query Match 80.6%; Score 631.4; DB 6; Length 878;
 Best Local Similarity 99.8%; Pred. No. 2e-157; 1; Indels 0; Gaps 0;
 Matches 632; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 151 GATPAGGTGAAAGAGAACTTCAATGAAATTTGTTATTCATTAATAAGCTTAAG 210
 Db 225 GATPAGGTGAAAGAGAACTTCAATGAAATTTGTTATTCATTAATAAGCTTAAG 284
 Qy 211 AGATGCAAGAAAGAGAGATCTTATCTTCTGCTGAAGCTGAGAGATGAGAGCA 270
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 Qy 391 AGTAATGCAAGATCGTTCTCAAGTGGCCCAAGAAAGATTTATCACTGAAAGCAAC 450
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 QY 631 CACAGTTCCTCCAGCTTTGCGAGCAGAGTCTGCTCACTGGGCGAGTGTGAATTA 690
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 QY 691 CAAGCTGTGCTTCTGTGTTTGTCAAGCTGATGAGCAAGCCAAAGTATCCAGAGTT 750
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 QY 751 GGCTTCTCATCTTTGGCTTACTCAAACTCTGA 783
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RESULT 15

AR085426

LOCUS AR085426 878 bp DNA linear PAT 01-SEP-2000

DEFINITION Sequence 22 from patent US 5981724.

ACCESSION AR085426

VERSION AR085426.1 GI:10012195

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 878)

AUTHORS Armitage,R.J., Fanslow,W.C., Spriggs,M.K., Srinivasan,S.,

Gibson,M.G., Morris,A.E. and McGrew,J.T.

TITLE DNA encoding CD40 ligand, a cytokine that binds CD40

JOURNAL Patent: US 5981724-A 22 09-NOV-1999;

FEATURES Location/Qualifiers

source 1..878

BASE COUNT 277 a 178 c 203 g 220 t

ORIGIN

Query Match 80.6%; Score 631.4; DB 6; Length 878;

Best Local Similarity 99.8%; Pred. No. 2e-157;

Matches 632; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 151 GATAAGGTGCAAGAGGAGTAACCTTCATGAAGATTTGTATTCTAATAAAGCTTAAG 210
 DB 225 GATAAGGTGCAAGAGGAGTAACCTTCATGAAGATTTGTATTCTAATAAAGCTTAAG 284
 QY 211 AGATGCAACAAAGAGAGATCTTTATCCTGCTGAACCTGAGAGATGAGAGCAA 270
 DB 285 AGATGCAACAAAGAGAGATCTTTATCCTGCTGAACCTGAGAGATGAGAGCAA 344
 QY 271 TTGAAGACCTTGTCAAGATATTAAGTTAAACAAAGAGAGAGAGAGAGAGAGAG 330
 DB 345 TTGAAGACCTTGTCAAGATATTAAGTTAAACAAAGAGAGAGAGAGAGAGAGAG 404
 QY 331 GAATGCAACAAAGAGAGATCTTTATCCTGCTGAACCTGAGAGATGAGAGCAA 390
 DB 405 GAATGCAACAAAGAGAGATCTTTATCCTGCTGAACCTGAGAGATGAGAGCAA 464
 QY 391 AGTAATGCAAGATCCGTTCTCAAGTGGGCGCAAGAGAGATTTATCACTGAAGAGCA 450
 DB 465 AGTAATGCAAGATCCGTTCTCAAGTGGGCGCAAGAGAGATTTATCACTGAAGAGCA 524
 QY 451 TTGGTAATGCTTGAATAAGGAAACAGCTGACGTTAAAGAGAGAGAGAGAGAGAG 510
 DB 525 TTGGTAATGCTTGAATAAGGAAACAGCTGACGTTAAAGAGAGAGAGAGAGAGAG 584
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 QY 571 GGCTTCTGGCTGAAGCCGACGATTTGATCTGAAGATCTTACTCAAGGCGCAATACC 630
 DB 645 GGCTTCTGGCTGAAGCCGACGATTTGATCTGAAGATCTTACTCAAGGCGCAATACC 704
 QY 631 CACAGTTCCTCCAGCTTTGCGAGCAGAGTCTGCTCACTGGGCGAGTGTGAATTA 690
 DB 705 CACAGTTCCTCCAGCTTTGCGAGCAGAGTCTGCTCACTGGGCGAGTGTGAATTA 764
 QY 691 CAAGCTGTGCTTCTGTGTTTGTCAAGCTGATGAGCAAGCCAAAGTATCCAGAGTT 750
 DB 765 CAAGCTGTGCTTCTGTGTTTGTCAAGCTGATGAGCAAGCCAAAGTATCCAGAGTT 824
 QY 751 GGCTTCTCATCTTTGGCTTACTCAAACTCTGA 783
 DB 825 GGCTTCTCATCTTTGGCTTACTCAAACTCTGA 857

Search completed: March 9, 2003, 02:11:24
 Job time : 2044.79 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 8, 2003, 21:32:03 ; Search time 1286.6 Seconds
(without alignment)
9856.249 Million cell updates/sec

Title: US-08-982-272-2

Perfect score: 783

Sequence: 1 ATGATAGAAACATACAGCA.....TTGGCTTACTCAACTCTGA 783

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 809774376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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2: em_escbm:*
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5: em_escov:*
6: em_escpl:*
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27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	245.2	31.3	398	10	AM486605 75217 MAR
3	72.8	9.3	638	9	AI982044 pat.PK007
4	55.8	7.1	997	17	CNS005TE
5	52.8	6.7	797	9	AL534423
6	51.2	6.5	1043	17	CNS0145P

7	51	6.5	1038	17	CNS0108N	AL098657 Drosophila
8	49.8	6.4	878	17	CNS0187R	AL108993 Drosophila
9	48.4	6.2	1101	17	CNS0039G	AL063921 Drosophila
10	47.6	6.1	920	17	AZ691914	ENTM26TR
11	46.8	6.0	423	17	AZ438784	1M0229106
12	46.8	6.0	458	17	AL514085	AL514085
13	45.6	5.8	802	17	CNS0383B	AL100719 Drosophila
14	45.6	5.8	828	17	CNS0181X	AL514085
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16	45.2	5.8	559	17	AQ373239	RPII1-14
17	44.8	5.7	1101	17	CNS0181N	AL108773 Drosophila
18	44.6	5.7	329	9	AL513719	AL513719
19	44.6	5.7	529	9	AL514657	AL514657
20	44.6	5.7	611	13	BI389827	BI389827
21	44.4	5.7	229	9	AV112562	AV112562
22	44.4	5.7	597	9	AL514721	AL514721
23	44.4	5.7	814	17	A2203738	A2203738
24	44.2	5.6	633	9	AL513979	AL513979
25	44.2	5.6	938	17	CNS006TU	AL100660 Drosophila
26	43.8	5.6	330	9	AL513817	AL513817
27	43.8	5.6	799	17	CNS011SA	AL100660 Drosophila
28	43.8	5.6	1101	17	CNS0182P	AL108811 Drosophila
29	43.6	5.6	588	17	AQ451757	AQ451757
30	43.6	5.6	828	17	CNS018FA	AQ451757
31	43.4	5.5	625	17	CNS036A2	AL109264 Drosophila
32	43	5.5	468	9	AL514541	AL128763 Tetradon
33	43	5.5	642	13	BJ096268	AL514541
34	42.8	5.5	807	17	CNS0119V	BU096268
35	42.6	5.4	415	14	R41111	BU096268
36	42.6	5.4	548	17	BO223382	R41111
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39	42.6	5.4	805	9	A1557564	AG044338
40	42.6	5.4	959	17	CNS00655	A1557564
41	42.6	5.4	1007	17	CNS06X9S	AL062806 Drosophila
42	42.4	5.4	634	9	AL514497	AL062806
43	42.4	5.4	918	17	CNS06X9S	AL514497
44	42.2	5.4	431	17	CNS04460	AL065768 Drosophila
45	42.2	5.4	950	17	CNS0134A	AL293145 Tetradon

ALIGNMENTS

RESULT 1
LOCUS 492 bp mRNA linear EST 25-APR-2001
DEFINITION 263218 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BF599437
VERSION BF599437.1 GI:11695919
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
Smith,T.P.L., Grose,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
1 (bases 1 to 492)

Caas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,
G.L., Heaton,M.P., Laegreid,W.M., Rohrer,G.A., Chalko-McKown,C.G.,
Petea,G., Holt,I., Karamcheva,S., Liang,F., Quackenbush,J. and
Keefe,J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)

JOURNAL MEDLINE
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred

v0.980904.e. Vector identified by cross_match with the -minscore 18 and -mismatch 12 options.

PCR Primers:
FORWARD: AGGAAACAGCTTATGACAT
BACKWARD: GTTTCCAGTCACGACG
Plate: 33 row: N column: 5
Seq primer: ATTAGGTGACACTATAG.

FEATURES

source

1. 492
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/db_xref="taxon:9913"
/clone_lib="MARC 3BOV"
/tissue_type="pooled"
/lab_host="DH10B"

/note="Vector: PCMV SPORTE; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendinosus muscle, and fetal
longissimus muscle."

BASE COUNT 163 a 103 c 104 g 122 t
ORIGIN

Query Match

Best Local Similarity 81.6%; Score 302.6; DB 12; Length 492;
Matches 363; Conservative 0; Mismatches 79; Indels 3; Gaps 1;

QY 1 ATGATGAAACATACAGCCACCTTCCCGAGATCCGTGGCACTGACCTTCCAGCGAGC 60
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DB 106 ATGAAATTTTATGATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 165
QY 121 CTTTTCGTGTATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
DB 166 CTTTTCGTGTATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 225
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DB 226 GAAGATTTTGTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 285
QY 241 TTGCTGAACGTGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAG 300
DB 286 TTACTGAACGTGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAG 345
QY 301 AACAAAGAG--AGAAAAAGAAACAGCTTTGAAAGCAAGAGTATGAGATCTT 357
DB 346 AACAAAGAGTAAAGAAAGAAAGAAAGAAAGTAAAGCAAGAGTATGAGAGCTT 405
QY 358 CAAATTCAGACACAGTGTAGAGCAACAGTAAATGAGATCCGTTTACAGTGG 417
DB 406 CAGATACCGGACATGTCATCAGTGAAGCCAGTAAACAACTCTGTTCCAGTGG 465
QY 418 GCCAAGAAAGATTTATATCATGA 442
DB 466 GCCCCCAAGATCTACACCTTA 490

RESULT 2

LOCUS AW486605 398 bp mRNA linear EST 25-APR-2001
DEFINITION 75217 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION AW486605
VERSION AW486605.1 GI:7056711
KEYWORDS EST.
SOURCE COW.
ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.

REFERENCE

1 (bases 1 to 398)
Smith,T.P.L., Grose,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett

G.L., Heaton,M.P., Laegreid,W.M., Rohrer,G.A., Chitko-McKown,C.G.,
Petea,G., Holt,I., Katamycheva,S., Liang,F., Quackenbush,J. and
Keefe,J.W.

Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
genome Res. 11 (4), 626-630 (2001)

JOURNAL

MEDLINE

COMMENT

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390

Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 20
and -mismatch 12 options.

PCR Primers:
FORWARD: AGGAAACAGCTTATGACAT
BACKWARD: GTTTCCAGTCACGACG
Plate: 34 row: F column: 23
Seq primer: ATTAGGTGACACTATAG.

FEATURES

source

1. 398
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 1BOV"
/tissue_type="pooled"
/lab_host="DH10B"

/note="Vector: PCMV SPORTE; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from lymph node, ovary,
fat, hypothalamus, and pituitary."

BASE COUNT 134 a 77 c 82 g 105 t
ORIGIN

Query Match

Best Local Similarity 83.8%; Score 245.2; DB 10; Length 398;
Matches 290; Conservative 0; Mismatches 53; Indels 3; Gaps 1;

QY 1 ATGATGAAACATACAGCCACCTTCCCGAGATCCGTGGCACTGACCTTCCAGCGAGC 60
DB 53 ATGATGAAACATACAGCTCACTTCTCCCGCTCCGTGGCACTGACCACTGTCACT 112
QY 61 ATGAAATTTTATGATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 120
DB 113 ATGAAATTTTATGATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 172
QY 121 CTTTTCGTGTATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
DB 173 CTTTTCGTGTATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 232
QY 181 GAAGATTTTGTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 240
DB 233 GAAGATTTTGTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 292
QY 241 TTGCTGAACGTGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAG 300
DB 293 TTACTGAACGTGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAG 352
QY 301 AACAAAGAG--AGAAAAAGAAACAGCTTTGAAAGCAAGAGTATGAGATCTT 343
DB 353 AACAAAGAGTAAAGAAAGAAAGAAAGTAAAGCAAGAGTATGAGAGCTT 398

RESULT 3

LOCUS A1982044 638 bp mRNA linear EST 07-MAY-2001
DEFINITION pat.p00072.c9.f chicken activated T cell cDNA Gallus gallus cDNA
ACCESSION A1982044
VERSION A1982044.1 GI:5885072
KEYWORDS EST.
SOURCE chicken.
ORGANISM Gallus gallus

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianidae; Gallus.
1 (bases 1 to 638)
Tsunaga, V.G., Soter, L., Cui, J. and Burnside, J.
An expressed sequence tag database of T-cell-enriched activated
chicken splenocytes: sequence analysis of 5251 clones
Genomics 66 (2), 144-151 (2000)

Contact: Joan Burnside
Molecular Endocrinology
University of Delaware
40 Townsend Hall, Newark, DE 19717, USA
Tel: 302 831-1345
Fax: 302-831-3411
Email: joan@udel.edu, www.chickest.udel.edu

Seq primer: T7.

FEATURES
source
1..638
/organism="Gallus gallus"
/db_xref="taxon:9031"
/clone="pat.pk0072.c9.f"
/clone_lib="chicken activated T cell cDNA"
/sex="male"
/cell_type="Con A-activated splenic T cell"
/lab_host="E.coli TOP10 F"
/note="Vector: pCDNA3"

BASE COUNT
132 a 171 c 151 g 180 t 4 others

ORIGIN

Query Match 9.3%; Score 72.8; DB 9; Length 638;
Best Local Similarity 58.3%; Pred. No. 3.1e-06;
Matches 169; Conservative 0; Mismatches 112; Indels 9; Gaps 2;

QY 495 AGGACTCTTATGCTCTACACTCAAGTCACTTCTGCTTAATCGGAGCTTGAATCA 554
DB 2 AGGCTCTACTACATCTACTCAAGTCAAGTCTTCTGCAAGCGCGCTTGG----- 56
QY 555 ACGCCCTCATCTGCGCGCTCTGCGTGAAGCCAGATTGATGAGATTTACT 614
DB 57 -GGCCCTTACCTCTTATTTTGTATCTCCCATGAGAGACCGGCTCTGAT 115
QY 615 CAAGCGGCAATATCCACAGTTCCTCCAG---CTTTGCAAGAGATCTGTTCACT 671
DB 116 GAAGGACTTGACAGCGCAACAGCTTCAAGGCTCTGTAGTCAATCCAGGGA 175
QY 672 GGGGAGTGTGATTAACAAGTGTCTGTGTTGTCAACGTGACTGAAGCAAG 731
DB 176 GGGCGAGTCTTGAAGCTCGGAGGCGAGCATGCTTTGTCAATGTGACGACTCAAC 235
QY 732 CCAGTATCCACAGAGTGTCTCATCTTTTGGCTTACTCAAACTCT 781
DB 236 AGCAGTGAAGTCAACCTTGGCAACCTACTTTGGCATGTTCAGCTGT 285

RESULT 4
CNS005TE/c 997 bp DNA linear GSS 03-JUN-1999
LOCUS
DEFINITION
Drosophila melanogaster genome survey sequence TERT end of BAC #
BACR12K22 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

AL060767.1 GI:4943573
GSS.
Drosophila melanogaster.
Drosophila melanogaster.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Empidoidea; Drosophilidae; Drosophila.
1 (bases 1 to 997)
Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

COMMENT

BP 191 91006 EVRY cedex - FRANCE [E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr]
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org> the BDGP Drosophila
melanogaster BAC library was prepared by Kazuo Ooegawa and
Aaron Mamoser in Pieter de Jong's laboratory in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
p1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES
source
1..997
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="BACR12K22"
/clone_lib="RPCI-98"
/note="end : TERT3"

BASE COUNT
89 a 99 c 13 g 258 t 538 others

ORIGIN

Query Match 7.1%; Score 55.8; DB 17; Length 997;
Best Local Similarity 19.5%; Pred. No. 0.019;
Matches 69; Conservative 131; Mismatches 153; Indels 0; Gaps 0;

QY 140 ATGAGACTTGATAGCTGCAAGAGCAATTAACCTTCATGAATTTGTATGATTA 199
DB 881 ATRRRRRARARARARARRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 822
QY 200 AAAAGCTTAAGATGCAACAAAGAGATCTTATCTTCTGTAATCTGAGAGAGA 259
DB 821 BGAARARARARARARARRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 762
QY 260 TGAGAGGCAATTTGAAGCCTTGTCAAGATATTAAGTTAAACAAGAGAAAAAG 319
DB 761 ARARARRARARARARARRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 702
QY 320 AAAACGCTTGAATGCAAGAGTGTATGATCTTCAATTTGACACAGCTGTA 379
DB 701 GAGARR 642
QY 380 GCGAAGCCCAAGTAATGAGATCGCTTCAAGTGGGCAAGAGATATTATCA 439
DB 641 RRRARR 582
QY 440 TGAAGCACTGTAATGCTTGAATATGGAACAGCTGACGCTTAAGAA 492
DB 581 GAGARR 529

RESULT 5
AL534423 797 bp mRNA linear EST 13-FEB-2001
LOCUS
DEFINITION
AL534423 LTI FL013.FBm1 Homo sapiens cDNA clone CSDF004YD24 5
prime, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

AL534423.1 GI:12797916
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 797)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope

```

Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: secrete@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1.1977
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DP004YD24"
/clone_1kb="LTI Fl013 Fbml"
/dev_stage="pooled tissue from post conception fetuses (20
week, 24 week and 26 week) "
/lab_host="DH108"
/note="Organ: Petal brain; Vector: pCMVSPORT 6; 3st strand
cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-stranded cDNA was digested with Not I
and cloned into the Not I and Eco RV sites of the
pCMVSPORT 6 vector. Library was constructed by Life
Technologies. Contact : Peng Liang Life Technologies, a
division of Invitrogen 9800 Central Express Drive Rockville
, Maryland 20850, USA Fax : (1) 301 610 8371 Email :
liang@lifetech.com URL :
http://fulllength.invitrogen.com"
43 c 120 g 152 t 75 others

```

Query Match	6.7%	Score 52.8;	DB 9;	Length 797;
Best Local Similarity	38.9%	Pred. No. 0.091;		
Matches 171; Conservative	36;	Mismatches 233.	Indels 0.	Cross 0

Qy 140 ATAGAAAGTTGGTATGAGCTGCAGAAGAGTAACCTTCATGAAGATTGTGATTCATAA 199
Dd 240 AGAGAGAGAAAAAAAAAWATTAAAAAAAAGAAAAAAATTAATGAAAAAAGAAAAAATA 259
Qy 200 AAAAGCTPAAAGANTCAACAAGAGAGACTTTTCCCTTGCGAACGTGAGAGA 259
Dd 300 AGGAAAAATRTAAAAAABAAAAAAGTAAATTTAAWTMTWMBAGATPAAAAATPAAAAA 359
Qy 260 TGAGAGGCCAATTGAGAAGCCTTGTCAGAGATATAAGCTTAAACAAAGAGAGAAAAAG 319
Dd 360 TGRMAAGAGAGAAAAAGAAAGAAATAPAAATGAAAAAABAAAAAARAAAAA 419
Qy 320 AAAACAGCTTTGAAATGCAAGAGAGTAGAGAGATCCCAAATTGCAGCACAGCTGTAA 379
Dd 420 AAAAAAGTAMAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAR 479
Qy 380 GCGAAGCCAAGTATAGCAGATCCGTTCTCAGGTGGGCGAAGAAAGATATATACC 439
Dd 480 AAGGATRGGAATTAATGATPAAAAAATTAATAAABAABAAAAAATTGAAAAA 539
Qy 440 TGAAGAGCACTTGGTATATGCTTGAATAAGGAAACGCTGACGTTAAAAAGAGAGAC 499
Dd 540 TAAAAAATTAATAAATGAAATGAAATGAAAAAAGAAAAAATTAATTAATAAAAAAAMM 559
Qy 500 TCATATTATGCTCAACTCAAGTCAGCTTGCTGCTCATAGGGAGCCTCGAGTCAAGCC 559
Dd 600 MTAAATGTWTMMMTMMTAAGMMMTMTMTTMMAAATMTTMCATTTTAAWTGTTM 659
Qy 560 CATTCAATCGCGCCTCTGG 579
Dd 660 TMTMMTAMTGTGTGGTGG 679

RESULT 6	
CNS0145P/c	
LOCUS	
DEFINITION	CNS0145P 1043 bp DNA linear GSS 26-JUL-1999
DESCRIPTION	Drosophila melanogaster genome survey sequence T7 end of BAC FLYB1N1811 of DrosBC library from Drosophila melanogaster [fruit fly] genomic survey sequence.
ACCESSION	AL103735
VERSION-	ALI03735.1 GI:5615346
KEYWORDS	GSS
SOURCE	Drosophila melanogaster.
ORGANISM	Drosophila melanogaster

REFERENCE
AUTHORS
TITLE
JOURNAL

Eularyota; Metazoa; Arthropoda; Hexapoda; Insecta; Peerygota;
Neopeptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Epiphyroidae; Drosophilidae; Drosophila.
1 (bases 1 to 1043)
Genoscope.
Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :

COMMENT

Determination of this BAC-end sequence was carried out as part of a

- Web : www.genoscope.cns.fr

- BP 191 91006 Evry cedex - FRANCE (E-mail : secref@genoscope.cns.fr)

genoscope - Centre National de Séquençage

15000 Evry - France

determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - <http://www.edgp.ebi.ac.uk> - This *Drosophila melanogaster* BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBeloBAC11.

FEATURES	Location/Qualifiers
source	1. .1043

BASE COUNT	277 a	96 c	121 g	382 t	167 others
ORIGIN					

```

Query Match      6.5%; Score 51.2; DB 17; Length 1043;
Best Local Similarity 36.2%; Pred. No. 0.2;
Matches 102; Conservative 48; Mismatches 132; Indels 0; Gaps 0;

```

OY 61 AAAAAATTTTAAAGTAATTACTACGTTTTCTTATCACCACCAATGATGGATCTGTG 120
Db 916 WIDATAWKTATTKTGATRTDRIKTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 85
OY 121 CTTTTCGTGTGATCTTATGAAGAATGATAAGCTGGAAGGAAAGTAAACCTCAT 187
Db 856 TTWTWTATATWTWATATATWTARGRABDDAAAAAAAAAATTTTWTMMWWMTTW 797
OY 181 GAAGATTTTGGATTCATAAAAAGCTAAAGATGCACAAGAGAGAGATCTTATCC 240
Db 796 WWWWMMMMTTTTTTTTTTTTAAAAAAAAAAAAAAAAAAAAAAAAANNTATWTWAAA 737
OY 241 TTGCTGAACGTGAGAGAGATGAGAGCAATTTGAAGACTTGTCAAGATTTAACGTTA 300
Db 736 TTTTAAATTTMAAAATTTMAATATATAATATATMAATATAATTTTATMAAAMWMTATATA 677
OY 301 AACCAAGAGAGAAAAAAGAAAAACGCTTTGAAATGCAAAGA 342
Db 676 TTMAMAAAAAMAMAMAMAAAAAAATATTTTTTMMWAATDTLAWA 635

LOCUS	CNS0108N	1038 bp	DNA	linear	SSS 26-JUL-1999
DEFINITION	Drosophila melanogaster genome survey sequence SP6 end of BAC BA003101 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.				
ACCESSION	AL098657				
VERSION	AL098657.1	GI:5610268			
KEYWORDS	GSS.				
SOURCE	Drosophila melanogaster.				
ORGANISM	Drosophila melanogaster				
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.				
	1 (bases 1 to 1038)				
REFERENCE	Genoscope.				
AUTHORS	Direct Submission				
TITLE	Submitted (22-JUL-1999) Genoscope - Centre National de Sequencage :				
JOURNAL	BP 1917 91006 EVRY cedex - FRANCE (E-mail : segreff@genoscope.cns.fr				
	- Web : www.genoscope.cns.fr/)				

COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (BDGP) - <http://www.edgp.ebi.ac.uk>. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.

FEATURES
source
1. 1038
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="BACN03101"
/clone_1lb="DrosBAC"
/plasmid="pBelobAC11"
/note="end : SP6"

BASE COUNT 372 a 119 g 219 t 322 others

ORIGIN

Query Match 6.5%; Score 51; DB 17; Length 1038;
Best Local Similarity 35.0%; Pred. No. 0.22;
Matches 157; Conservative 20; Mismatches 271; Indels 0; Gaps 0;

Qy 72 TATGATTTACTTACTTTCTTCTTATACCCAAATGATGATCTGCTTTGCTG 131
Db 37 TTTNNNTTTTNNNNNTTTTGTANNACCTTTTATTTTATTTTATTTT 96
Qy 132 GTATCTTCATGAGATTGATTAAGTCGAGAGAGTAACCTTCATGAGTTTGT 191
Db 97 TTAATAAGYRCANNCNTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 156
Qy 192 ATTCATTAAGGCTTAAGATGCAAGAGAGAGATCTTATCTGCTGACTG 251
Db 157 TTNNTTTTATNANNANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 216
Qy 252 TGAGAGATGAGAGCAATTGAGACCTTCTCAAGATTAAGTTAAAGAAAGA 311
Db 217 NNNNTNANNNTAAANAAATTTAAAAAAGAGAGAGAGAGAGAGAGAG 276
Qy 312 GAAAAAGAAACACCTTGAATGCAAGAGAGAGAGAGAGAGAGAGAGAG 371
Db 277 AAAAAAGAAACACCTTGAATGCAAGAGAGAGAGAGAGAGAGAGAGAG 336
Qy 372 CGTTGAGGAGCAACAGTAATGCAATCGCTTCTACAGTGGCCAAAGAGTA 431
Db 337 AAAAAAGAAACACCTTGAATGCAAGAGAGAGAGAGAGAGAGAGAGAG 396
Qy 432 TTATACATGAAAGCACTGTAATGCTTGAATGCAAGAGAGAGAGAGAGAG 491
Db 397 TAAATAAADAAAAAATTAATTAATTAATTAATTAATTAATTAATTAAT 456
Qy 492 AGAAGACCTTATATGCTACACTCA 519
Db 457 ADMDAAAAAAATWDTGKKAASAAAA 484

RESULT 8
CNS0187R 878 bp DNA linear GSS 26-JUL-1999
LOCUS Drosophila melanogaster genome survey sequence SP6 end of BAC
DEFINITION BACN04E04 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION AL108993
VERSION AL108993.1 GI:5629297
KEYWORDS GSS.
SOURCE Drosophila melanogaster.
ORGANISM Drosophila melanogaster.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 878)
AUTHORS Genoscope.
TITLE Direct Submission

JOURNAL Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage; BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr

COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (BDGP) - <http://www.edgp.ebi.ac.uk>. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.

FEATURES
source
1. 878
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="BACN04E04"
/clone_1lb="DrosBAC"
/plasmid="pBelobAC11"
/note="end : SP6"

BASE COUNT 279 a 132 c 120 g 182 t 165 others

ORIGIN

Query Match 6.4%; Score 49.8; DB 17; Length 878;
Best Local Similarity 25.1%; Pred. No. 0.42; Mismatches 98; Indels 0; Gaps 0;
Matches 60; Conservative 81

Qy 257 ACATGAGAGCAATTGAGACCTTGTCAAGATTAACGTTAAACAAAGAGAAA 316
Db 88 AAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 147
Qy 317 AAGAAACAGCTTTGAAAGAGAGATGAGATGCAATTCAGACAGCTTG 376
Db 148 AAAAAAATTTGCTGATGATTTGTTTAAATTTAAATTTAAATTTAAATTT 207
Qy 377 TAAGCAAGCCACAGTAATGCAATCGCTTCTACAGTGGCCAAAGAGTA 436
Db 208 WARGWMMRGMAAAARAAWMMWRCCTWRCMAAAMMAAAMMAAAMMAAARCA 267
Qy 437 CCATGAAGAAGAACTGTAATGCTTGAATGCAAGAGAGAGAGAGAGAGAG 495
Db 268 WMMWMAAAMCBAAMGMAAABATTRAAMWMAAAMMAAAMMAAAMMAAAM 326

RESULT 9
CNS0039G 1101 bp DNA linear GSS 03-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence TET3 end of BAC #
DEFINITION BACR08K10 of RCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION AL063921
VERSION AL063921.1 GI:4941778
KEYWORDS GSS.
SOURCE Drosophila melanogaster.
ORGANISM Drosophila melanogaster.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 1101)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage; BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr

COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutomo Oosegawa and Aaron Mammoss in Pletier de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the

```

BASE COUNT      201 a      64 C      131 g      202 t      503 others
ORIGIN
/originism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="BACRO8K10"
/clone_1ib="RPT-98"
/notes="end : TET3"

```

[illegible][illegible][illegible]

243 **67776** *Asplenium* *platyneuron* (L.) Oakes

0 / YYYYYYYY

.....NDNDDDDNDNAGTAGKWKRIWKKRKRDRTRWDADADDRTARDDR 704

703 RRGDDGADAGKGGKKTGKKRRRRDRATWDRTDAAWWADAAWTTTDTTDTTDDWDPKDPBPCKA 644

[illegible]

Db 583 RRDRARARADRR 571

07691974

genomic, DNA sequence.

Ensemble: **Ensemble**

AUTHORS Loftus, B., Van Aken, S., and Fraser C

contact: Brendan J Loftus

Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel.: 301 838 0208
Fax: 301 838 3543
Email: bjloftus@igr.org
Clones are derived from the *Entamoeba histolytica* HMI-1MSD sheared
DNA library

FEATURES	Location/Qualifiers
source	1. .920

```
/clone lib="Entamoeba histolytica sheared DNA"
```

using a method described by Clark and Diamond (Clark,

the library construction is described in detail in [13].

Barell, Oxford University Press, 1999), "

Query Match

100

628

889 629

689

749 ATGGCGGAGGGGGGAGGAGAAAGAAAAGAAAAAAGAAAAA 808

809 AAAAGATGGAAGAACAACCACTT

RESULT 11

clone IMAGE30672 rat placenta UGCLM library Mus musculus genomic

KEYWORDS GSS.

1. *Planirostris*; *Euchneria*; *Kocentia*; *Sciurognathus*; *Muridae*; *Murinae*; *Mus*.

M., Rose, M., Rose, R., Stokes B., Tinday A., von Niederhousen A., M., Rose, M., Rose, R., Stokes B., Tinday A., von Niederhousen A.

TOYENNYE
plastic inserts
1944-1945

Journal
Unpublished (2000)
Comment
Contact: Robert B. Weiss
University of Utah Genome Center

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0229 row: 1 column: 06
Seq primer: CGTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 423.

FEATURES

source

1..423
Location/Qualifiers

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U08C1M0229106"
/clone_lib="Mouse 10kb plasmid U08C1M library"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: pMD42nv, Purified genomic DNA from M. Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (91473114[gb]/AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 119 a 90 c 40 g 174 t
ORIGIN

Query Match 6.0%; Score 46.8; DB 17; Length 423;
Best Local Similarity 50.4%; Pred. No. 2.3; Indels 0; Gaps 0;
Matches 114; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

Qy 100 ACCCAATGATGATCTGCTCTTCTGCTGATCTTCATGAGAGATGATGATGATC 159
Db 423 ACTGAGCTGCTGATTTGATTTAGGAACATATGATTAATGATTTGATTAAT 364
Qy 160 GAAG 219
Db 363 GACTATGTAACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 304
Qy 220 AAAGAGAGAGATCTTATCTCTGTAAGTGAAGAGAGAGAGAGAGAGAGAG 279
Db 303 ATAG 244
Qy 280 CTTCAGAGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGAT 325
Db 243 CTGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 198

RESULT 12
AL514085/c 458 bp mRNA linear EST 13-PEB-2001
LOCUS AL514085 LTI NFI006 PL2 Homo sapiens cDNA clone C10B0404E10 3
DEFINITION prime mRNA sequence.
ACCESSION AL514085
VERSION AL514085.1 GI:1277579
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 458)
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polyes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES

source

1..458
Location/Qualifiers

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="C10B0404E10"
/clone_lib="LTI NFI006 PL2"
/tissue_type="Placenta"
/note="Vector: pCMVSPORT 6; Site 1: NotI, 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by life technologies. Contact : Feng Liang life technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@life.com URL : http://fulllength.invitrogen.com"

BASE COUNT 186 a 13 c 3 g 207 t 49 others
ORIGIN

Query Match 6.0%; Score 46.8; DB 9; Length 458;
Best Local Similarity 42.5%; Pred. No. 2.3;
Matches 117; Conservative 14; Mismatches 144; Indels 0; Gaps 0;

Qy 68 TTTTNGATGATGATCTGCTCTTCTGCTGATCACCAGAGATGATGATGATGATG 127
Db 304 TTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTT 245
Qy 128 CTGTGATCTTCATGAGAGATGATGATGATGATGATGATGATGATGATGAT 187
Db 244 TTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNTTTTNT 185
Qy 188 TTGTATCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 247
Db 184 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 125
Qy 248 ACTGTGAG 307
Db 124 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 65
Qy 308 AAG 342
Db 64 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 30

RESULT 13
CNS0383B/c 802 bp DNA linear GSS 15-MAY-2000
LOCUS CNS0383B Tetradon nigriviridis genome survey sequence PUC-ORI end of clone
DEFINITION 004012 of library G from Tetradon nigriviridis, genomic survey
sequence.
ACCESSION AL232112
VERSION AL232112.1 GI:7891247
KEYWORDS GSS; genome survey sequence.
SOURCE Tetradon nigriviridis.
ORGANISM Tetradon nigriviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetradon.
REFERENCE 1 (bases 1 to 802)
Roest-Crolius, H., Vaillon, O., Basilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fitzames, C., Wincker, P., Brothier, P., Quetier, F.,

Submitted (23-JUL-1999) Genoscope - Centre National de Sequenc

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/organism="Homo sapiens"
```

/db_xref="taxon:9606"
 /clone="CLOBA0042E10"
 /clone_id="LTI_NFL006_P12"
 /issue_type="placenta"
 /note="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-stranded cDNA was digested with Not I and
 cloned into the Not I and Eco RV sites of the pCMVSPORT 6
 vector. Library was normalized. Library was constructed by
 Life Technologies. Contact: Feng Liang Life Technologies,
 a division of Invitrogen 9800 Medical Center Drive
 Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
 Email: fliang@life-tech.com URL:
 http://fulllength.invitrogen.com"

BASE COUNT 186 a 13 c 3 g 207 t 49 others
 ORIGIN

Query Match 5.8%; Score 45.2; DB 9; Length 458;
 Best Local Similarity 41.1%; Pred. No. 5.2; 144; Indels 0; Gaps 0;
 Matches 113; Conservative 18; Mismatches 144; Indels 0;

```

Qy 68 TTTTATGTAATTTACTGCTTTTCCTTATCACCCCAATGATGATCTGCTTTTG 127
    ||||| : ||||| |||||
Db 162 TTTTATGTAATTTACTGCTTTTCCTTATTTNNNNNTTNNNTTTTNTTTTTCCTCC 221
    ||||| : ||||| |||||

Qy 128 CTGTGTATCTTCATAGAGATTGATAGGTCGAGAGAGTAACCTTCATGAAGATT 187
    ||||| : ||||| |||||
Db 222 CACCTTGCTTTAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAA 281
    ||||| : ||||| |||||

Qy 188 TTGTATTCATAAAAAGCTTAAGAGATGCAACAAGAGAGAGATCTTTATCCTTGCTGA 247
    ||||| : ||||| |||||
Db 282 AAGAAATTTAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAA 341
    ||||| : ||||| |||||

Qy 248 ACTGTGAGAGATGAGAGCAATTGGAAGCCTGTGAGAGATTAACGTTAAACAAG 307
    ||||| : ||||| |||||
Db 342 AATTTTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 401
    ||||| : ||||| |||||

Qy 308 AAGAGAAAAAGAAAAACAGCTTTGAAATGCAAGA 342
    ||||| : ||||| |||||
Db 402 AAAAAAATAAATAAATAAATAAATAAATAAATAA 436
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Search completed: March 9, 2003, 04:42:03
 Job time : 1295.6 secs

10

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: March 8, 2003, 18:30:53 ; Search time 163.589 Seconds
(without alignments)
10778.963 Million cell updates/sec

Title: US-08-982-272-2

Perfect score: 783
Sequence: 1 ATGATGAAACATACAGCCA.....TTGGCTTACTCAACTCTGA 783

Scoring table:
Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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24: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	783	100.0	783	19	AAV38998
2	783	100.0	783	19	AAV61062
3	781.4	99.8	783	15	AAO63960
4	781.4	99.8	783	19	AAV12853
5	781.4	99.8	783	20	AAZ27524
6	777.2	99.3	782	14	AAQ41507
7	760.6	97.1	783	19	AAV39001
8	751	95.9	783	19	AAV38999
9	664.6	84.9	818	16	AAO5762

10	645.2	82.4	1477	22	AAH25527	Nucleotide sequenc
11	631.4	80.6	1778	20	AAZ27538	Mouse trimetric CD4
12	616.6	78.7	783	19	AAV42184	Exemplary nucleoti
13	592.4	75.7	786	19	AAV39003	Exemplary CD40 lig
14	582.8	74.4	786	19	AAV39002	Exemplary CD40 lig
15	570	72.8	786	19	AAV39000	Exemplary CD40 lig
16	560.4	71.6	786	19	AAO63959	Human CD40-L type
17	560.4	71.6	786	19	AAV38997	CD40 ligand gene u
18	560.4	71.6	786	19	AAV12852	CD40 ligand coding
19	560.4	71.6	786	19	AAO41506	CD40-L DNA. Homo
20	560.4	71.6	840	15	AAO67123	Human CD40 ligand
21	560.4	71.6	840	16	AAO57653	CDNA of CD40L, a n
22	560.4	71.6	840	19	AAV39782	Human CD40 ligand
23	560.4	71.6	840	19	AAV61065	Human CD40-L codin
24	560.4	71.6	840	20	AAZ27525	Nucleotide sequenc
25	560.4	71.6	879	22	AAV55539	Human CD40 ligand
26	560.4	71.6	1816	21	AAAS1745	DNA encoding novel
27	560.4	71.6	1816	23	AAH86571	Human CD40L mutain
28	559	71.4	840	18	AAO57984	Genomic sequence o
29	558.8	71.4	840	15	AAO94091	Human CD40-L CDNA.
30	555.6	71.0	840	16	AAV39004	CD40 ligand gene u
31	551.6	67.9	864	21	AAZ35540	Feline CD154 CDNA.
32	517.4	66.1	885	21	AAZ35541	Feline CD154 CDNA
33	517.4	66.1	885	21	AAZ35542	Feline CD154 CDNA
34	514.4	65.7	780	21	AAZ55543	Feline CD154 CDNA
35	514.4	65.7	780	21	AAZ55544	Canine CD154 CDNA
36	511	65.3	1878	21	AAZ55535	Canine CD154 CDNA
37	511	64.9	780	21	AAZ55536	Canine CD154 CDNA
38	508	64.9	780	21	AAZ55537	Nucleotide sequenc
39	508	64.9	780	21	AAZ55538	HIV-1 gp120 v3 100
40	454.6	58.1	1552	22	AAH25525	HIV-1 gp120 v3 100
41	449.2	57.4	865	22	AAH82933	HIV-1 gp120 v3 100
42	449.2	57.4	906	22	AAH82932	HIV-1 gp120-human
43	449.2	57.4	2209	22	AAH82929	Human CD40-L/Fc fu
44	449.2	57.4	2252	22	AAH82928	
45	446.2	57.0	1425	14	AAQ41516	

ALIGNMENTS

AAV38998	AAV38998 standard; DNA; 783 BP.
AAV38998	AAV38998; (first entry)
23-SEP-1998	CD40 ligand gene used in the course of the invention.
CD40 ligand	alteration; immunoreactivity; human cell;
accessory molecule	ligand; AM; gene therapy; treatment; neoplasia;
autoimmune disorder;	rheumatoid arthritis; vaccine; ss.
Homo sapiens.	
MO9826061-A2.	
18-JUN-1998.	
08-DEC-1997;	97MO-US22740.
01-DEC-1997;	97US-0982272.
09-DEC-1996;	96US-0032145.
(RBGC) UNIV CALIFORNIA.	
Cantwell M, Kipps TV, Sharma S;	
WPI; 1998-348521/30.	
Vectors containing accessory molecule ligand genes - used for	

altering immunoreactivity of cells, particularly for treatment of neoplasia or autoimmune disorders, e.g. rheumatoid arthritis

Disclosure, Pages 104-105; 167pp; English.

The present sequence represents a CD40 ligand gene. The sequence is used to exemplify the method of the invention. The specification describes a method for altering the immunoreactivity of human cells which comprises introducing a gene encoding an accessory molecule ligand (AML) into the cells so that the AML is expressed on the surface of the cells. Vectors containing the AML genes can be used in gene therapy for treating neoplasia or autoimmune disorders such as rheumatoid arthritis. They can also be used for vaccination to produce immunity against a virus cell, bacteria, proteins, fungus or neoplasia.

Sequence 783 BP; 243 A; 159 C; 177 G; 204 T; 0 other;

Query Match 100.0%; Score 783; DB 19; Length 783;

Best Local Similarity 100.0%; Pred. No. 1.9e-208;

Matches 783; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGATAGAAAATACATACGACCTTCCCGGATCCGTCGCACTGCACTTCCAGGAGC 60
DB 1 ATGATAGAAAATACATACGACCTTCCCGGATCCGTCGCACTGCACTTCCAGGAGC 60
QY 61 ATGAAGATTTTATGATTTTACTTACTGTTTCTTATGACCAATGATTTGATCTGTG 120
DB 61 ATGAAGATTTTATGATTTTACTTACTGTTTCTTATGACCAATGATTTGATCTGTG 120
QY 121 CTTTTCGCTGATATCTTATGAAAGATTTGATTAAGTGAAGGAAAGTAACTTAT 180
DB 121 CTTTTCGCTGATATCTTATGAAAGATTTGATTAAGTGAAGGAAAGTAACTTAT 180
QY 181 GAAATTTTGTATTTTAAAGGATTAAGATGCAAAAGAGAGATCTTATCC 240
DB 181 GAAATTTTGTATTTTAAAGGATTAAGATGCAAAAGAGAGATCTTATCC 240
QY 241 TTGCTGAAGTGTAGAGATGAGAAAGCAATTTGAAGCTTTGCAAGATTAACGTTA 300
DB 241 TTGCTGAAGTGTAGAGATGAGAAAGCAATTTGAAGCTTTGCAAGATTAACGTTA 300
QY 301 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
DB 301 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
QY 361 ATTGACAGACACGTTGTAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 361 ATTGACAGACACGTTGTAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
QY 421 AAGAAAGATATTAATACATACGACCTTCCCGGATCCGTCGCACTGCACTTCCAGGAGC 480
DB 421 AAGAAAGATATTAATACATACGACCTTCCCGGATCCGTCGCACTGCACTTCCAGGAGC 480
QY 481 ACGGTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
DB 481 ACGGTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
QY 541 GAGCCTTCGATGCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
DB 541 GAGCCTTCGATGCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
QY 601 GAGAGATCTTACTCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
DB 601 GAGAGATCTTACTCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
QY 661 TCTGTTCACTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
DB 661 TCTGTTCACTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY 721 ACTGAAGCAAGCAAGTATCAAGAGTGTGCTTCTATCTTTGGCTTCAAACTC 780
DB 721 ACTGAAGCAAGCAAGTATCAAGAGTGTGCTTCTATCTTTGGCTTCAAACTC 780

```

QY 781 TGA 783
DB 781 TGA 783

RESULT 2
AAV61062
ID AAV61062 standard; DNA; 818 BP.

AC AAV61062;

DT 08-DEC-1998 (first entry)

DE Murine CD40 ligand encoding DNA sequence.

XX Murine; mouse; CD40 ligand; TNF receptor family; activated T cell;
KW type 2 membrane glycoprotein; cell proliferation; differentiation;
KW B cell; ds.

OS Mus sp.

Key Location/Qualifiers
FT CDS 13..795
FT /tag= a
FT /product= "CD40 ligand"

PN US5817516-A.

PD 06-OCT-1998.

PF 28-APR-1995; 95US-0431055.

PR 28-APR-1995; 95US-0431055.
PR 28-APR-1994; 94US-0234580.

PA (BOEH) BOEHRINGER INGELHEIM PHARM INC.

PI Castle B. Kehry M;

DR WPI: 1998-556393/47.
DR P-PSDB; AAW71750.

PT Increased proliferation of B cells in culture - by incubating them
in the presence of membrane-bound CD40 ligand

Example 2; Fig 1; 37pp; English.

The present sequence encodes murine CD40 ligand which is used in the method of the invention. The method has been developed for proliferating B cells to increase their number at least 100-fold. The method comprises: (a) providing high density, membrane bound CD40 ligand, and (b) culturing one or more B cells in the presence of this ligand. The culture results in a proliferation in the number of B cells of at least 100 fold. Also described is a method as above where the B cells are induced to differentiate into antibody-producing cells in the presence of one or more cytokines. The method can be used for stimulating B-cell proliferation in vitro or in vivo, e.g. for treating conditions in which B-cell proliferation and activation is suppressed. Eight rounds of division over six days can be achieved, corresponding to a 256-fold increase in cell numbers, which is a vast increase compared to previous culturing methods.

Sequence 818 BP; 249 A; 170 C; 186 G; 213 T; 0 other;

Query Match 100.0%; Score 783; DB 19; Length 818;

Best Local Similarity 100.0%; Pred. No. 1.9e-208;

Matches 783; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGATAGAAAATACATACGACCTTCCCGGATCCGTCGCACTGCACTTCCAGGAGC 60
DB 13 ATGATAGAAAATACATACGACCTTCCCGGATCCGTCGCACTGCACTTCCAGGAGC 72
QY 61 ATGAAGATTTTATGATTTTACTTACTGTTTCTTATGACCAATGATTTGATCTGTG 120

```

```

Db 73 ATGAAAGATTTTATGATTTACTTACTGTTTCTTATCACCAGCAAGATGATCTGTG 132
      |||
Oy 121 CTTTGTGCTGTATTTCTTATGAAAGATGATGATGATGATGATGATGATGATGAT 180
      |||
Db 133 CTTTGTGCTGTATTTCTTATGAAAGATGATGATGATGATGATGATGATGATGAT 192
      |||
Oy 181 GAAGATTTTGTATTCATTAAGAAAGATGATGATGATGATGATGATGATGATGAT 240
      |||
Db 193 GAAGATTTTGTATTCATTAAGAAAGATGATGATGATGATGATGATGATGATGAT 252
      |||
Oy 241 TTGCTGAAGCTGTGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 300
      |||
Db 253 TTGCTGAAGCTGTGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 312
      |||
Oy 301 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
      |||
Db 313 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 372
      |||
Oy 361 ATTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
      |||
Db 373 ATTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 432
      |||
Oy 421 AAGAAAGATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 480
      |||
Db 433 AAGAAAGATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 492
      |||
Oy 481 ACGGTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
      |||
Db 493 ACGGTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 552
      |||
Oy 541 GAGCTTGAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
      |||
Db 553 GAGCTTGAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 612
      |||
Oy 601 GAGAGATCTTACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
      |||
Db 613 GAGAGATCTTACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 672
      |||
Oy 661 TCTGTCTACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
      |||
Db 673 TCTGTCTACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 732
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Oy 721 ACTGAAGCAAGCAAGTATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
      |||
Db 733 ACTGAAGCAAGCAAGTATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 792
      |||
Oy 781 TGA 783
      |||
Db 793 TGA 795
      |||

RESULT 3
AA063960
ID AA063960 standard; cDNA to mRNA; 783 BP.
AC AA063960;
XX
DT 12-JAN-1995 (first entry)
DE Mouse CD40-L type II transmembrane protein coding sequence.
XX
KW Leucine zipper; trimerisation; trimeric CD40-L; fusion protein;
KW hetero-oligomer; homo-oligomer; type II transmembrane protein;
KW soluble CD40-L; tumour necrosis factor family; ss.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT CDS 1..783
FT /product= mouse_CD40-L
FT /note= "nucleotides 148-780 code for the

```

extracellular region (amino acids 50-260) "

FT
XX
EN W09410308-A.

XX
PD 11-MAY-1994.

XX
PF 20-OCT-1993; 93WO-US10034.

XX
PR 23-OCT-1992; 92US-0969703.

XX
PR 13-AUG-1993; 93US-0107353.

XX
PA (IMMUNEX CORP.

XX
PI Spriggs MK, Strinivasan S;

XX
DR WPI, 1994-167465/20.

XX
DR P-PsDB; AAR53970.

XX
PT Prepn. of soluble oligomeric mammalian proteins - using host

XX
PT cells to express a fusion protein comprising a leucine zipper

XX
PT domain and a heterologous mammalian protein

XX
PS Example 1; Page 25-26; 35pp; English.

XX
CC A DNA fragment encoding the extracellular (soluble) region of mouse

XX
CC CD40-L was ligated to a synthetic oligonucleotide sequence coding

XX
CC for a leader peptide, a 33 amino acid leucine zipper sequence

XX
CC (AAR53968) and the flag (RPM) linker sequence. Cells expressing the

XX
CC fusion construct are grown to accumulate oligomeric, soluble CD40-L

XX
CC in the supernatant. The leucine zipper sequence spontaneously

XX
CC trimerises in solution and fusion proteins comprising

XX
CC the sequence fused to a heterologous mammalian protein also form

XX
CC oligomers.

XX
SQ Sequence 783 BP; 243 A; 159 C; 178 G; 203 T; 0 other;

XX
Query Match 99.8%; Score 781.4; DB 15; Length 783;

XX
Best Local Similarity 99.9%; Pred. No. 5.3e-208;

XX
Matches 782; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 ATGATGAAATCATACAGCAAGTCTCCCAAGATCCGAGGCAATGACCTTCCAGGAGC 60

Db 1 ATGATGAAATCATACAGCAAGTCTCCCAAGATCCGAGGCAATGACCTTCCAGGAGC 60

Oy 61 ATGAAATTTTATGATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 120

Db 61 ATGAAATTTTATGATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 120

Oy 121 CTTTGTGCTGTATTTCTTATGAAAGATGATGATGATGATGATGATGATGATGAT 180

Db 121 CTTTGTGCTGTATTTCTTATGAAAGATGATGATGATGATGATGATGATGATGAT 180

Oy 181 GAAGATTTTGTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 240

Db 181 GAAGATTTTGTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 240

Oy 241 TTGCTGAAGCTGTGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 300

Db 241 TTGCTGAAGCTGTGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 300

Oy 301 AACAAAG 360

Db 301 AACAAAG 360

Oy 361 ATTGAG 420

Db 361 ATTGAG 420

Oy 421 AAGAAAGATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 480

Db 421 AAGAAAGATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 480

Oy 481 ACGGTTAAAG 540

Db 481 ACGGTTAAAG 540

Example 1; column 23-24; 21p; English.

CC This sequence is the coding sequence for the mouse CD40 ligand (CD40-L).
CC The encoded protein can be used in a fusion protein produced using the
CC method of the invention. The method is for preparing soluble oligomeric
CC protein by culturing a host cell transfected with a vector for the

QY 1 ATGATGAAACATACAGCCAACTTCCCCAGATCCGTCGCACTGACTTCCAGCAGC 60

22	1	GAAGAGAAACATACAGCCCAACCTTCCCCAGATCCGAGCAACTGACCTTCAAGCAGAG	60
QY	61	ATGAAGATTTTATATGATTTACTTACGTGTTTCTTTATCAACCCAAATGATTTGATCTGAG	12
Dp	61	ATGAAGATTTTATGATTTACTTACTGTTTTCTTATCAACCCAAATGATTTGATCTGAG	12
QY	121	CTTTTGTGCTGATCTTCAATGAAGATTTGATTAAGTCCGAGAGGAATTAACCTTCAT	18
Dp	121	CTTTTGTGCTGATCTTCAATGAAGATTTGATTAAGTCCGAGAGGAATTAACCTTCAT	18
QY	181	GAAATTTTGTATTCATTAATAAAAGCTTAAAGAGATGCACAACAAAGAGAGATCTTTATAC	24
Dp	181	GAAATTTTGTATTCATTAATAAAAGCTTAAAGAGATGCACAACAAAGAGAGATCTTTATAC	24
QY	241	TTGCTGATCTGAGAGATATGAGAAAGCAATTTGAAATCCTTGTCAAGATATTAACGTTA	30
Dp	241	TTGCTGATCTGAGAGATATGAGAAAGCAATTTGAAATCCTTGTCAAGATATTAACGTTA	30
QY	301	AACAAAGAGAGAAAAAGAAAACAGCTTTGAAAATGCAAAAGAGTGAATGAGATCTCTCA	36
Dp	301	AACAAAGAGAGAAAAAGAAAACAGCTTTGAAAATGCAAAAGAGTGAATGAGATCTCTCA	36
QY	361	ATTGCAACACGTTGTATACGAGCAACAGTAAATGACGATCCGTTTCAACATGAGGACC	42
Dp	361	ATTGCAACACGTTGTATACGAGCAACAGTAAATGACGATCCGTTTCAACATGAGGACC	42
QY	421	AAGAAAGATATATATACATGAAAAGCACTTGATATCTTGAAAAATGGGAAACAGCTG	48
Dp	421	AAGAAAGATATATATACATGAAAAGCACTTGATATCTTGAAAAATGGGAAACAGCTG	48
QY	481	ACGGTTAAAGAGAGACCTATATATGTCTCAACATCAAGTCACTTCTGCTTAAATGGG	54
Dp	481	ACGGTTAAAGAGAGACCTATATATGTCTCAACATCAAGTCACTTCTGCTTAAATGGG	54
QY	541	GAGCTTGAAGTCAAGGCCCATTTCAATGCTGCGCTTGCGCTGAAAGCCAGATTTGATCT	60
Dp	541	GAGCTTGAAGTCAAGGCCCATTTCAATGCTGCGCTTGCGCTGAAAGCCAGATTTGATCT	60
QY	601	GAGAGATCTTACTCAAGCCGCAAAATACCAAGTCTCTCCAGCTTTGGAGAGACAG	66
Dp	601	GAGAGATCTTACTCAAGCCGCAAAATACCAAGTCTCTCTCCAGCTTTGGAGAGACAG	66
QY	661	TCGTTCACCTGGGCGGAGATGTTGAATTAACAAGCTGGATGCTCTGTGTTGTCAAGTG	72
Dp	661	TCGTTCACCTGGGCGGAGATGTTGAATTAACAAGCTGGATGCTCTGTGTTGTCAAGTG	72
QY	721	ACTGAAGCAACCAAGTATACAGAGTTGCTCTCATCTTTTGGCTACTCAAACTC	78

Db 721 ACTGAAAGCCAGGATGATCCAGAGTGGCTTCATCTTTGGCTTACTCAAACTC 780
 QY 781 TGA 783
 Db 781 TGA 783

RESULT 5
 AA27524
 ID AA27524 standard; cDNA; 783 BP.

AC AA27524;
 DT 13-DEC-1999 (first entry)
 XX

DE Mouse CD40-L coding sequence.

KX CD40-L; CD40 receptor ligand; anti-human CD40-L monoclonal antibody;
 KM binding inhibitor; trimeric CD40-L; anti-immunoglobulin M;
 KM peripheral blood B cell; proliferation inhibitor; ss.

OS Mus sp.

PN US5961974-A.

PD 05-OCT-1999.

PF 24-MAY-1994; 94US-0249189.

PR 25-OCT-1991; 91US-0783707.

PR 05-DEC-1991; 91US-0805723.

PR 23-OCT-1992; 92US-0969703.

XX (IMMV) IMMUNEX CORP.

XX Spriggs MK, Fanslow WC, Armitage RJ;

XX WPI; 1999-579604/49.

XX P-P-SDB; AA39937.

XX Anti-human CD40-L ligand monoclonal antibodies -

XX Disclosure; Fig 1; 59pp; English.

XX This sequence encodes the mouse CD40 receptor ligand (CD40-L). The

XX invention relates to anti-human CD40-L monoclonal antibodies M90 secreted

XX by hybridoma hCD40L-M90 (ATCC HB-12055) and M91 secreted by hybridoma

XX hCD40L-M91 (ATCC HB-12056). M90 and M91 inhibit CD40-L binding to CD40

XX and the ability of trimeric CD40-L and anti-immunoglobulin M to induce

XX proliferation of peripheral blood B cells.

XX Sequence 783 BP; 243 A; 159 C; 178 G; 203 T; 0 other;

XX Query Match 99.8%; Score 781.4; DB 20; Length 783;

XX Best Local Similarity 99.9%; Pred. No. 5.3e-208;

XX Matches 782; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGATGAAACATACAGCAACCTTCCCGAGATCCGAGCACTTCCAGGAGC 60

Db 1 ATGATGAAACATACAGCAACCTTCCCGAGATCCGAGCACTTCCAGGAGC 60

QY 61 ATGAGATTTTATGATTTTACTTCTTTTCTTATCACCCAATGATGATCTGTG 120

Db 61 ATGAGATTTTATGATTTTACTTCTTTTCTTATCACCCAATGATGATCTGTG 120

QY 121 CTTTGGCTGATCTTCAATGAGATGATGATGATGATGATGATGATGATGATGAT 180

Db 121 CTTTGGCTGATCTTCAATGAGATGATGATGATGATGATGATGATGATGATGAT 180

QY 241 TTGCTGAACCTGAGAGATGAGAGCAATTTGAAGCCTTGTCAAGATATAACGTTA 300

Db 241 TTGCTGAACCTGAGAGATGAGAGCAATTTGAAGCCTTGTCAAGATATAACGTTA 300

QY 301 AACAAAG 360

Db 301 AACAAAG 360

QY 361 ATTGCAGCAGAGCTTGAAGAGCAAGATGATGATGATGATGATGATGATGATGATG 420

Db 361 ATTGCAGCAGAGCTTGAAGAGCAAGATGATGATGATGATGATGATGATGATGATG 420

QY 421 AAGAAAGATATTTATCCATGAAAGCACTTGTATGCTTGAATAATGGAAACAGCTG 480

Db 421 AAGAAAGATATTTATCCATGAAAGCACTTGTATGCTTGAATAATGGAAACAGCTG 480

QY 481 ACGGTTAAAG 540

Db 481 ACGGTTAAAG 540

QY 541 GAGCCTTCGAGTCAAGCCCATTCATCTGCGCTCTGCTGAAGCCCAAGATCTT 600

Db 541 GAGCCTTCGAGTCAAGCCCATTCATCTGCGCTCTGCTGAAGCCCAAGATCTT 600

QY 601 GAGAGATCTTACTCAAGGCGGCAATACCAAGTCTCCAGCTTTGCGAGCAGAG 660

Db 601 GAGAGATCTTACTCAAGGCGGCAATACCAAGTCTCCAGCTTTGCGAGCAGAG 660

QY 661 TCTGTCACTTGGGCGAGGTGTTGAATTAAGAGTGTCTTGTGTTTGTCAAGCTG 720

Db 661 TCTGTCACTTGGGCGAGGTGTTGAATTAAGAGTGTCTTGTGTTTGTCAAGCTG 720

QY 721 ACTGAGCAAGCAAGTATCCACAGAGTGGCTTCTCATCTTTGGCTTACTCAACTC 780

Db 721 ACTGAGCAAGCAAGTATCCACAGAGTGGCTTCTCATCTTTGGCTTACTCAACTC 780

QY 781 TGA 783

Db 781 TGA 783

RESULT 6
 AAQ41507
 ID AAQ41507 standard; DNA; 782 BP.

XX AAQ41507;

XX 12-AUG-1993 (first entry)

XX Murine CD40-L DNA.

XX Human; CD40-L; CD40; type II; membrane; polypeptide; extracellular;

XX transmembrane; region; intracellular; soluble; activity; B cell;

XX proliferation; induction; antibody; secretion; IgE; agonist;

XX antagonist; binding assay; ss.

XX Mus musculus.

XX W09308207-A.

XX 29-APR-1993.

XX 23-OCT-1992; 92MO-US08990.

XX 25-OCT-1991; 91US-0783707.

XX 05-DEC-1991; 91US-0805723.

XX (IMMV) IMMUNEX CORP.

XX Armitage RJ, Fanslow WC, Spriggs MK;

XX WPI; 1993-152417/18.

DR P-PSDB; AAR36702.

XX New cytokine CD40-L as CD40 agonist and antagonist - is used for
PT treating allergies, lupus, rheumatoid arthritis,
PT graft-versus-host disease and insulin-dependent diabetes mellitus
XX
XX Disclosure; Fig 1; 80pp; English.

XX This sequence encodes a murine CD40-L polypeptide which binds to CD40.
CC CD40-L is a type II membrane polypeptide which has an extracellular
CC region at its C-terminus, a transmembrane region and an
CC intracellular region at its N-terminus. A soluble form of CD40-L
CC lacks the transmembrane domain. CD40-L activity is mediated by
CC binding with CD40 and induces B cell proliferation and induction of
CC antibody secretion, including IgE. Membrane bound CD40-L acts as a
CC CD40 agonist and soluble CD40-L acts as a CD40 antagonist. CD40-L
CC can be used in a binding assay to detect cells expressing CD40.
XX

SQ Sequence 782 BP; 242 A; 157 C; 180 G; 203 T; 0 other;

Query Match 99.3%; Score 777.2; DB 14; Length 782;

Best Local Similarity 99.6%; Pred. No. 7,9e-207;

Matches 779; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGATAGAAACATACAGCCACCTTCCCGAGATCCGTGGCACTGACCTCCAGCAGC 60
DB 1 ATGATAGAAACATACAGCCACCTTCCCGAGATCCGTGGCACTGACCTCCAGCAGC 60
QY 61 ATGAGAGATTTTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 120
DB 61 ATGAGAGATTTTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 120
QY 121 CTTTTCGCTGTATCTTATGAGAAATGATGATGATGATGATGATGATGATGATGAT 180
DB 121 CTTTTCGCTGTATCTTATGAGAAATGATGATGATGATGATGATGATGATGATGAT 180
QY 181 GAAGATTTTGTATTCATTAATAAGTAAAGATGAAAGATGAAAGATGAAAGATGAAAG 240
DB 181 GAAGATTTTGTATTCATTAATAAGTAAAGATGAAAGATGAAAGATGAAAGATGAAAG 240
QY 241 TTGCTGAACCTGTAGAGATGAAAGCAATTTGAAGCTTGTCAAGATTAACGTTA 300
DB 241 TTGCTGAACCTGTAGAGATGAAAGCAATTTGAAGCTTGTCAAGATTAACGTTA 300
QY 301 AACAAAG 360
DB 301 AACAAAG 360
QY 361 ATTGACGACAGCTGTAAAGCAAGCAAGTAAAGCAAGTAAAGCAAGTAAAGCAAGTAA 420
DB 361 ATTGACGACAGCTGTAAAGCAAGCAAGTAAAGCAAGTAAAGCAAGTAAAGCAAGTAA 420
QY 421 AAGAAAGATATTAATCATGTAAGCACTGTGTAAGCTTGAAGTAAAGTAAAGTAAAG 480
DB 421 AAGAAAGATATTAATCATGTAAGCACTGTGTAAGCTTGAAGTAAAGTAAAGTAAAG 480
QY 481 ACGGTTAAAG 540
DB 481 ACGGTTAAAG 540
QY 541 GAGCCTTCAGATCAAGCCCATCATGATGATGATGATGATGATGATGATGATGATGAT 600
DB 541 GAGCCTTCAGATCAAGCCCATCATGATGATGATGATGATGATGATGATGATGATGAT 600
QY 601 GAGAGAGATTTTACTCAAGGCGCAATATCCACAGTTCTCCACAGCTTTGCGAGCAGAG 660
DB 601 GAGAGAGATTTTACTCAAGGCGCAATATCCACAGTTCTCCACAGCTTTGCGAGCAGAG 660
QY 661 TCTGTTCACTGGGCGAGAGTGTGTAATTAAGAGTGTGTTCTGTGTTTCTCAAGTGTG 720
DB 661 TCTGTTCACTGGGCGAGAGTGTGTAATTAAGAGTGTGTTCTGTGTTTCTCAAGTGTG 720
QY 721 ACTGAAG 780
DB 721 ACTGAAG 780

DB 721 ACTGAAG 780
QY 781 TG 782
DB 781 TG 782

RESULT 7

AAV39001
ID AAV39001 standard; DNA; 783 BP.

AC AAV39001;

DT 23-SEP-1998 (first entry)

DE Exemplary CD40 ligand gene used in the course of the invention.

KW CD40 ligand; alteration; immunoreactivity; human cell;

KW accessory molecule ligand; AMU; gene therapy; treatment; neoplasia;

OS Chimeric - Mus sp.

OS Chimeric - Homo sapiens.

PN WO9826061-A2.

PD 18-JUN-1998.

PF 08-DEC-1997; 97WO-US222740.

PR 01-DEC-1997; 97US-0982272.

PR 09-DEC-1996; 96US-0032145.

PA (REGC) UNIV CALIFORNIA.

PI Cantwell M, Kipps TJ, Sharma S;

DR WPI; 1998-348521/30.

XX Vectors containing accessory molecule ligand genes - used for

PT altering immunoreactivity of cells, particularly for treatment of

PT neoplasia or autoimmune disorders, e.g. rheumatoid arthritis

PS Disclosure; Page 106; 167pp; English.

XX The present sequence represents an exemplary CD40 ligand gene,

CC comprising nucleotides encoding the extracellular domains (Domains III

CC and IV) and transmembrane domain (Domain II) the murine CD40 ligand gene

CC (AAV3997) operatively linked to nucleotides encoding the cytoplasmic

CC domain of the human CD40 ligand gene (AAV38998). The sequence is used to

CC exemplify the method of the invention. The specification describes a

CC method for altering the immunoreactivity of human cells which comprises

CC introducing a gene encoding an accessory molecule ligand (AMU) into the

CC cells so that the AMU is expressed on the surface of the cells. Vectors

CC containing the AMU genes can be used in gene therapy for treating

CC neoplasia or autoimmune disorders such as rheumatoid arthritis. They can

CC also be used for vaccination to produce immunity against a virus cell,

CC bacteria, protein, fungus or neoplasia.

SQ Sequence 783 BP; 243 A; 161 C; 174 G; 205 T; 0 other;

Query Match 97.1%; Score 760.6; DB 19; Length 783;

Best Local Similarity 98.2%; Pred. No. 3.4e-202;

Matches 769; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGATAGAAACATACAGCCACCTTCCCGAGATCCGTGGCACTGACCTCCAGCAGC 60
DB 1 ATGATAGAAACATACAGCCACCTTCCCGAGATCCGTGGCACTGACCTCCAGCAGC 60
QY 61 ATGAGAGATTTTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 120
DB 61 ATGAGAGATTTTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 120

Db 541 GAGCCTTCAGTCAAGCCCATTCATCTGCGCCTTGGCTGAAGCCCAAGATTGGAATCT 600
 QY 601 GAGAGAACTTTACTCAAGCGGCAAAATPACCAAGTTCTCCAGCTTTGGCAGAGCAG 660
 Db 601 GAGAGAACTTTACTCAAGCGGCAAAATPACCAAGTTCTCCAGCTTTGGCAGAGCAG 660
 QY 661 TCTGTTCACTTGGGCGGAGTGTGTAATTACAGCTGAGTCTGTGTGTTGCAACGTG 720
 Db 661 TCTGTTCACTTGGGCGGAGTGTGTAATTACAGCTGAGTCTGTGTGTTGCAACGTG 720
 QY 721 ACTGAGCAAGCCCAAGTATCCAGAGTTGGCTTCTCATCTTTGGCTTACTCAACTC 780
 Db 721 ACTGAGCAAGCCCAAGTATCCAGAGTTGGCTTCTCATCTTTGGCTTACTCAACTC 780
 QY 781 TGA 783
 Db 781 TGA 783
 RESULT 9
 AAT05762
 ID AAT05762 standard; DNA; 818 BP.
 AC AAT05762;
 XX
 DT 18-MAR-1996 (first entry)
 XX
 DE Murine CD40 ligand DNA.
 XX
 KW High density membrane-bound CD40 ligand; B-lymphocyte; B-cell;
 KM differentiation; proliferation; baculovirus; Spodoptera frugiperda;
 SF9; insect cell culture; tumour necrosis factor receptor; ss.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT CDS 13..795
 FT /*tag= a
 FT
 WT W09529935-A1.
 XX
 PN 09-NOV-1995.
 PD
 XX 28-APR-1995; 95WO-US05448.
 PF
 XX 28-APR-1994; 94US-0234580.
 PR
 XX (BOEH) BOEHRINGER INGELHEIM PHARM INC.
 PA
 XX Caetle BE, Kehry M;
 PI
 XX WPI; 1995-393038/50.
 DR P-PSDB; AAR85485.
 DR
 XX High density membrane bound CD40 ligand - for stimulating the
 PT proliferation of B cells in vitro or in vivo, partic. for producing
 PT differentiated cells
 XX
 PS Disclosure; Fig 1; 74pp; English.
 XX
 CC The nucleotide sequence given in AAT05762 encodes a mouse high-density,
 CC membrane-bound (hmb) CD40 ligand (AAR85485) that induces long-term
 CC proliferation of B-cells in culture. These proliferating B-cells
 CC can be induced to differentiate into antibody-prod. cells. The
 CC nucleotide sequence is incorporated into a baculovirus vector that
 CC is used to transfect SF9 insect cells for prodn. of recombinant
 CC hmbCD40.
 XX
 SQ Sequence 818 BP; 237 A; 182 C; 188 G; 211 T; 0 other;
 Query Match 84.9%; Score 664.6; DB 16; Length 818;
 Best Local Similarity 90.5%; Pred. No. 2.2e-175;
 Matches 709; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 1 ATGATGAAACATPACAGCCAACTTTCCCGAGATCGGTGGCAACTGACCTTCCAGCGAGC 60
 Db 13 ATGATGAAACATPACAGCCAACTTTCCCGAGATCGGTGGCAACTTCCAGCGAGC 72
 QY 61 ATGAAATTTTAAATTTTACTTAACTGTTTTCCCTTATCAACCAATGATGATGATCTG 120
 Db 73 ATGAAATTTTAAATTTTACTTAACTGTTTTCCCTTATCAACCAATGATGATGATCTG 132
 QY 121 CTTTGGTCTGTGTATCTTCAATGAAATTTGATTAAGGTGAGAGAGAAATTAACCTTCA 180
 Db 133 CTTTGGTCTGTGTATCTTCAATGAAATTTGATTAAGGTGAGAGAGAAATTAACCTTCA 192
 QY 181 GAAATTTTGTATTCATTAATAAGCTTAAAGATGCAACAAAGAGAGAGATCTTTATCC 240
 Db 193 GAAATTTTGTATTCATTAATAAGCTTAAAGATGCAACAAAGAGAGAGATCTTTATCC 252
 QY 241 TTGCTGAACCTGTGAGAGATGAGAGAGCAATTTGAAAGCTTGTCAAGATATTAAGTTA 300
 Db 253 TTGCTGAACCTGTGAGAGATGAGAGAGCAATTTGAAAGCTTGTCAAGATATTAAGTTA 312
 QY 301 AACAAAG 360
 Db 313 AACAAAG 372
 QY 361 ATTGCGACACAGCTTGTAAAGCAAGCAACGTATACAGATCCGTTCTCAAGTGGGCC 420
 Db 373 ATTGCGACACACAGCTTGTAAAGCAAGCAACGTATACAGATCCGTTCTCAAGTGGGCC 432
 QY 421 AAGAAAGATATTTATACATGAAAGCAACTTGTGTAATGCTGAAATGAGAAACAGCTG 480
 Db 433 CTAAGCGGCAAAATPACCAAGTTCTCCAGCTTTGGAGAGAGAGAGAGAGAGAGAG 492
 QY 481 ACGTTTAAAG 540
 Db 493 ACGTTTAAAG 552
 QY 541 GAGCCTTCAGTCAAGCCCATTCATCTGCGCCTTGGCTGAAGCCCAAGATTGGAATCT 600
 Db 553 GAGCCTTCAGTCAAGCCCATTCATCTGCGCCTTGGCTGAAGCCCAAGATTGGAATCT 612
 QY 601 GAGAGAACTTTACTCAAGCGGCAAAATPACCAAGTTCTCCAGCTTTGGCAGAGCAG 660
 Db 613 GAGAGAACTTTACTCAAGCGGCAAAATPACCAAGTTCTCCAGCTTTGGCAGAGCAG 672
 QY 661 TCTGTTCACTTGGGCGGAGTGTGTAATTACAGCTGAGTCTGTGTGTTGCAACGTG 720
 Db 673 TCTGTTCACTTGGGCGGAGTGTGTAATTACAGCTGAGTCTGTGTGTTGCAACGTG 732
 QY 721 ACTGAGCAAGCCCAAGTATCCAGAGTTGGCTTCTCATCTTTGGCTTACTCAACTC 780
 Db 733 ACTGAGCAAGCCCAAGTATCCAGAGTTGGCTTCTCATCTTTGGCTTACTCAACTC 792
 QY 781 TGA 783
 Db 793 TGA 795
 RESULT 10
 AAH25527
 ID AAH25527 standard; DNA; 1477 BP.
 AC AAH25527;
 XX
 DT 22-AUG-2001 (first entry)
 XX
 DE Nucleotide sequence of surfactant protein D fused to CD40 ligand.
 XX
 KW Fusion protein; CD40 ligand; tumour necrosis factor; TNF; collectin;
 KM pulmonary surfactant protein D; SPD; immunocompetent cell;
 KW cell antigenicity; vaccine adjuvant; chimera; ss.
 XX
 OS Chimeric - Mus sp.

Db 541 GAAGCTTGAGTCAGCTCATTTATAGCAAGCTTCTGCTTAAGTCCCGGCTAGATTC 600
 Qy 601 GAGAGATCTTACTCAAGCGGCAATACCAGAGTTCTCCAGCTTTGCGAGCAG 660
 Db 601 GAGAGATCTTACTCAAGCTCAATATCCAGAGTTCTCCAGAGCTTTGCGAGCAG 660
 Qy 661 TCTGTTCACTGGCGGAGTGTTTAATACAGCGTGTCTGTTGTTGCAACG 720
 Db 661 TCCATTCACTGGGAGAGTATTTAATGACAGGAGTCTGCGTGTGTTGCAATG 720
 Qy 721 ACTGAAGCAAGCCAGTGAATCCAGAGTTGGCTTCATCTTTGGTTACTCAATC 780
 Db 721 ACTGATCCAGCAAGTGAAGCCAGTGGCTTACGCTTGGCTTACTCAATC 780
 Qy 781 TGA 783
 Db 781 TGA 783
 RESULT 13
 AAV39003
 ID AAV39003 standard; DNA; 786 BP.
 XX AAV39003;
 AC 23-SEP-1998 (first entry)
 DT 23-SEP-1998 (first entry)
 DE Exemplary CD40 ligand gene used in the course of the invention.
 XX CD40 ligand; alteration; immunoreactivity; human cell;
 KW accessory molecule; ligand; AMU; gene therapy; treatment; neoplasia;
 KM autoimmune disorder; rheumatoid arthritis; vaccine; chimera; ss.
 OS Chimeric - Mus sp.
 OS Chimeric - Homo sapiens.
 XX WO982061-A2.
 PN 18-JUN-1998.
 PD 08-DEC-1997; 97WO-0622740.
 PF 01-DEC-1997; 97US-0982272.
 PR 09-DEC-1996; 96US-0032145.
 XX (REGC) UNIV CALIFORNIA.
 PA Cantwell M, Kipps TJ, Sharma S;
 PI WP1; 1998-348521/30.
 DR Vectors containing accessory molecule ligand genes - used for
 PT altering immunoreactivity of cells, particularly for treatment of
 PT neoplasia or autoimmune disorders, e.g. rheumatoid arthritis
 XX
 PS Disclosure; Page 107; 167pp; English.
 XX The present sequence represents an exemplary CD40 ligand gene,
 CC comprising nucleotides encoding the extracellular domains (Domains III
 CC and IV) of the human CD40 ligand gene (AAV38998) operatively linked to
 CC nucleotides encoding the cytoplasmic domain (Domain I) and transmembrane
 CC domain (Domain II) of the murine CD40 ligand gene (AAV38997). The
 CC sequence is used to exemplify the method of the invention. The
 CC specification describes a method for altering the immunoreactivity of
 CC human cells which comprises introducing a gene encoding an accessory
 CC molecule ligand (AMU) into the cells so that the AMU is expressed on the
 CC surface of the cells. Vectors containing the AMU genes can be used in
 CC gene therapy for treating neoplasia or autoimmune disorders such as
 CC rheumatoid arthritis. They can also be used for vaccination to produce
 CC immunity against a virus cell, bacteria, protein, fungus or neoplasia.
 XX Sequence 786 BP; 250 A; 166 G; 170 G; 200 T; 0 other;

Query Match 75.7%; Score 592.4; DB 19; Length 786;
 Beel Local Similarity 85.5%; Pred. No. 3.1e-155;
 Matches 672; Conservative 0; Mismatches 111; Indels 3; Gaps 1;
 Qy 1 ATGATGAAACATACAGCAACCTTCCCAATCCCGGCACTGGAATCTCCAGCAG 60
 Db 1 ATGATGAAACATACAGCAACCTTCCCAATCCCGGCACTGGAATCTCCAGCAG 60
 Qy 61 ATGAAAGTTTATGATTTTACTTACTGTTTCTTATCAACCAATGATGATCTGTG 120
 Db 61 ATGAAAGTTTATGATTTTACTTACTGTTTCTTATCAACCAATGATGATCTGTG 120
 Qy 121 CTTTTCCTGTATCTTCAATGAAAGTTGATAGGTCGAAAGGAATGAACCTTCAT 180
 Db 121 CTTTTCCTGTATCTTCAATGAAAGTTGATAGGTCGAAAGGAATGAACCTTCAT 180
 Qy 181 GAAGTTTGTATTTCAAAAAAGCTTAAAGATGCAACAAAGAGAGATCTTTATCC 240
 Db 181 GAAGTTTGTATTTCAAAAAAGCTTAAAGATGCAACAAAGAGAGATCTTTATCC 240
 Qy 241 TTGCTGAACTGTGAGAGATGAGAGCAATTTTGAAGCTTTGCAAGATATACGTTA 300
 Db 241 TTGCTGAACTGTGAGAGATGAGAGCAATTTTGAAGCTTTGCAAGATATACGTTA 300
 Qy 301 AACAAAGAGA--GAAAAAAGAAAAAGCTTTGAAATGCAAGAGGTGATGAGATCTT 357
 Db 301 AACAAAGAGAGAGAAAAAGAAAAAGCTTTGAAATGCAAGAGGTGATGAGATCTT 357
 Qy 358 CAAATGAGACACCTTTGTATGAGAGCCCAAGATGAGAGATGAGATGAGATGAG 417
 Db 358 CAAATGAGACACCTTTGTATGAGAGCCCAAGATGAGAGATGAGATGAGATGAG 417
 Qy 418 GCAAGAAAGATATTTATCATGAAAAAGCACTGTGATGCTTGAATGAGAAACAG 477
 Db 418 GCAAGAAAGATATTTATCATGAAAAAGCACTGTGATGCTTGAATGAGAAACAG 477
 Qy 478 CTGACGTTTAAAGAAAGAAAGAAAGTATTTATGTTATCACTCAAGTCACTTCTCTAAT 537
 Db 478 CTGACGTTTAAAGAAAGAAAGAAAGTATTTATGTTATCACTCAAGTCACTTCTCTAAT 537
 Qy 481 CTGACGTTTAAAGAAAGAAAGAAAGTATTTATGTTATCACTCAAGTCACTTCTCTAAT 540
 Db 481 CTGACGTTTAAAGAAAGAAAGAAAGTATTTATGTTATCACTCAAGTCACTTCTCTAAT 540
 Qy 538 CGGAGACCTTGAAGTCAAGCCCATTCATGCTGCGCTTGGCTGAAGCCAGATGGA 597
 Db 538 CGGAGACCTTGAAGTCAAGCCCATTCATGCTGCGCTTGGCTGAAGCCAGATGGA 597
 Qy 541 CGGAGACCTTGAAGTCAAGCCCATTCATGCTGCGCTTGGCTGAAGCCAGATGGA 600
 Db 541 CGGAGACCTTGAAGTCAAGCCCATTCATGCTGCGCTTGGCTGAAGCCAGATGGA 600
 Qy 598 TCTGAGAGATCTTACTCAAGGCGGCAATACCAAGTCTCTCCAGCTTTGCGAGCAG 657
 Db 598 TCTGAGAGATCTTACTCAAGGCGGCAATACCAAGTCTCTCCAGCTTTGCGAGCAG 657
 Qy 601 TTGAGAGATCTTACTCAAGGCGGCAATACCAAGTCTCTCCAGCTTTGCGAGCAG 660
 Db 601 TTGAGAGATCTTACTCAAGGCGGCAATACCAAGTCTCTCCAGCTTTGCGAGCAG 660
 Qy 658 CAGTCTGTCACTTGGCGGAGTGTGATTAACAAGTGTGCTTCTGTGTTTGCAC 717
 Db 658 CAGTCTGTCACTTGGCGGAGTGTGATTAACAAGTGTGCTTCTGTGTTTGCAC 717
 Qy 661 CATTCATTCACCTTGGAGAGAGTATTAATGCAACAGGCTTCCGTTGTTGCAT 720
 Db 661 CATTCATTCACCTTGGAGAGAGTATTAATGCAACAGGCTTCCGTTGTTGCAT 720
 Qy 718 GTGACGAAAGAAAGCAAGTGAATCCAGAGATTTGCGCTTCATCTTTGGCTTACCA 777
 Db 718 GTGACGAAAGAAAGCAAGTGAATCCAGAGATTTGCGCTTCATCTTTGGCTTACCA 777
 Qy 721 GTGACGAAAGAAAGCAAGTGAATCCAGAGATTTGCGCTTCATCTTTGGCTTACCA 780
 Db 721 GTGACGAAAGAAAGCAAGTGAATCCAGAGATTTGCGCTTCATCTTTGGCTTACCA 780
 Qy 778 CTCTGA 783
 Db 781 CTCTGA 786
 RESULT 14
 AAV39002
 ID AAV39002 standard; DNA; 786 BP.
 XX AAV39002;
 AC 23-SEP-1998 (first entry)
 DT 23-SEP-1998 (first entry)
 DE Exemplary CD40 ligand gene used in the course of the invention.
 XX CD40 ligand; alteration; immunoreactivity; human cell;
 KM accessory molecule ligand; AMU; gene therapy; treatment; neoplasia;

CC cytoplasmic domain (Domain I). The sequence is used to exemplify the
CC method of the invention. The specification describes a method for
CC altering the immunoreactivity of human cells which comprises introducing
CC a gene encoding an accessory molecule ligand (AML) into the cells so that
CC the AML is expressed on the surface of the cells. Vectors containing the
CC AML genes can be used in gene therapy for treating neoplasia or
CC autoimmune disorders such as rheumatoid arthritis. They can also be used
CC for vaccination to produce immunity against a virus cell, bacteria,
CC protein, fungus or neoplasia.
XX

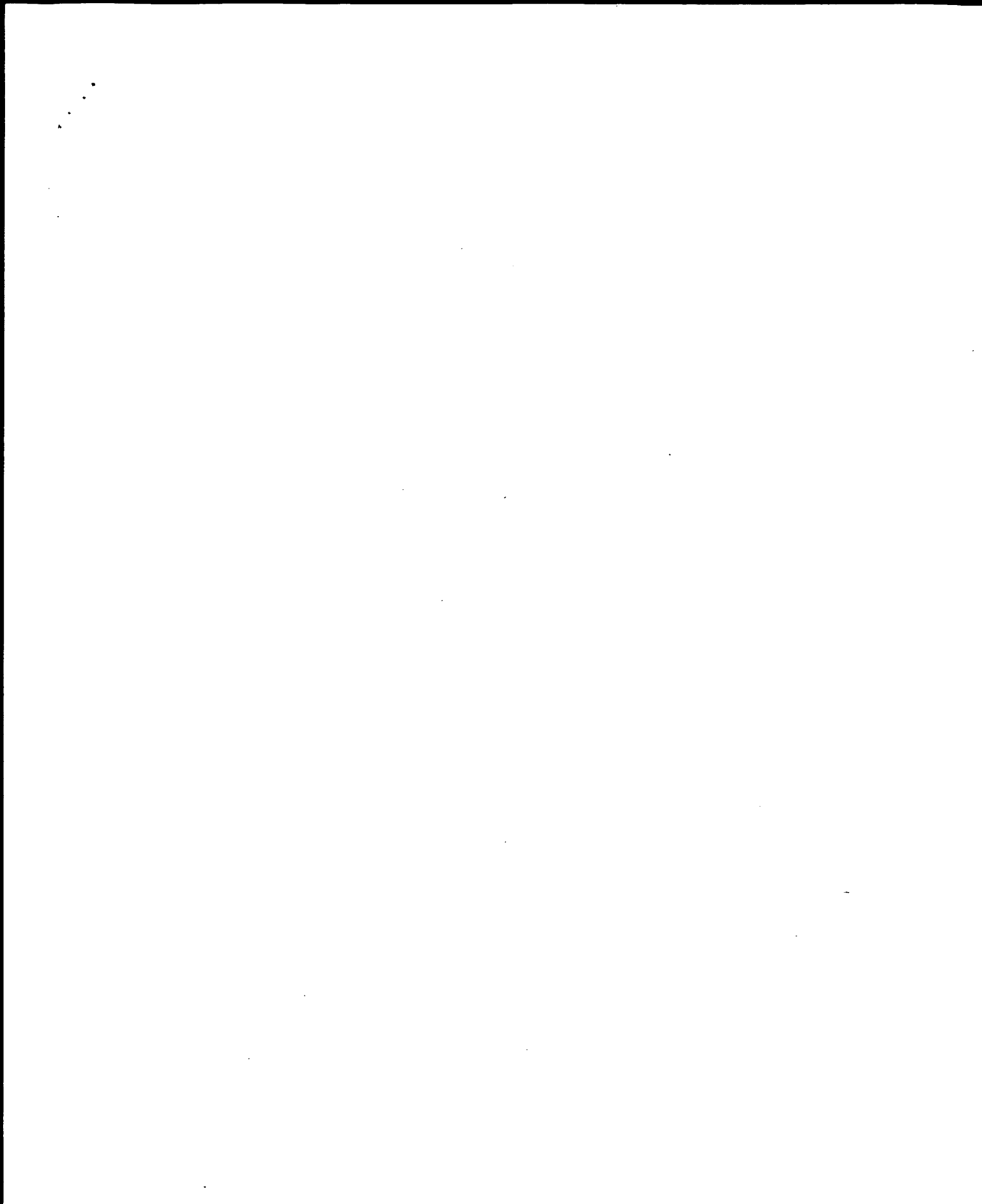
SQ Sequence 786 BP; 250 A; 168 C; 167 G; 201 T; 0 other;

Query Match 72.8%; Score 570; DB 19; Length 786;

Best Local Similarity 83.7%; Pred. No. 5,6e-149;
Matches 658; Conservative 0; Mismatches 125; Indels 3; Gaps 1;

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Db 1 ATGATCGAAACATACCAACCACTTCCCGAGATCCGTCGCACTGAGACTGCGCATCAGC 60
Qy 61 ATGAAGATTTTATGATTTTACTTACTGTTTCTTATCACCCTAATGATGATCTGTG 120
Db 61 ATGAAGATTTTATGATTTTACTTACTGTTTCTTATCACCCTAATGATGATCTGTG 120
Qy 121 CTTTGTGCTGATCTCATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 180
Db 121 CTTTGTGCTGATCTCATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 180
Qy 181 GAAGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATGATTT 240
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Qy 241 TTGCTGAACCTGTGAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 300
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Qy 301 AACAAAGAGA--GAAAAAGAAAAGCTTTGAATGCAAGAGATGATGAGATCCT 357
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Qy 358 CAAATTTGAGACAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 417
Db 358 CAAATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 417
Qy 418 GCCAAGAAAGAGATTTATTAACATGAAAAAGCTTTGATGATGATGATGATGATGAT 477
Db 421 GCTGAAAAAGAGATTTATTAACATGAAAAAGCTTTGATGATGATGATGATGATGAT 477
Qy 478 CTGACGTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 537
Db 481 CTGACGTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Qy 538 CGGAGGCTTGTGAGTCAAGCCATTCATCGTGGCTTGTGAGTCAAGCCATTCAGTGA 597
Db 541 CGGAGGCTTGTGAGTCAAGCCATTCATCGTGGCTTGTGAGTCAAGCCATTCAGTGA 600
Qy 598 TCTGAGAGATCTTACATCAAGGCGGCAATTAACCAAGTCTTCCAGCTTTGCGAGAG 657
Db 601 TCTGAGAGATCTTACATCAAGGCGGCAATTAACCAAGTCTTCCAGCTTTGCGAGAG 660
Qy 658 CAGTCTGTTCACTTGGGCGAGGTTGATTAACAAGCTGTGCTTGTGTTGTCAAC 717
Db 661 CAAATCAATTCATCTTGGGAGAGATTTGAATGCAACAGGCTGTGCTTGTGTTGTCAAT 720
Qy 718 GTGACTGAAGCAAGCAAGTATCCAGAGTTGGCTTCACTTTGGCTTACTCAAA 777
Db 721 GTGACTGAATCCAAGCAAGTATCCAGAGTTGGCTTCACTTTGGCTTACTCAAA 780
Qy 778 CTCTGA 783
Db 781 CTCTGA 786
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Search completed: March 8, 2003, 22:12:40
Job time : 166.589 secs



GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: March 9, 2003, 02:11:48 ; Search time 54.0541 Seconds
(Without alignments)
9675.146 Million cell updates/sec

Title: US-08-982-272-2

Sequence: 1 ATGATGAAACATACAGCCCA.....TTGACTTACTCAACTCTGA 783

Scoring table: IDENTITY_NUC
Gapext 10.0, Gapext 1.0

Searched: 478924 seqs, 33395956 residues

Total number of hits satisfying chosen parameters: 957848

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing filter 45 summaries

Database: Published Applications NA:

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11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	783	100.0	1250	9	US-10-182-093-1	Sequence 1, Appl1
2	123.8	15.8	2395	9	US-09-875-453-9	Sequence 9, Appl1
3	46	5.9	9121	10	US-09-070-9278-221	Sequence 221, App
4	44	5.6	2220	10	US-09-897-214-15	Sequence 15, Appl1
5	40.4	5.2	176373	9	US-10-095-407-17	Sequence 17, Appl1
6	37	4.7	424	10	US-09-960-352-11218	Sequence 11218, A
7	37	4.7	1758	12	US-10-071-751-29	Sequence 29, Appl1
8	36.4	4.6	391	10	US-09-813-358-196	Sequence 196, App
9	36.2	4.6	262	10	US-09-919-580-896	Sequence 896, App
10	36.2	4.6	2430	9	US-10-105-695-1	Sequence 1, Appl1
11	36.2	4.6	2430	9	US-10-105-695-1	Sequence 1, Appl1
12	36.2	4.6	2430	10	US-09-747-521-1	Sequence 1, Appl1
13	36.2	4.6	2430	12	US-10-106-014-1	Sequence 1, Appl1
14	36	4.6	544	9	US-09-864-761-7124	Sequence 7124, Ap
15	36	4.6	25377	9	US-10-061-119-4	Sequence 4, Appl1
16	35.6	4.5	736	10	US-09-772-1348-31	Sequence 31, Appl1
17	35.6	4.5	24768	10	US-09-764-887-602	Sequence 602, App
18	35.2	4.5	4956	10	US-09-070-9278-291	Sequence 291, App
19	35.2	4.5	335913	9	US-09-754-853A-2	Sequence 2, Appl1

20	35.2	4.5	335913	9	US-09-754-853A-3	Sequence 3, Appl1
21	35	4.5	2272	10	US-09-873-438-1	Sequence 1, Appl1
22	34.8	4.4	337	10	US-09-960-352-14232	Sequence 14232, A
23	34.8	4.4	399	10	US-09-960-352-14574	Sequence 14574, A
24	34.8	4.4	404	10	US-09-960-352-9259	Sequence 9259, Ap
25	34.8	4.4	420	10	US-09-960-352-7144	Sequence 7144, Ap
26	34.8	4.4	431	10	US-09-960-352-5558	Sequence 5558, Ap
27	34.8	4.4	433	10	US-09-960-352-3058	Sequence 3058, Ap
28	34.8	4.4	555	9	US-09-736-457-380	Sequence 380, App
29	34.8	4.4	555	9	US-09-902-941-380	Sequence 380, App
30	34.8	4.4	555	9	US-09-849-626-380	Sequence 380, App
31	34.8	4.4	2000	9	US-09-938-842A-3039	Sequence 3039, App
32	34.8	4.4	3202	10	US-09-833-790-421	Sequence 421, App
33	34.8	4.4	46237	10	US-09-933-980-78	Sequence 78, Appl1
34	34.6	4.4	717	10	US-09-939-980-78	Sequence 232, App
35	34.6	4.4	725	10	US-09-910-943-232	Sequence 8414, Ap
36	34.4	4.4	312	10	US-09-960-352-8414	Sequence 12302, A
37	34.2	4.4	341	10	US-09-960-352-12302	Sequence 675, App
38	34.2	4.4	422	10	US-09-764-864-675	Sequence 292, App
39	34.2	4.4	20561	10	US-09-070-9278-292	Sequence 1, Appl1
40	34	4.3	766	9	US-10-125-258-1	Sequence 137, App
41	34	4.3	1710	9	US-10-078-770-137	Sequence 78, Appl1
42	34	4.3	1744	10	US-09-804-682-78	Sequence 315, App
43	33.8	4.3	1354	10	US-09-925-301-315	Sequence 9094, Ap
44	33.6	4.3	170	10	US-09-867-701-9094	Sequence 765, App
45	33.6	4.3	340	10	US-09-919-580-765	

ALIGNMENTS

RESULT 1
US-10-182-093-1
Sequence 1, Application US/10182093
Publication No. US20030021808A1
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as represented by
APPLICANT: c/o Center for Disease Control and Prevention
APPLICANT: Trilip, Ralph
APPLICANT: Jones, Les
APPLICANT: Anderson, Larry
APPLICANT: Brown, Michael
TITLE OF INVENTION: CD40 Ligand Adjuvant for Respiratory
FILE REFERENCE: 14114.030102
CURRENT APPLICATION NUMBER: US/10/182.093
CURRENT FILING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: 60/179,905
PRIOR FILING DATE: 2000-02-02
NUMBER OF SEQ ID NOS: 1
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1250
TYPE: DNA
ORGANISM: Murine
US-10-182-093-1

Query Match 100.0%; Score 783; DB 9; Length 1250;
Best Local Similarity 100.0%; Pred. No. 8.9e-203;
Matches 783; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGATGAAACATACAGCCCACTTCCCGAGATCGGTGCAACTGCACTTCAGAGAC 60
13 ATGATGAAACATACAGCCCACTTCCCGAGATCGGTGCAACTGCACTTCAGAGAC 72
61 ATGATGAAACATACAGCCCACTTCCCGAGATCGGTGCAACTGCACTTCAGAGAC 120
73 ATGATGAAACATACAGCCCACTTCCCGAGATCGGTGCAACTGCAACTGCACTTCAGAGAC 132
121 CTTTTCCTGCTGATCTTCATACAGATTTGGTATGAGTGGAGAGAGAGTAACTTCAT 180
133 CTTTTCCTGCTGATCTTCATACAGATTTGGTATGAGTGGAGAGAGAGTAACTTCAT 192

Query Match 5.9%; Score 46; DB 10; Length 9121;
Best Local Similarity 52.6%; Pred. No. 0.025;
Matches 100; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

Qy 161 AAGAGAAATTAACCTTCAATGAGTTTGTATTTCAAAAAAGCTTAAGAGATGCAACA 220
Db 8754 AAGAAAAAGCAAAAAAATTTCTAGTATTTTGAAGAGAAAAAACAATGAAATTTTATA 8813
Qy 221 AAGAGAAAGATCTTATCTTCTGCTGAACGTGAGAGATGAGAAAGCAATTTGAAGAC 280
Db 8814 AATGAAAGAACTTATTTTGTATTAATCCCTTAAGATGAAAAACAATTTTAAAAAC 8873
Qy 281 TTGCAAGATATATACGTTAAACAAGAGAAAAAAGAAAAAGCACTTTGAATGCAAA 340
Db 8874 TTTACAGATATTTGTTTCCGAGAGTAAAGAGCAAAAAAATTTTGTGATGATGAAAA 8933
Qy 341 GAGGTGATGA 350
Db 8934 CAATTGATTA 8943

RESULT 4

US-09-897-214-15/C
Sequence 15, Application US/09897214
Patent No. US2002007679A1
GENERAL INFORMATION:
APPLICANT: Thayer, Edward C.
APPLICANT: Sheppard, Paul O.
APPLICANT: Preenell Scott R.
TITLE OF INVENTION: Leucine-Rich Repeat Proteins, Zlrr7,
TITLE OF INVENTION: Zlrr8, and Zlrr9
FILE REFERENCE: 01-27
CURRENT APPLICATION NUMBER: US/09/897, 214
CURRENT FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: 60/215,446
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 15
LENGTH: 2220
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificial polynucleotide sequence
NAME/KEY: misc_feature
LOCATION: (1)...(2220)
OTHER INFORMATION: n = A,T,C or G
US-09-897-214-15

Query Match

5.6%; Score 44; DB 10; Length 2220;
Best Local Similarity 25.3%; Pred. No. 0.044;
Matches 96; Conservative 70; Mismatches 212; Indels 1; Gaps 1;

Qy 262 AGAAGCAATTTGAAGACCTTCAAGATATACGTTAAACAAGAGAAAAAGAA 321
Db 925 AANARTTDAATNSWNRNACCTGNSWNRNACCTGNSWNRNACCTGNSWNRNACCT 866
Qy 322 AACGCTTGAATGCAAGAGGTGAGATCTCTCAATTCAGACACAGCT-TGTAAG 380
Db 865 TRCARTTGTGAAAN 806
Qy 381 CGAAGCCACAGTAATGAGACATCGTTTCAAGTGGGCCCAAGAAAGATATTAACAT 440
Db 805 CNSWNGNANANGNCGNSWNRNACCTGNSWNRNACCTGNSWNRNACCTGNSWNRNACCT 746
Qy 441 GAAAGCACTTGTGATGCTTGAAGAAACGCTGACGCTTAAAGAGAGACT 500
Db 745 ADATRTCCCTGNAANGNNGNANANANANANANANANANANANANANANANANAN 686
Qy 501 CTATATGCTTACACTCAAGTCACTCTCTCTTAATGGGAGACCTTCAGATCAAGCC 560
Db 685 TNGNARTCNCDATCCANCCNSWYTCANCKYTCNARRANGTNCNSWNRNACCT 626

Qy 561 ATTCACTGCGGCTCTGCTGAGCCGACGATTTGATGAGAGATCTTACTCAAGGC 620
Db 625 RNCCTYCNANNGTAN 566
Qy 621 GGCMAATACCCAGCTTC 639
Db 565 CMCCTYGNCGNCCNCKNC 547

RESULT 5

US-10-095-407-17
Sequence 17, Application US/10095407
Patent No. US20020164330A1
GENERAL INFORMATION:
APPLICANT: Pan, Yang
APPLICANT: Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/10/095,407
CURRENT FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/091,650
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: US 60/054,646
PRIOR FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 17
LENGTH: 176373
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(176373)
OTHER INFORMATION: n = A,T,C or G
US-10-095-407-17

Query Match

5.2%; Score 40.4; DB 9; Length 176373;
Best Local Similarity 48.3%; Pred. No. 3.2;
Matches 113; Conservative 0; Mismatches 121; Indels 0; Gaps 0;

Qy 213 ATGCAACAAAGAGAGATCTTATCTTCTGCTGAACCTGTGAGATGAGAGCAATT 272
Db 114639 ATGAAAAATGAAATGAGATATTAATCTGAAACGTCAGGAAAAATTTGAAATA 114698
Qy 273 TGAAGACCTTCTCAAGATATTAACGTTAAACAAGAGAAAAAGAAAAAGCTTTGA 332
Db 114699 AGAAATCTGACCAAAAAATCTCTGATCAATCAAAAAAAGAAAAAGAAAAAG 114758
Qy 333 AATGCAAGAGGTGATGAGATCTTCAATTTGACGACACCTTTGACGACCAAGC 392
Db 114759 TTGCGAAGAGAAAAATCAAGCATGAAAAAGCGGACAAATGAAAGTGGAAAAAG 114818
Qy 393 TATGAGATCTGCTTCAAGTGGGCCCAAGAAAGATTTTATACATGAAAG 446
Db 114819 GGTAGAAAGACAGTCCAGAAATATCACTAGTCACTAAATCAACATTAAG 114872

RESULT 6

US-09-960-352-11218
Sequence 11218, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Byatt, John C.
APPLICANT: Mathiasagen, Negapan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112

SEQ ID NO 11218
 LENGTH: 424
 TYPE: DNA
 ORGANISM: Bos taurus
 OTHER INFORMATION: Clone ID: 48-LIB3058-026-Q1-K1-D12
 US-09-960-352-11218

Query Match 4.7%; Score 37; DB 10; Length 424;
 Best Local Similarity 49.4%; Pred. No. 1.6;
 Matches 126; Conservative 0; Mismatches 125; Indels 4; Gaps 1;

Qy 68 TTTTATGATTTCTACGTTTCTTCTATCCCAAGATGATCTGCTTTTG 127
 Db 30 TTTTATGATTTCTACGTTTCTTCTATCCCAAGATGATCTGCTTTTG 89
 Qy 128 CTGTATCTCATAGAGATTGATAGGTCGAGAGAGAACTTATCATGATTT 187
 Db 90 TTTTATGATTTCTACGTTTCTTCTATCCCAAGATGATCTGCTTTTG 149
 Qy 188 TTGTATTCATTAAGCTTAAGATGATGATGATGATGATGATGATGATGAT 247
 Db 150 TTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 209
 Qy 248 ACTGT---GAGGATGAGAGAGATTTGAGACCTTCTCATGATATTAAC 303
 Db 210 AATATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 269
 Qy 304 AAG 318
 Db 270 AAAAAAAAAATGAAA 284

RESULT 7

US-10-071-751-29
 Sequence 29, Application US/10071751
 Patent No. US20020142352A1
 GENERAL INFORMATION:
 APPLICANT: Hunter, Shirley Wu
 Sim, Gek-Kee

TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA PROTEINS AND
 APPARATUS TO COLLECT SUCH PROTEINS
 NUMBER OF SEQUENCES: 88
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SHERIDAN ROSS P.C.
 STREET: 1560 BROADWAY, SUITE 1200
 CITY: DENVER
 STATE: CO
 COUNTRY: U.S.A.
 ZIP: 80202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/071,751
 FILING DATE: 07-Feb-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/171,156
 FILING DATE: 1998-10-09
 ATTORNEY/AGENT INFORMATION:
 NAME: Connell, Gary J.
 REGISTRATION NUMBER: 32,020
 REFERENCE/DOCKET NUMBER: 2618-17-C4-PUS
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 303/863-9700
 TELEFAX: 303/863-0223
 INFORMATION FOR SEQ ID NO: 29:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1758 base pairs
 TYPE: nucleic acid

STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..1758
 NAME/KEY: W = A or T
 LOCATION: 1136
 SEQUENCE DESCRIPTION: SEQ ID NO: 29:

US-10-071-751-29

Query Match 4.7%; Score 37; DB 12; Length 1758;
 Best Local Similarity 47.2%; Pred. No. 3.2; Mismatches 121; Indels 0; Gaps 0;
 Matches 109; Conservative 1;

Qy 155 AGCTGAT 214
 Db 1043 AAGATGATGAT 1102
 Qy 215 GCAACAAAGAT 274
 Db 1103 AAGAACTAAGAT 1162
 Qy 275 AAGACCTTGTCAAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 334
 Db 1163 ATACTGTTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1222
 Qy 335 TGCAGAT 385
 Db 1223 TTGAAGCTCCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1273

RESULT 8

US-09-813-358-196/c
 Sequence 196, Application US/09813358
 Patent No. US20020048759A1
 GENERAL INFORMATION:
 APPLICANT: Xu, Jiangchun
 APPLICANT: Pyle, Ruth A.
 APPLICANT: Stolk, John A.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 FILE REFERENCE: 210121.501
 CURRENT APPLICATION NUMBER: US/09/813,358
 CURRENT FILING DATE: 2001-03-21
 NUMBER OF SEQ ID NOS: 222
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 196
 LENGTH: 391
 TYPE: DNA
 ORGANISM: Homo sapien
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1) ... (391)
 OTHER INFORMATION: n = A, T, C or G
 US-09-813-358-196

Query Match 4.6%; Score 36.4; DB 10; Length 391;
 Best Local Similarity 51.0%; Pred. No. 2.3; Mismatches 79; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

Qy 68 TTTTATGATTTCTACGTTTCTTCTATCCCAAGATGATGATGATGATGATGAT 127
 Db 369 TTTTATGATTTCTACGTTTCTTCTATCCCAAGATGATGATGATGATGATGAT 310
 Qy 128 CTGTATCTCATAGAGATTGATAGGTCGAGAGAGAACTTATCATGATTT 187
 Db 309 TTTTATGATTTCTACGTTTCTTCTATCCCAAGATGATGATGATGATGATGAT 250
 Qy 188 TTGTATTCATTAAGCTTAAGATGATGATGATGATGATGATGATGATGATGAT 222
 Db 249 TTAATTAAGAT 215

RESULT 9

US-09-919-580-896
; Sequence 896, Application US/09919580
; Patent No. US20020110832A1
; GENERAL INFORMATION:
; APPLICANT: Fyle, Ruth
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.552
; CURRENT APPLICATION NUMBER: US/09/919,580
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 896
; LENGTH: 262
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 58, 132, 133, 139, 140, 147, 262
; OTHER INFORMATION: n = A,T,C or G
US-09-919-580-896

Query Match

4.6%; Score 36.2; DB 10; Length 262;
Best Local Similarity 48.2%; Pred. No. 2.2;
Matches 92; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 135 TCTTCATGAGATGGATGATGAGGAGAGAGGATTAACCTTCATGAGATTGGATT 194
DB 56 TTTTATGAGCTGCTCACTTTATTAATGAAATGAAATGATGAAATGCGAACT 115
QY 195 CATTAAGAGGCTTAAGATGCAACAAAGAGAGATCTTTATCTTCTGCTGAATCTGA 254
DB 116 ACTATCACTTAATATNNCTGCTNNCAAGTAAAGATCTTTATGCTTAATCACTTAA 175
QY 255 GGAGATGAGAGGCAATTTGAGACCTTGTCAGAGATATTAAGTTTAAACAAGAGAGAA 314
DB 176 ATATTAAGCAAGATTAATTAATTTGCTTTTGTATTAATTAATTAATTAATTAATTAAT 235
QY 315 AAAAGAAAACA 325
DB 236 AAAAATAAAAA 246

RESULT 10

US-10-105-695-1
; Sequence 1, Application US/10105695
; Publication No. US20020197272A1
; GENERAL INFORMATION:
; APPLICANT: Galloway, Darrel R.
; APPLICANT: Mateczun, Alfred J.
; TITLE OF INVENTION: Methods for Protection Against Lethal Infection with Bacillus And
; FILE REFERENCE: 22727/04115
; CURRENT APPLICATION NUMBER: US/10/105,695
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US 09/747,521
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2430
; TYPE: DNA
; ORGANISM: Bacillus anthracis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2430)
; OTHER INFORMATION:
US-10-105-695-1

Query Match 4.6%; Score 36.2; DB 9; Length 2430;
Best Local Similarity 50.3%; Pred. No. 6.1;
Matches 89; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 158 TCGAAGAGAGATTAACCTTCATGAGAGATTGTTATTCATTAATAAGAGATGCA 217
DB 1053 TCTTAAGAGATTAACAAATGATGATGATTTTATCTTCTGAGAGAAAGAGCTTTT 1112
QY 218 ACAAGAGAGAGATCTTTATCTGCTGAGAGATGAGAGATGAGAGCAATTGAG 277
DB 1113 AAAAAGCTCAAAATGATGATGATTTTATCTTCTGAGAGAGAAAGAGCTTTTAA 1172
QY 278 ACTTTCAGAGATTAACCTTAAACAAGAGAGAAAGAGAAAGAGAGCTTTGAA 334
DB 1173 TAGAATACAGTGATGATGATGATTTTATCTTCTGAGAGAGAAAGAGAGCTTTTAA 1229

RESULT 11

US-10-105-694-1
; Sequence 1, Application US/10105694
; Publication No. US20030003109A1
; GENERAL INFORMATION:
; APPLICANT: Galloway, Darrel R.
; APPLICANT: Mateczun, Alfred J.
; TITLE OF INVENTION: Methods for Protection Against Lethal Infection with Bacillus
; FILE REFERENCE: 22727/04116
; CURRENT APPLICATION NUMBER: US/10/105,694
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US 09/747,521
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2430
; TYPE: DNA
; ORGANISM: Bacillus anthracis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2430)
; OTHER INFORMATION:
US-10-105-694-1

Query Match 4.6%; Score 36.2; DB 9; Length 2430;
Best Local Similarity 50.3%; Pred. No. 6.1;
Matches 89; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 158 TCGAAGAGAGATTAACCTTCATGAGAGATTGTTATTCATTAATAAGAGATGCA 217
DB 1053 TCTTAAGAGATTAACAAATGATGATGATTTTATCTTCTGAGAGAAAGAGCTTTT 1112
QY 218 ACAAGAGAGAGATCTTTATCTGCTGAGAGATGAGAGATGAGAGCAATTGAG 277
DB 1113 AAAAAGCTCAAAATGATGATGATTTTATCTTCTGAGAGAGAAAGAGCTTTTAA 1172
QY 278 ACTTTCAGAGATTAACCTTAAACAAGAGAGAAAGAGAGAAAGAGAGCTTTGAA 334
DB 1173 TAGAATACAGTGATGATGATGATTTTATCTTCTGAGAGAGAAAGAGAGCTTTTAA 1229

RESULT 12

US-09-747-521-1
; Sequence 1, Application US/09747521
; Patent No. US20020051791A1
; GENERAL INFORMATION:
; APPLICANT: Galloway, Darrel
; APPLICANT: Mateczun, Alfred
; TITLE OF INVENTION: Methods for Protection Against Lethal Infection with Bacillus
; FILE REFERENCE: 22727/04079
; CURRENT APPLICATION NUMBER: US/09/747,521
; CURRENT FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1

LENGTH: 2430
TYPE: DNA
ORGANISM: Bacillus anthracis
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(2430)
US-09-747-521-1

Query Match
Best Local Similarity 50.3%; Score 36.2; DB 10; Length 2430;
Pred. No. 6.1;
Matches 89; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 158 TCGAAGAGAGTAACCTTCATGAAAGTTTGTATCATTAAGGCTTAAGATGCA 217
DB 1053 TCTAAAAAGAAATACAAATTGATGATGATTTTATCTACTGAGAAAAGGTTTTT 1112
QY 218 ACAAGAGAGAGATCTTTATCTCTGTAAGCTGAGAGATGAGAGCAATTTGAAG 277
DB 1113 AAAAAAGCTACAAATGATTCGTGATTTCTTTATCTGAGAGAAAAGGCTTTTAA 1172
QY 278 ACCTGTCAAGATATACGTTAAACAAAGAGAAAAAGAAACGCTTTGAAA 334
DB 1173 TAGAATACAGGTGATGATGATGATGATTTTCTGAAAAAGGTTTTTAA 1229

RESULT 13
US-10-106-014-1
Sequence 1, Application US/10106014
Patent No. US20020142002A1
GENERAL INFORMATION:
APPLICANT: Galloway, Darrel R.
APPLICANT: Mateczun, Alfred J.
TITLE OF INVENTION: Methods for Protection Against Lethal Infection with Bacillus Anthracis
FILE REFERENCE: 22727/04114
CURRENT APPLICATION NUMBER: US/10/106,014
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER: US 09/747,521
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 2430
TYPE: DNA
ORGANISM: Bacillus anthracis
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(2430)
OTHER INFORMATION:
US-10-106-014-1

Query Match
Best Local Similarity 4.6%; Score 36.2; DB 12; Length 2430;
Pred. No. 6.1;
Matches 89; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 158 TCGAAGAGAGTAACCTTCATGAAAGTTTGTATCATTAAGGCTTAAGATGCA 217
DB 1053 TCTAAAAAGAAATACAAATTGATGATGATTTTATCTACTGAGAAAAGGTTTTT 1112
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DB 1113 AAAAAAGCTACAAATGATTCGTGATTTCTTTATCTGAGAGAAAAGGCTTTTAA 1172
QY 278 ACCTGTCAAGATATACGTTAAACAAAGAGAAAAAGAAACGCTTTGAAA 334
DB 1173 TAGAATACAGGTGATGATGATGATGATTTTCTGAAAAAGGTTTTTAA 1229

RESULT 14
US-09-864-761-7124/C
Sequence 7124, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.

APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecmics-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annotmax Sequence Listing Engine vers. 1.1
SEQ ID NO 7124
LENGTH: 544
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL157405.2
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.8
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.5
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.2
US-09-864-761-7124

Query Match
Best Local Similarity 4.6%; Score 36; DB 10; Length 544;
Pred. No. 3.4;
Matches 90; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

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QY 189 TGTATCTTCATGAGAGATGAGTAAGCTGAGAGAGTAACCTTCATGAGATTT 248
DB 356 TGTATCTTCATGAGAGATGAGTAAGCTGAGAGAGTAACCTTCATGAGATTT 297

Qy 249 CTGTGAGGATATAGAAGGCATTTGAAACCTTGTCAAGATATACTTAACAAGA 308
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RESULT 15
THE 10-063

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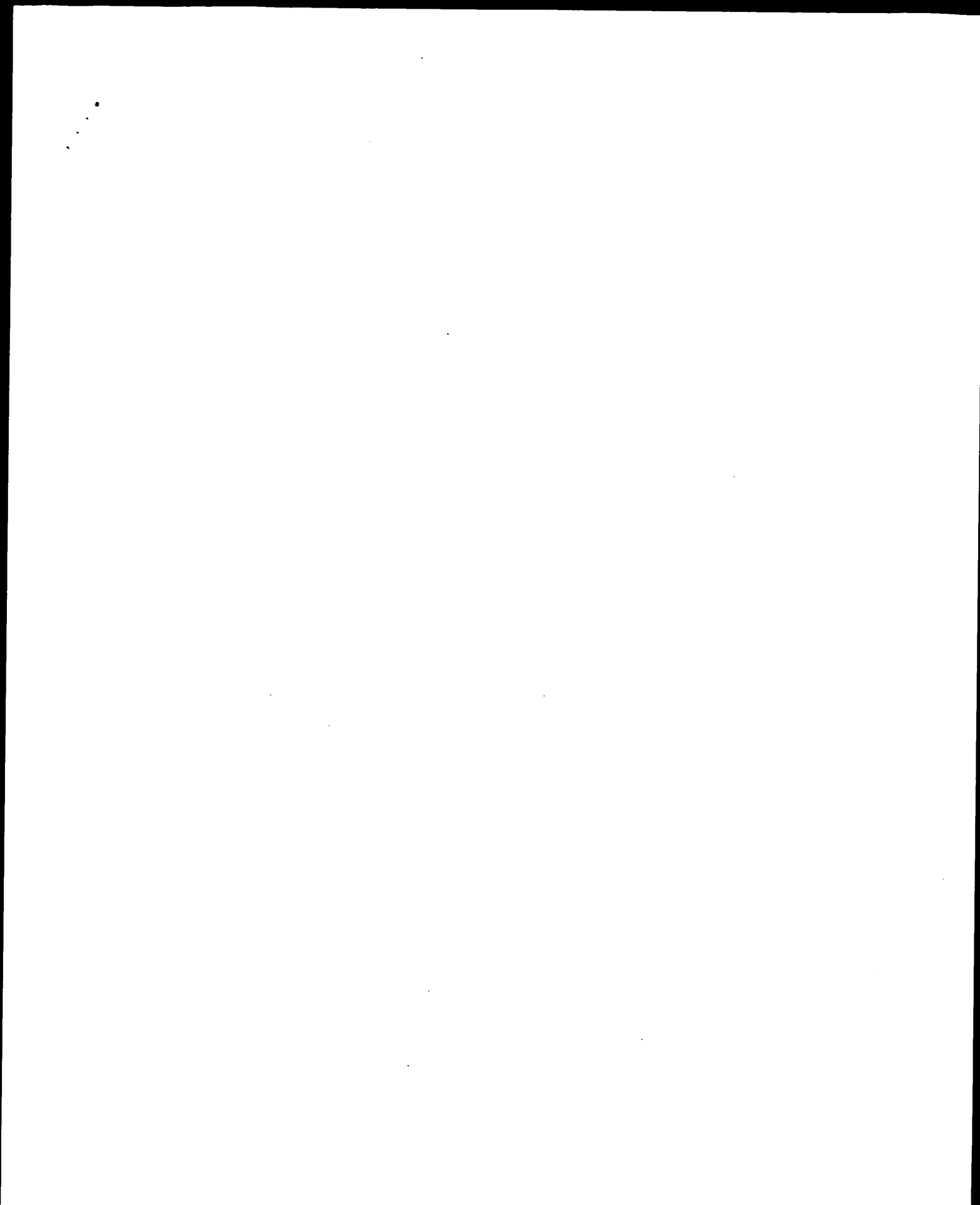
US-10-061-119-4
; Sequence 4, Application US/10061119
; Publication No. US20030008031A1
GENERAL INFORMATION:
APPLICANT: Sklar, Pamela
APPLICANT: Lander, Eric S.
APPLICANT: Schwab, Sibylle
APPLICANT: Wildenauer, Dieter
TITLE OF INVENTION: Association Between Schizophrenia and a
TITLE OF INVENTION: Two-Marker Haplotype Near P11B Gene
FILE REFERENCE: 2825-2027-001
CURRENT APPLICATION NUMBER: US/10/061,119
CURRENT FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 60/265,910
PRIOR FILING DATE: 2001-02-02
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 25377
TYPE: DNA
ORGANISM: Homo sapiens
US-10-061-119-4

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Query Match	4.6%;	Score 36;	DB 9;	Length 25377;
Best Local Similarity	49.5%;	Pred. No. 20;		
Matches 93; Conservative		0; Mismatches	95; Indels	0; Gaps

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Db	6816	TGGAGCTTGAATTTTAATTAAGGTCACACATGGTTTAACTTGGGACAGTCCCTCTTT	6875
Qy	98	TCACCCAATGATTGATCTGTGCTTTTGGCTGTATCTTCATTAAGAGATGTGATPAG	157
Db	6876	TCATATATTTTCCCTCAATTTTCATTATGATTTTTTTCTTCATGAGCACTGATGAAT	6938
Qy	158	TCGAAGAGAGATTAACCTTCATGAATTTGTTCATTAATAAAGCTAAAGATGAC	217
Db	6936	GTTTTTCAGCAGGAAAACCTTACTGTGATGTGTCTCTTCCAGAGCATCATCAGAA	6995
Qy	218	ACAAAGA 225	
Db	6996	ACACAGGA 7003	

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Job time : 212.054 BECS



GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: March 8, 2003, 21:49:58 ; Search time 33.5164 Seconds
(without alignments)
7164.491 Million cell updates/sec

Title: US-08-982-272-2

Perfect score: 783

Sequence: 1 ATGATAGAAACATACAGCCA.....TTGGCTTACTCAAACTCTGA 783

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	783	100.0	818	1	US-08-431-055-1
2	783	100.0	818	4	US-08-858-197-1
3	781.4	99.8	783	1	US-08-446-922-5
4	781.4	99.8	783	2	US-08-249-189-1
5	781.4	99.8	783	2	US-08-484-624A-1
6	781.4	99.8	783	2	US-08-477-733B-1
7	781.4	99.8	783	3	US-08-088-913A-1
8	781.4	99.8	783	4	US-08-769-819-1
9	781.4	99.8	783	4	US-08-770-974-1
10	781.4	99.8	783	4	US-08-770-974-1
11	781.4	99.8	783	4	US-09-399-106-1
12	781.4	99.8	783	5	PCT-US93-10034-5
13	781.4	99.8	783	2	US-08-249-189-22
14	781.4	99.8	783	2	US-08-484-624A-22
15	781.4	99.8	783	2	US-08-477-733B-22
16	781.4	99.8	783	3	US-09-088-913A-22
17	781.4	99.8	783	4	US-08-769-819-22
18	781.4	99.8	783	4	US-08-770-974-22
19	781.4	99.8	783	4	US-08-770-974-22
20	781.4	99.8	783	4	US-09-399-106-22
21	781.4	99.8	783	4	US-08-446-922-3
22	781.4	99.8	783	5	PCT-US93-10034-3
23	781.4	99.8	783	1	US-07-940-605A-1
24	781.4	99.8	783	1	US-08-184-422-7
25	781.4	99.8	783	1	US-08-360-923A-1
26	781.4	99.8	783	1	US-08-431-055-3
27	781.4	99.8	783	2	US-08-690-096-1

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29	560.4	71.6	840	2	US-08-484-624A-11	Sequence 11, Appl
30	560.4	71.6	840	2	US-08-477-733B-11	Sequence 11, Appl
31	560.4	71.6	840	3	US-08-763-995-1	Sequence 11, Appl
32	560.4	71.6	840	3	US-09-088-913A-11	Sequence 11, Appl
33	560.4	71.6	840	3	US-08-589-771B-7	Sequence 11, Appl
34	560.4	71.6	840	4	US-08-769-819-11	Sequence 11, Appl
35	560.4	71.6	840	4	US-08-770-974-11	Sequence 11, Appl
36	560.4	71.6	840	4	US-08-858-197-3	Sequence 11, Appl
37	560.4	71.6	840	4	US-08-770-981-11	Sequence 11, Appl
38	560.4	71.6	840	4	US-09-399-106-11	Sequence 11, Appl
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40	446.2	57.0	1425	2	US-08-484-624A-15	Sequence 15, Appl
41	446.2	57.0	1425	2	US-08-477-733B-15	Sequence 15, Appl
42	446.2	57.0	1425	3	US-09-088-913A-15	Sequence 15, Appl
43	446.2	57.0	1425	4	US-08-769-819-15	Sequence 15, Appl
44	446.2	57.0	1425	4	US-08-770-974-15	Sequence 15, Appl
45	446.2	57.0	1425	4	US-08-770-981-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-08-431-055-1
Sequence 1, Application US/08431055
Patent No. 5817516
GENERAL INFORMATION:
APPLICANT: KEHRY, MERILYN R
APPLICANT: CASTLE, BRIAN E
TITLE OF INVENTION: METHODS FOR PROLIFERATING AND
TITLE OF INVENTION: DIFFERENTIATING B CELLS, AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
STREET: 100 NEW YORK AVE. N.W. SUITE 600
CITY: WASHINGTON
STATE: D.C.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,055
FILING DATE: 28-Apr-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: US 08/234,580
FILING DATE: 28-Apr-1994
ATTORNEY/AGENT INFORMATION:
NAME: MILLMAN, ROBERT A
REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 1011.1030000/RAM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 818 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 13..795
US-08-431-055-1
Query Match 100.0%; Score 783; DB 1; Length 818;
Best Local Similarity 100.0%; Pred. No. 2.8e-224;
Matches 783; Conservative 0; Mismatches 0; Indels 0;

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Db	73	ATGAAAGATTTTATATGATTTTACTTACTGTTTTCTTATCAACCAATGATTTGATCTGTG	13
QY	121	CTTTTCTGTGATCTTATAGAAAGTTGATAGATAGCAAGAGAAAGTAACTTCACT	18
Db	133	CTTTTCTGTGATCTTATAGAAAGTTGATAGATAGCAAGAGAAAGTAACTTCACT	19
QY	161	GAAATTTTGTATCTATATAAAAAGCTTAAAGATGCAACAAAGAAAGATCTTTATCC	24
Db	193	GAAATTTTGTATCTATATAAAAAGCTTAAAGATGCAACAAAGAAAGATCTTTATCC	25
QY	241	TTTCTGACCTGTAGAGAGATATAGAGCAATTTGAAACCTTGTCAGAAATATACGTTA	30
Db	253	TTTCTGACCTGTAGAGAGATATAGAGCAATTTGAAACCTTGTCAGAAATATACGTTA	31
QY	301	AACAAAGAAAGAAAAAAGAAACAGCTTGAATATGCAAAAGGTGATGAGATCTCTCA	36
Db	313	AACAAAGAAAGAAAAAAGAAACAGCTTGAATATGCAAAAGGTGATGAGATCTCTCA	37
QY	361	ATTGCAACACAGTTGTAGAGAGCAACAGTATATGCAAGATCCGTTCTACAGTGGGC	42
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QY	421	AAGAAAGATATTTATACATGAAAGCAACTTGGTAAATGCTTGAATAATGAGAAACAGCTG	48
Db	433	AAGAAAGATATTTATACATGAAAGCAACTTGGTAAATGCTTGAATAATGAGAAACAGCTG	49
QY	481	ACGGTTAAAGAGAGAGACTCTTTATGCTACACTCAAGTACCTCTGCTTAATGG	54
Db	493	ACGGTTAAAGAGAGAGACTCTTTATGCTACACTCAAGTACCTCTGCTTAATGG	55
QY	541	GACCTTCAAGTCAACGCCCATTCATCGTGGGCTCTGGCTGAAGCCCAATTTGATCT	60
Db	553	GACCTTCAAGTCAACGCCCATTCATCGTGGGCTCTGGCTGAAGCCCAATTTGATCT	61
QY	601	GAGAGATCTTACTCAAGGCGGCAATATCCCAAGTTCCTCCAGCTTTCGAGAGAG	66
Db	613	GAGAGATCTTACTCAAGGCGGCAATATCCCAAGTTCCTCCAGCTTTCGAGAGAG	67
QY	661	TCTGTTCACTTGGCGGAGTGTTTAATTAATCAAGCTGGGCTTCTGTTTTCACAGTG	72
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QY	721	ACTGAAGCAACCAAGTATCCACAGATTTGGCTGTCACTTTTGGCTTACTCAAACTC	78
Db	733	ACTGAAGCAACCAAGTATCCACAGATTTGGCTGTCACTTTTGGCTTACTCAAACTC	79
QY	781	TGA 783	
Db	793	TGA 795	

RESULT 2
US-08-858-197-1
Sequence 1, Application US/08858197
Patent No. 6297052
GENERAL INFORMATION:
APPLICANT: KEHRY, MERILYN R.
APPLICANT: CASTLE, BRIAN E.
TITLE OF INVENTION: METHODS FOR PROLIFERATING AND
TITLE OF INVENTION: DIFFERENTIATING B CELLS, AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
STREET: 100 NEW YORK AVE. N.W. SUITE 600
CITY: WASHINGTON
STATE: D.C.

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1 ZIP: 20005
2 COMPUTER READABLE FORM:
3 MEDIUM TYPE: Floppy disk
4 COMPUTER: IBM PC compatible
5 OPERATING SYSTEM: PC-DOS/MS-DOS
6 SOFTWARE: Patent Release #1.0, Version #1.25
7 CURRENT APPLICATION DATA:
8 APPLICATION NUMBER: US/08/858,197
9 FILING DATE:
10 CLASSIFICATION:
11 PRIOR APPLICATION DATA:
12 APPLICATION NUMBER: US/08/234,580
13 FILING DATE: 28-APR-1994
14 ATTORNEY/AGENT INFORMATION:
15 NAME: MILLMAN, ROBERT A
16 REGISTRATION NUMBER: 36,217
17 REFERENCE/DOCKET NUMBER: 1011.1030000/RAM
18 TELECOMMUNICATION INFORMATION:
19 TELEPHONE: (202)371-2600
20 TELEFAX: (202)371-2540
21 INFORMATION FOR SEQ. ID NO.: 1:
22 SEQUENCE CHARACTERISTICS:
23 LENGTH: 818 base pairs
24 TYPE: nucleic acid
25 STRANDEDNESS: both
26 TOPOLOGY: linear
27 MOLECULE TYPE: DNA
28 FEATURE:
29 NAME/KEY: CDS
30 LOCATION: 13..795
31 US-08-858-197-1
32
33 Query Match 100.0%; Score 783; DB 4; Length 818;
34 Best Local Similarity 100.0%; Pred. No. 2,8e-224;
35 Matches 783; Conservative 0; Mismatches 0; Indels 0; Gaps 0
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41 121 CTTTTCGCTGATCTTCATATAGAGATTTGATAGTGGAAAGAGAACTTTCAT 180
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43 181 GAAGATTTTGATCATATAAAAAGCTTAAGAGATGCAACAAAGAGAGATCTTTATCC 240
44 193 GAAGATTTTGATCATATAAAAAGCTTAAGAGATGCAACAAAGAGAGATCTTTATCC 252
45 241 TTGCTGAAGCTGAGAGAGATGAGAGGCAATTTGAAGACCTTGCAAGATTTAAAGCTTA 300
46 253 TTGCTGAAGCTGAGAGATGAGAGGCAATTTGAAGACCTTGCAAGATTTAAAGCTTA 312
47 301 AACCAAGAGAGAAAAAGAAAACAGCTTTGAATCAAGAGAGTATGAGATCTTCAA 360
48 313 AACCAAGAGAGAAAAAGAAAACAGCTTTGAATCAAGAGAGTATGAGATCTTCAA 372
49 361 ATTGCAGACAGGTGTATACGCAAGCAACGATATGCGAGATCCGTTCTAAGTGGGCC 420
50 373 ATTGCAGACAGGTGTATACGCAAGCAACGATATGCGAGATCCGTTCTAAGTGGGCC 432
51 421 AAGAAAGATTTATACCATGAAAAGCACTTGGTATGCTTGAATAAGGAAAACAGCTG 480
52 433 AAGAAAGATTTATACCATGAAAAGCAACGATATGCGAGATCCGTTCTAAGTGGGCC 492
53 481 ACGGTTAAAGAGAGAGCTCTATATATGTCTAATCACTCAAGTCACTTTCGCTTAATCG 540
54 493 ACGGTTAAAGAGAGAGCTCTATATATGTCTAATCACTCAAGTCACTTTCGCTTAATCG 552
55 541 GAGCTTCAAGTCAAGCCCAATCAATGCTGAGCCTTGGCTGAAGCCCAATGATGATCT 600

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Db 553 GAGCTTGAAGTCAAGCCGATTCAGTGGGCTCTGCTGAGAGCCGAGCATTTGATTT 612
Qy 601 GAGAGATCTTACTCAAGGGGCAATATCCAGTTCCTCCAGCTTTGGAGCAGCG 660
Db 613 GAGAGATCTTACTCAAGGGGCAATATCCAGTTCCTCCAGCTTTGGAGCAGCG 672
Qy 661 TCGTTCACTTGGGGGAGTGTGAATTAAGAGCTGGGCTTCTGAGTTCAGAGTG 720
Db 673 TCGTTCACTTGGGGGAGTGTGAATTAAGAGCTGGGCTTCTGAGTTCAGAGTG 732
Qy 721 ACTGAAGCAAGCCAGATGATCCAGAGTGGCTTCTCATCTTTGGCTTACGAACTC 780
Db 733 ACTGAAGCAAGCCAGATGATCCAGAGTGGCTTCTCATCTTTGGCTTACGAACTC 792
Qy 781 TGA 783
Db 793 TGA 795

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RESULT 3
US-08-446-922-5
; Sequence 5, Application US/08446922
; Patent No. 5716805
; GENERAL INFORMATION:
; APPLICANT: Spriggs, Melanie
; APPLICANT: Srinivasan, Subhashini
; TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.1
; SOFTWARE: Microsoft Word for Apple, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,922
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US98 08/107,353
; FILING DATE: 08-13-93
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 1003-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 783 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Mouse
; STRAIN: CD40-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..780
; US-08-446-922-5

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Query Match 99.8%; Score 781.4; DB 1; Length 783;
Best Local Similarity 99.9%; Pred. No. 8,28-224;
Matches 782; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGATGAAACATPACAGCCAACTTCCCGAGATCCGTGCAACTGACCTTCCAGCAGC 60
Db 1 ATGATGAAACATPACAGCCAACTTCCCGAGATCCGTGCAACTGACCTTCCAGCAGC 60
Qy 61 ATGAAAGTTTATGATTTTACTTACTGTTTCTTATCAACCAATGATGATCTGTG 120
Db 61 ATGAAAGTTTATGATTTTACTTACTGTTTCTTATCAACCAATGATGATCTGTG 120
Qy 121 CTTTTCCTGTATCTTCATPAGAAAGTTGATAGCTGCAAGAGAAATGAACTTAT 180
Db 121 CTTTTCCTGTATCTTCATPAGAAAGTTGATAGCTGCAAGAGAAATGAACTTAT 180
Qy 181 GAAATTTTGTATTTCAATAAAGCTAAAGATGCAACAAGAGAGATCTTATCC 240
Db 181 GAAATTTTGTATTTCAATAAAGCTAAAGATGCAACAAGAGAGATCTTATCC 240
Qy 241 TTGCTGAACCTGTGAGAGATGAGAGCAATTTGAAGCTTTGCAAGATATACGTTA 300
Db 241 TTGCTGAACCTGTGAGAGATGAGAGCAATTTGAAGCTTTGCAAGATATACGTTA 300
Qy 301 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Db 301 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Qy 361 ATTCAGACACCTGTGTAAGCAAGCCAAAGTAAGCAAGCAAGCAAGCAAGCAAG 420
Db 361 ATTCAGACACCTGTGTAAGCAAGCCAAAGTAAGCAAGCAAGCAAGCAAGCAAG 420
Qy 421 AAGAAAGATATATATACATGAAAGCACTGTGATGCTTGAATGGAATGGAAGAC 480
Db 421 AAGAAAGATATATATACATGAAAGCACTGTGATGCTTGAATGGAATGGAAGAC 480
Qy 481 AGCGTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Db 481 AGCGTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Qy 541 GAGCCTTCAGTCAAGCCCATTCATGCTGCGGCTCTGCTGAAGCCAGCATGATCT 600
Db 541 GAGCCTTCAGTCAAGCCCATTCATGCTGCGGCTCTGCTGAAGCCAGCATGATCT 600
Qy 601 GAGAGATCTTACTCAAGGGGCAATATCCAGTTCCTCCAGCTTTGGAGCAGCG 660
Db 601 GAGAGATCTTACTCAAGGGGCAATATCCAGTTCCTCCAGCTTTGGAGCAGCG 660
Qy 661 TCGTTCACTTGGGGGAGTGTGAATTAAGAGCTGGCTTCTGTGTTGCAAGTG 720
Db 661 TCGTTCACTTGGGGGAGTGTGAATTAAGAGCTGGCTTCTGTGTTGCAAGTG 720
Qy 721 ACTGAAGCAAGCCAGATGATCCAGAGATGGGCTTCATCTTTGGCTTACGAACTC 780
Db 721 ACTGAAGCAAGCCAGATGATCCAGAGATGGGCTTCATCTTTGGCTTACGAACTC 780
Qy 781 TGA 783
Db 781 TGA 783

RESULT 4
US-08-249-189-1
; Sequence 1, Application US/08249189
; Patent No. 5961974
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: FANSLAW, WILLIAM
; APPLICANT: SPRIGGS, MELANIE
; APPLICANT: SRINIVASAN, SUBHASHINI
; APPLICANT: GIBSON, MARYLOU
; TITLE OF INVENTION: NOVEL CYTOKINE

```

```

NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSER: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.1
SOFTWARE: Microsoft Word for Apple, version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/249,189
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,703
FILING DATE: October 23, 1992
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/805,723
FILING DATE: December 5, 1991
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/783,707
FILING DATE: October 25, 1991
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET INFORMATION: 2802-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 783 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: MOUSE
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 1..783
US-08-249-189-1

Query Match 99.8%; Score 781.4; DB 2; Length 783;
Best Local Similarity 99.9%; Pred. No. 8,2e-224;
Matches 782; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

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QY 241 TTGCTGAAGTGTGAGAGATGAGAGGCAATTTGAAGACTTGTCAAGATATAACGTTA 300
DB 241 TTGCTGAAGTGTGAGAGATGAGAGGCAATTTGAAGACTTGTCAAGATATAACGTTA 300
QY 301 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
DB 301 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
QY 361 ATTGACACACAGCTGTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 361 ATTGACACACAGCTGTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
QY 421 AAGAAAGATATATATACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
DB 421 AAGAAAGATATATATACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
QY 481 ACGGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
DB 481 ACGGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
QY 541 GAGCTTCAGATCAAGCCCATTCATGTCGAGCTCTGAGTGAAGCCAGAGAGAGAGAGAG 600
DB 541 GAGCTTCAGATCAAGCCCATTCATGTCGAGCTCTGAGTGAAGCCAGAGAGAGAGAGAG 600
QY 601 GAGGAAATCTTACTCAAGGCGGCAATACCCAGATTCCTCCAGCTTTGGAGAGAGAG 660
DB 601 GAGGAAATCTTACTCAAGGCGGCAATACCCAGATTCCTCCAGCTTTGGAGAGAGAGAG 660
QY 661 TCTGTTCACTTGGGCGGAGTGTGTAATTACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
DB 661 TCTGTTCACTTGGGCGGAGTGTGTAATTACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY 721 ACTAAGCAAGCAAGAGATGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
DB 721 ACTAAGCAAGCAAGAGATGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
QY 781 TGA 783
DB 781 TGA 783

RESULT 5
US-08-484-624A-1
Sequence 1, Application US/08484624A
Patent No. 5962406
GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: FANSLAW, WILLIAM
APPLICANT: SPRIGGS, MELANIE
APPLICANT: SRINIVASAN, SUBHASHINI
APPLICANT: GIBSON, MARYLOU
APPLICANT: MORRIS, ARVIA E.
APPLICANT: MCGREW, JEFFERY
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSER: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,624A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:

```

APPLICATION NUMBER: 08/477,733
 FILING DATE: June 07, 1995
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/969,703
 FILING DATE: October 23, 1992
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/805,723
 FILING DATE: December 5, 1991
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/783,707
 FILING DATE: October 25, 1991
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Perkins, Patricia A.
 REGISTRATION NUMBER: 34,693
 REFERENCE/DOCKET NUMBER: 2802-D
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 2065870430
 TELEFAX: 2065870606
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 783 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHEICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: MOUSE
 IMMEDIATE SOURCE:
 CLONE: CD40-L
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..783
 US-08-484-624A-1

Query Match 99.8%; Score 781.4; DB 2; Length 783;
 Best Local Similarity 99.8%; Pred. No. 8.2e-224;
 Matches 782; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGATGAAACATACAGCCAACTTCCCAAGATCCGTGCAACTGACCTTCACGCAAC 60
 DB 1 ATGATGAAACATACAGCCAACTTCCCAAGATCCGTGCAACTGACCTTCACGCAAC 60

QY 61 ATGAGATTTTATATATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 120
 DB 61 ATGAGATTTTATATATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 120

QY 121 CTCTTCTGCTGTATCTTATGAAAGATTTGATAGTGTGAAAGAGATTAACCTTCAT 180
 DB 121 CTCTTCTGCTGTATCTTATGAAAGATTTGATAGTGTGAAAGAGATTAACCTTCAT 180

QY 181 GAAGATTTTGTATCTTATGAAAGATTTGATAGTGTGAAAGAGATTAACCTTCAT 240
 DB 181 GAAGATTTTGTATCTTATGAAAGATTTGATAGTGTGAAAGAGATTAACCTTCAT 240

QY 241 TTGCTGAACCTGTAGAGATTAAGAGCAATTTGAAGACCTTGTCAAGATTAACCTTCA 300
 DB 241 TTGCTGAACCTGTAGAGATTAAGAGCAATTTGAAGACCTTGTCAAGATTAACCTTCA 300

QY 301 AACAAAG 360
 DB 301 AACAAAG 360

QY 361 ATTGAGACACAGCTGTGTAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 420
 DB 361 ATTGAGACACAGCTGTGTAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 420

QY 421 AAGAAAGATTTATATCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480

DB 421 AAGAAAGATTTATATCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480

QY 481 ACGGTTAAAG 540

DB 481 ACGGTTAAAG 540

QY 541 GAGCCTTGAGTCAAGCCATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600

DB 541 GAGCCTTGAGTCAAGCCATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600

QY 601 GAGGATTTTATATCAAGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660

DB 601 GAGGATTTTATATCAAGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660

QY 661 TCTGTTCACTTGGGCGAG 720

DB 661 TCTGTTCACTTGGGCGAG 720

QY 721 ACTGAG 780

DB 721 ACTGAG 780

QY 781 TGA 783

DB 781 TGA 783

RESULT 6
 US-08-477-733B-1
 Sequence 1, Application US/08477733B
 Patent No. 5981724
 GENERAL INFORMATION:
 APPLICANT: ARMITAGE, RICHARD
 APPLICANT: FANSLAW, WILLIAM
 APPLICANT: SPRIGGS, MELANIE
 APPLICANT: SRINIVASAN, SUBHASHINI
 APPLICANT: GIBSON, MARYLOU
 APPLICANT: MORRIS, ARVIA B.
 APPLICANT: MCGREW, JEFFERY
 TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: IMMUNEX CORPORATION
 STREET: 51 UNIVERSITY STREET
 CITY: SEATTLE
 STATE: WASHINGTON
 COUNTRY: USA
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: Apple Operating System 7.5.5
 SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1
 CURRENT APPLICATION DATA:
 FILING DATE: June 07, 1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/249,189
 FILING DATE: May 24, 1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/969,703
 FILING DATE: October 23, 1992
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/805,723
 FILING DATE: December 5, 1991
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/783,707
 FILING DATE: October 25, 1991

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 783 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: MOUSE
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 1..783
US-08-477-733B-1

Query Match 99.8%; Score 781.4; DB 2; Length 783;
Best Local Similarity 99.9%; Pred. No. 8.2e-224;
Matches 782; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGATGAAACATTCACCCCACTTCCCGATCGGTGGCACTGACCTTCCAGGAGC 60
Db 1 ATGATGAAACATTCACCCCACTTCCCGATCGGTGGCACTGACCTTCCAGGAGC 60

Qy 61 ATGAGATTTTATGATTTACTTCTGTTTCTTATCACCACCAATGATGATCGTG 120
Db 61 ATGAGATTTTATGATTTACTTCTGTTTCTTATCACCACCAATGATGATCGTG 120

Qy 121 CTTTGTGCTGATCTCTGATGAAGATGATGATGATGATGATGATGATGATGAT 180
Db 121 CTTTGTGCTGATCTCTGATGAAGATGATGATGATGATGATGATGATGATGAT 180

Qy 181 GAAATTTTGTATCTATTAAGGCTTAAGATGCAAGAGGATGATGATGATGAT 240
Db 181 GAAATTTTGTATCTATTAAGGCTTAAGATGCAAGAGGATGATGATGATGAT 240

Qy 241 TTGCTGAACGTGAGAGATGAGAGATGAGATGAGATGAGATGAGATGAGATG 300
Db 241 TTGCTGAACGTGAGAGATGAGAGATGAGATGAGATGAGATGAGATGAGATG 300

Qy 301 AACAAAG 360
Db 301 AACAAAG 360

Qy 361 ATTGAGACACGCTGTAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Db 361 ATTGAGACACGCTGTAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420

Qy 421 AAGAAAGATATTAATCATGAAAGCACTTGATGCTTGAATGGAATGGAACAG 480
Db 421 AAGAAAGATATTAATCATGAAAGCACTTGATGCTTGAATGGAATGGAACAG 480

Qy 481 ACGTTAAAG 540
Db 481 ACGTTAAAG 540

Qy 541 GAGCTTGAAGTCAAGCCATTCATGCTGAGGCTTGGCTGAAGCCAGCATGATCT 600
Db 541 GAGCTTGAAGTCAAGCCATTCATGCTGAGGCTTGGCTGAAGCCAGCATGATCT 600

Qy 601 GAGAGATCTTACTCAAGGCGGCAATATCCAGATGCTCCAGCTTTGCGAGAGAG 660
Db 601 GAGAGATCTTACTCAAGGCGGCAATATCCAGATGCTCCAGCTTTGCGAGAGAG 660

Qy 661 TCTGTTCACTTGGCGGAGAGTGTGAATTAAGAGTGTGCTCTGTTGTCAACGTG 720
Db 661 TCTGTTCACTTGGCGGAGAGTGTGAATTAAGAGTGTGCTCTGTTGTCAACGTG 720

Qy 721 ACTGAAG 780
Db 721 ACTGAAG 780

Qy 781 TGA 783
Db 781 TGA 783

RESULT 7
US-09-088-913A-1
Sequence 1, Application US/09088913A
Patent No. 6087329
GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: FANLOW, WILLIAM
APPLICANT: SPRIGGS, MELANIE
APPLICANT: SRINIVASAN, SUBHASHINI
APPLICANT: GIBSON, MARYLOU
APPLICANT: MORRIS, ARVIA E.
APPLICANT: MCGREW, JEFFERY
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/088,913A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484,624
FILING DATE:
APPLICATION NUMBER: 08/477,733
FILING DATE: June 07, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,703
FILING DATE: October 23, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/805,723
FILING DATE: December 5, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/783,707
FILING DATE: October 25, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 783 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO

Qy	61	ATGAGATTTTATGATTTACTCTATCTCTTTCTTATACCAAAAGATGGATCTGTG	1200
Db	61	ATGAGATTTTATGATTTACTCTATCTCTTTCTTATACCAAAAGATGGATCTGTG	1200
Qy	121	CTTTTTCCTGTGATCTTCACTGAAGATTGGATPAAGTCGAAGGAAGTAAACCTTCAT	1800
Db	121	CTTTTTCCTGTGATCTTCACTGAAGATTGGATPAAGTCGAAGGAAGTAAACCTTCAT	1800
Qy	181	GAGATTTTGTATTCATTAATAAAGCTAAAGAGATGCAAAAGGAGAGGATCTTTATCC	2400
Db	181	GAGATTTTGTATTCATTAATAAAGCTAAAGAGATGCAAAAGGAGAGGATCTTTATCC	2400
Qy	241	TTCCTGAACCTGTGAAGATGGAAGGCAATTTGAAGACTTTGTCAAGATATAAGTTA	3000
Db	241	TTCCTGAACCTGTGAAGATGGAAGGCAATTTGAAGACTTTGTCAAGATATAAGTTA	3000
Qy	301	AACAAAGAAGAGAAAAAAGAAAAGCTTTGGAATGCAAAAGGATGATGAGATCCTAA	3600
Db	301	AACAAAGAAGAGAAAAAAGAAAAGCTTTGGAATGCAAAAGGATGATGAGATCCTAA	3600
Qy	361	ATTGCAGACAACGTTGTAAGCGAAGCCAAACAGTAATGCGATCCGTTCTAACGTGGCC	4200
Db	361	ATTGCAGACAACGTTGTAAGCGAAGCCAAACAGTAATGCGATCCGTTCTAACGTGGCC	4200
Qy	421	AAGAAAGAATTTATACATGAAAGCAACMTGATATGCTTGAATAATGGGAAACAGCTG	4800
Db	421	AAGAAAGAATTTATACATGAAAGCAACMTGATATGCTTGAATAATGGGAAACAGCTG	4800
Qy	481	ACGGTTAAAAAGAGAGGACTCTATATATGTCTAACCTCAAGTCAACCTTGCTCTATCCG	5400
Db	481	ACGGTTAAAAAGAGAGGACTCTATATATGTCTAACCTCAAGTCAACCTTGCTCTATCCG	5400
Qy	541	GAGCCTTGAATCAAGGCCATTCACTGCTGGGCTCTGGCTGAAGCCCAATGGATCT	6000
Db	541	GAGCCTTGAATCAAGGCCATTCACTGCTGGGCTCTGGCTGAAGCCCAATGGATCT	6000
Qy	601	GAGAGAAATCTTACTCAAGCGGCAATTAACCAAGTTCTCTCCAGCTTTGCGAGACGAG	6600
Db	601	GAGAGAAATCTTACTCAAGCGGCAATTAACCAAGTTCTCTCCAGCTTTGCGAGACGAG	6600
Qy	661	TCTGTTCACTTGGGCGGAGATGTTGAATTAACAAGCTGGGTCTGTGTTTGTCAAGCTG	7200
Db	661	TCTGTTCACTTGGGCGGAGATGTTGAATTAACAAGCTGGGTCTGTGTTTGTCAAGCTG	7200
Qy	721	ACTGAAGCAACCCAGATGATCCACAGATTTGGCTTCTCATCTTTTGGCTTACTCAATCC	7800
Db	721	ACTGAAGCAACCCAGATGATCCACAGATTTGGCTTCTCATCTTTTGGCTTACTCAATCC	7800
Qy	781	TGA 783	
Db	781	TGA 783	

RESULT 9
 US-08-770-974-1
 : Sequence 1, Application US/08770974
 : Patent No. 630972
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: ARMITAGE, RICHARD
 : APPLICANT: FANSLAW, WILLIAM
 : APPLICANT: SPRIGGS, MELANIE
 : APPLICANT: SRINIVASAN, SUBHASHINI
 : APPLICANT: GIBSON, MARYLOU
 :
 : TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
 :
 : NUMBER OF SEQUENCES: 24
 :
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: IMMUNEX CORPORATION
 : STREET: 51 UNIVERSITY STREET
 : CITY: SEATTLE
 : STATE: WASHINGTON
 : COUNTRY: USA
 :
 : ZIP: 98101
 :
 : COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: Apple Operating System 7.1
 SOFTWARE: Microsoft Word for Apple, version 5.1a
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/770,974
 FILING DATE: 20-DEC-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/477,733
 FILING DATE: 02-AUG-1995
 APPLICATION NUMBER: 08/249,189
 FILING DATE: May 24, 1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/969,703
 FILING DATE: October 23, 1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/805,723
 FILING DATE: December 5, 1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/783,707
 FILING DATE: October 25, 1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Perkins, Patricia A.
 REGISTRATION NUMBER: 34,693
 REFERENCE/DOCKET NUMBER: 2802-D
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 2065870430
 TELEFAX: 2065870606
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 783 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: MOUSE
 IMMEDIATE SOURCE:
 CLONE: CD40-L
 FEATURES:
 NAME/KEY: CDS
 LOCATION: 1..783

	Query Match	99.8%;	Score 781.4;	DB 4;	Length 783;
	Best Local Similarity	99.9%;	Pred. No. 8,2e-224;		
	Matches 782;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	1 ATGATAGAAACATCAACGCCACTTCCCGCAGATCCGTGGCAACTGAGCTTCACAGAGC	60			
Db	1 ATGTATGAACAACATCACCCAACCTTCCCCCAGATCCGTGCACATGGACTTCCACACAGC	60			
Qy	61 ATGAAGAATTTTAATGATATTACATCTACTCTTTCTTACTACACCACAAATGATATGACGTG	120			
Db	61 ATGAAGAATTTTAATGATATTACTACTCTTTCTTATDCCCACAAATGATGGATCTGTG	120			
Qy	121 CTTTTGCTGTGTATCTTCATAGAAGATTGGATTAAGTCGAAAGAGNAGTAACCTTCAT	180			
Db	121 CTTTTGCTGTGTATCTTCATAGAGATTGGATTAAGTCGAAAGAGNAGTAACCTTCAT	180			
Qy	181 GAAATTTTGATATCATAAAAAGCTAAAGAGATGCACAAAGAGAGAGATCTTATCC	240			
Db	181 GAAGATTTTGATATCATMAAAAAGCTAAAGAGATGCACAAAGAGAGAGATCTTATCC	240			
Qy	241 TTGCTGAACGTGAGAGAGATGAGAAGCAATTTGAAGACCTTGTCAAAGATATAAGCTTA	300			
Db	241 TTGCTGAACGTGAGAGAGATGAGAAGCAATTTGAAGACCTTGTCAAAGATATAAGCTTA	300			
Qy	301 AACAAAGAGAGAAAAAGAAAAACGCTTTGAATGCAAAGAGGTGATGAGATCTTCAA	360			

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Prior Application Data:	
Application Number: 07/805,723	
Filing Date: December 5, 1991	
Classification: 435	
Prior Application Data:	
Application Number: 07/783,707	
Filing Date: October 25, 1991	
Classification: 435	
Attorney/Agent Information:	
Name: Perkins, Patricia A.	
Registration Number: 34,693	
Reference/Docket Number: 2802-D	
Telecommunication Information:	
Telephone: 2065870430	
Telefax: 2065870606	
Information for SEQ ID NO: 1:	
Sequence Characteristics:	
Length: 783 base pairs	
Type: nucleic acid	
Strandedness: single	
Topology: linear	
Molecule Type: cDNA	
Hypothetical: NO	
Anti-Sense: NO	
Original Source:	
Organism: MOUSE	
Immediate Source:	
Clone: CD40-L	
Feature:	
Name/Key: CDS	
Location: 1..783	
US-08-770-981-1	
Query Match	99.8%; Score 781.4; DB 4; Length 783;
Best Local Similarity	99.9%; Pred. No. 8.2e-224;
Matches 782; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Oy	1 ATGATAGAAACCTACAGCCACTTCCCCCGATCGGTGGCACTGCATTCACAGCAGC 60
Ds	1 ATGATAGAAACCTACAGCCACTTCCCCCGATCGGTGGCACTGCATTCACAGCAGC 60
Oy	61 ATGAAGATTTTTAAGTATTTACTACTGTTTTCTTATCACCCAATGATGGATCTGTG 120
Ds	61 ATGAAGATTTTTAAGTATTTACTACTGTTTTCTTATCACCCAATGATGGATCTGTG 120
Oy	121 CTTTTCCTGTGTATCTTCATAGAGATTGGATTAAGTGCAAGAGAACTTCAT 180
Ds	121 CTTTTCCTGTGTATCTTCATAGAGATTGGATTAAGTGCAAGAGAACTTCAT 180
Oy	181 GAAATTTTGATTCATPAAAAAAGCTAAAGATGCACAAAGAGAGAGATCTTATCC 240
Ds	181 GAAATTTTGATTCATPAAAAAAGCTAAAGATGCACAAAGAGAGAGATCTTATCC 240
Oy	241 TTGCTGACTGTGAGAGATGAGAAGCAATTGTAAGACTTGTCAGATAATACGTTA 300
Ds	241 TTGCTGACTGTGAGAGATGAGAAGCAATTGTAAGACTTGTCAGATAATACGTTA 300
Oy	301 AACCAAGAGAAAAGAAAAGAAAACGCTTTGAATCAAGAGTGATGAGATCTCTCA 360
Ds	301 AACCAAGAGAAAAGAAAAGAAAACGCTTTGAATCAAGAGTGATGAGATCTCTCA 360
Oy	361 ATTGCAGACAAGCTGTGTAAGCGAAGCAAGTAGATGAGCATCCGTTCTACAGTGGCC 420
Ds	361 ATTGCAGACAAGCTGTGTAAGCGAAGCAAGTAGATGAGCATCCGTTCTACAGTGGCC 420
Oy	421 AAGAAAGAGATTTATCAATGAAAAGCACTGGTAAATGCTTGAATAATGGAAAACAGCTG 480
Ds	421 AAGAAAGAGATTTATCAATGAAAAGCACTGGTAAATGCTTGAATAATGGAAAACAGCTG 480
Oy	481 AGGTTAAAGAGAGACTTATATATCTTACACTCAAGTCACTTGTCTTATCGG 540
Ds	481 AGGTTAAAGAGAGACTTATATATCTTACACTCAAGTCACTTGTCTTATCGG 540

Db 721 ACTGAAGCAAGCCAGTATCCACAGATTGGCTTCTCATCTTTGGCTACTCAAACTC 780
QY 781 TGA 783
Db 781 TGA 783

RESULT 12

PCT-US93-10034-5

; Sequence 5, Application PC/TUS9310034

; GENERAL INFORMATION:

; APPLICANT: Spriggs, Melanie

; APPLICANT: Srinivasan, Subhashini

; TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US93/10034

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Perkins, Patricia A

; REGISTRATION NUMBER: 34,693

; REFERENCE/DOCKET NUMBER: 1003

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206)587-0430

; TELEFAX: (206)233-0644

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 783 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA to mRNA

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; ORIGINAL SOURCE:

; ORGANISM: Mouse

; STRAIN: CD40-L

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..780

; PCT-US93-10034-5

Query Match 99.8%; Score 781.4; DB 5; Length 783;

Best Local Similarity 99.9%; Pred. No. 8.2e-224;

Matches 782; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGATAGAAACATACAGCCCACTTCCCGAGATCCGTGGCACTGAGCTTCCAGGAGC 60
Db 1 ATGATAGAAACATACAGCCCACTTCCCGAGATCCGTGGCACTGAGCTTCCAGGAGC 60
QY 61 ATGAAGATTTTATGATTTACTTCTGTTTCTTATACCCCAATGATGGATCTGTG 120
Db 61 ATGAAGATTTTATGATTTACTTCTGTTTCTTATACCCCAATGATGGATCTGTG 120
QY 121 CTTTGGCTGTATCTTCTGATAGATTTGATTAAGTGAAGAGAGAACTTCTCAT 180
Db 121 CTTTGGCTGTATCTTCTGATAGATTTGATTAAGTGAAGAGAGAACTTCTCAT 180
QY 181 GAAGATTTTGTATTCATTAATAAGCTAAAGATGCAAAAGAGAAAGATCTTATCC 240

Db 181 GAAGATTTTGTATTCATTAATAAGCTAAAGATGCAAAAGAGAAAGATCTTATCC 240
QY 241 TTGCTGAACCTGTAGAGATGAGAGCAATTTGAAAGCTTGTCAAGATTTAACTGA 300
Db 241 TTGCTGAACCTGTAGAGATGAGAGCAATTTGAAAGCTTGTCAAGATTTAACTGA 300
QY 301 AACCAAG 360
Db 301 AACCAAG 360
QY 361 ATTCCAGCACACCTGTGTAAGCAAGCCCACTGTAATGAGATTCCTTTAAGTGGCC 420
Db 361 ATTCCAGCACACCTGTGTAAGCAAGCCCACTGTAATGAGATTCCTTTAAGTGGCC 420
QY 421 AAGAAAGATTTATATCCATGAAAGCACTTGTATGCTTGAATAAGAGAGAGAGAG 480
Db 421 AAGAAAGATTTATATCCATGAAAGCACTTGTATGCTTGAATAAGAGAGAGAGAG 480
QY 481 ACGGTAAAAAG 540
Db 481 ACGGTAAAAAG 540
QY 541 GAGCCTTCAGTCAACGCCCATTCATGCTGCGCTCTGCTGAAGCCAGCATTTGATC 600
Db 541 GAGCCTTCAGTCAACGCCCATTCATGCTGCGCTCTGCTGAAGCCAGCATTTGATC 600
QY 601 GAGGATATCTTACTCAAGCGGCAATATCCCACTTCTCCAGCTTTGGAGAGAGAG 660
Db 601 GAGGATATCTTACTCAAGCGGCAATATCCCACTTCTCCAGCTTTGGAGAGAGAG 660
QY 661 TCTGTTCACTTGGGCGAGAGTGTGAATTACAGCTGAGCTTCTGTTTGTCAAGTG 720
Db 661 TCTGTTCACTTGGGCGAGAGTGTGAATTACAGCTGAGCTTCTGTTTGTCAAGTG 720
QY 721 ACTGAACCAAGCAAGTATCCACAGATTTGGCTTCTGATTTGGCTTAACTC 780
Db 721 ACTGAACCAAGCAAGTATCCACAGATTTGGCTTCTGATTTGGCTTAACTC 780

RESULT 13
US-08-249-189-22
; Sequence 22, Application US/08249189
; Patent No. 5961974
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: FANSLAW, WILLIAM
; APPLICANT: SPRIGGS, MELANIE
; APPLICANT: SRINIVASAN, SUBHASHINI
; APPLICANT: GIBSON, MARYLOU
; TITLE OF INVENTION: NOVEL CYTOKINE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.1
; SOFTWARE: Microsoft Word for Apple, version 5.1a
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/249,189
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/969,703
FILING DATE: October 23, 1992
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/805,723
FILING DATE: December 5, 1991
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/783,707
FILING DATE: October 25, 1991
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Petkine, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ. ID NO.: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 878 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
STRAIN: Murine CD40-L trimer
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 15..92
FEATURE:
NAME/KEY: CDS
LOCATION: 15..857
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 93..857
US-08-249-189-22

Query Match 80.6%; Score 631.4; DB 2; Length 878;
Best Local Similarity 99.8%; Pred. No. 5.4e-179;
Matches 632; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

151 GATAAGGTGGAAGAGAGTAACCTTCATGAAAGTTTGTATTGTAATAAAGGTAAG 210
Db 225 GATAAGGTGGAAGAGAGTAACCTTCATGAAAGTTTGTATTGTAATAAAGGTAAG 284
Qy 211 AGATGCAACAAAGAGAGATCTTATCTCTGTAACCTGTGAGAGATGAAAGCAA 270
Db 285 AGATGCAACAAAGAGAGATCTTATCTCTGTAACCTGTGAGAGATGAAAGCAA 344
Qy 271 TTGTAAGACCTTGTCAAGATATTAAGTTAAACAAGAAAGAAAGAAAGAGCTTT 330
Db 345 TTGTAAGACCTTGTCAAGATATTAAGTTAAACAAGAAAGAAAGAGCTTT 404
Qy 331 GAAATGCAAAAGAGTGTAGAGATCTTCAAAATTTGACGACACGTTGTAAAGCGAAC 390
Db 405 GAAATGCAAAAGAGTGTAGAGATCTTCAAAATTTGACGACACGTTGTAAAGCGAAC 464
Qy 391 AGTAATGACAGATCGTCTCAAGTGGGCAAGAAAGATTTATTCATGAAAGCAAC 450
Db 465 AGTAATGACAGATCGTCTCAAGTGGGCAAGAAAGATTTATTCATGAAAGCAAC 524
Qy 451 TTGTAATGCTTGAATAATGGAACACGCTGACGTTAAAGAGAGAGACTTATTTATGTC 510
Db 525 TTGTAATGCTTGAATAATGGAACACGCTGACGTTAAAGAGAGACTTATTTATGTC 584
Qy 511 TACACTCAAGTCACTTCTGCTTAATCGGAGACCTGTGAGTCAAGCCCATTTAGTGC 570
Db 585 TACACTCAAGTCACTTCTGCTTAATCGGAGACCTGTGAGTCAAGCCCATTTAGTGC 644
Qy 571 GGCTCTGCTGAGAGCCAGCAATTTGATGAGAGATCTTACTCAAGCGGCAATATCC 630
Db 645 GGCTCTGCTGAGAGCCAGCAATTTGATGAGAGATCTTACTCAAGCGGCAATATCC 704

Qy 631 CACAGTCTCCGACGCTTTCGAGAGAGAGTCTTCACTGGGGGAGTGTGAATTA 690
Db 705 CACAGTCTCCGACGCTTTCGAGAGAGAGTCTTCACTGGGGGAGTGTGAATTA 764
Qy 691 CAAGCTGTGCTCTGTGTGTGTGTCACGTCGACGTAAGCAAGCAAGTATCAAGATT 750
Db 765 CAAGCTGTGCTCTGTGTGTGTGTCACGTCGACGTAAGCAAGCAAGTATCAAGATT 824
Qy 751 GGCTCTCACTCTTTGGCTTACTCAAGCTTGA 783
Db 825 GGCTCTCACTCTTTGGCTTACTCAAGCTTGA 857

RESULT 14
US-08-484-624A-22
Sequence 22, Application US/08484624A
Patent No. 5962406
GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: FANSLAW, WILLIAM
APPLICANT: SPRIGGS, MELANIE
APPLICANT: SRINIVASAN, SUBHASHINI
APPLICANT: GIBSON, MARYLOU
APPLICANT: MORRIS, ARVIA E.
APPLICANT: MCGREW, JEFFERY
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,624A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/477,733
FILING DATE: June 07, 1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,703
FILING DATE: October 23, 1992
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/805,723
FILING DATE: December 5, 1991
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/783,707
FILING DATE: October 25, 1991
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Petkine, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ. ID NO.: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 878 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
CLONE: Murine CD40-L trimer
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 15..92
FEATURE:
NAME/KEY: CDS
LOCATION: 15..857
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 93..857
US-08-484-624A-22

Query Match 80.6%; Score 631.4; DB 2; Length 878;
Best Local Similarity 99.8%; Pred. No. 5.4e-179;
Matches 632; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 151 GATAGGTGGAAGAGAGTAAACCTTCATGAGATTTTGTATTCATATAAAGCTTAAG 210
DB 225 GATAGGTGGAAGAGAGTAAACCTTCATGAGATTTTGTATTCATATAAAGCTTAAG 284
QY 211 AGATGCAACAAAGAGAGATCTTTATCTTGTGTAAGTGTAGAGATGAGAGCA 270
DB 285 AGATGCAACAAAGAGAGATCTTTATCTTGTGTAAGTGTAGAGATGAGAGCA 344
QY 271 TTGGAAGACCTTGTCAAGATATTAAGTTAAACAAAGAGAGAGAGAGAGAGAGAG 330
DB 345 TTGGAAGACCTTGTCAAGATATTAAGTTAAACAAAGAGAGAGAGAGAGAGAGAG 404
QY 331 GAAATGCAAGAGAGAGAGATCTTCAATTTGCAAGCAACGTTGTAAAGAGAGCAAC 390
DB 405 GAAATGCAAGAGAGAGAGATCTTCAATTTGCAAGCAACGTTGTAAAGAGAGCAAC 464
QY 391 AGTAATGAGAGATCCGTTCAAGTGGGCGCAAGAGAGATTTATACAGTAAAGCAAC 450
DB 465 AGTAATGAGAGATCCGTTCAAGTGGGCGCAAGAGAGATTTATACAGTAAAGCAAC 524
QY 451 TTGTAATGCTTGAAG 510
DB 525 TTGTAATGCTTGAAG 584
QY 511 TACACTCAAGTCACTTGTGCTCTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 570
DB 585 TACACTCAAGTCACTTGTGCTCTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 644
QY 571 GGCCTCTGAG 630
DB 645 GGCCTCTGAG 704
QY 631 CACAGTCTCCGAG 690
DB 705 CACAGTCTCCGAG 764
QY 691 CAAAGTGTGCTTGTGTTGTCAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 750
DB 765 CAAAGTGTGCTTGTGTTGTCAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 824
QY 751 GGCCTCTCATCTTTGTGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 783
DB 825 GGCCTCTCATCTTTGTGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 857

RESULT 15
US-08-477-733B-22
Sequence 22, Application US/08477733B
Patent No. 5981724
GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: RANSLOW, WILLIAM
APPLICANT: SPRIGGS, MELANIE
APPLICANT: SRINIVASAN, SUBHASHINI
APPLICANT: GIBSON, MARYLOU

APPLICANT: MORRIS, ARVIA E.
APPLICANT: MCGREW, JEFFERY
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,733B
FILING DATE: June 07, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,189
FILING DATE: May 24, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,703
FILING DATE: October 23, 1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/805,723
FILING DATE: December 5, 1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/783,707
FILING DATE: October 25, 1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870606
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 878 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
CLONE: Murine CD40-L trimer
FEATURES:
NAME/KEY: sig_peptide
LOCATION: 15..92
FEATURE:
NAME/KEY: CDS
LOCATION: 15..857
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 93..857
US-08-477-733B-22

Query Match 80.6%; Score 631.4; DB 2; Length 878;
Best Local Similarity 99.8%; Pred. No. 5.4e-179;
Matches 632; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 151 GATAGGTGGAAGAGAGTAAACCTTCATGAGATTTTGTATTCATATAAAGCTTAAG 210
DB 225 GATAGGTGGAAGAGAGTAAACCTTCATGAGATTTTGTATTCATATAAAGCTTAAG 284
QY 211 AGATGCAACAAAGAGAGAGATCTTTATCTTGTGTAAGTGTAGAGATGAGAGCA 270

Db 285 AGATGCAACAAAGAGAGATCTTTATCTTGCTGAACCTGAGAGATGAGAAAGCAA 344
Qy 271 TTTGAAGACCTTGTCAAGATTTAACTTAACAAAGAAAGAAAAAGAAACAGCTTT 330
Db 345 TTTGAAGACCTTGTCAAGATTTAACTTTAAACAAAGAAAGAAAAAGAAACAGCTTT 404
Qy 331 GAAATGCAAAAGAGATGAGATCTTCAAAATTGCAGCAACGTTTGAAGCAAGCCAAAC 390
Db 405 GAAATGCAAAAGAGATGAGATCTTCAAAATTGCAGCAACGTTTGAAGCAAGCCAAAC 464
Qy 391 AGTAATGACATCCGTCTCAAGTGGGCCAAGAAAGATTTATACATGAAAGCAAC 450
Db 465 AGTAATGACATCCGTCTCAAGTGGGCCAAGAAAGATTTATACATGAAAGCAAC 524
Qy 451 TTTGTAATGCTTGAATAATGGAAACAGCTGACGTTAAAGAGAGACTTATATGTC 510
Db 525 TTTGTAATGCTTGAATAATGGAAACAGCTGACGTTAAAGAGAGACTTATATGTC 584
Qy 511 TTAACCTCAAGTCACTTCTGCTTAATCGGAGCCTTCAAGTCAACGCCCATTCATCGTC 570
Db 585 TTAACCTCAAGTCACTTCTGCTTAATCGGAGCCTTCAAGTCAACGCCCATTCATCGTC 644
Qy 571 GGCTCTGCTGAAGCCAGCATTTGATCTGAGAGATCTTACTCAAGCGCGCAATACC 630
Db 645 GGCTCTGCTGAAGCCAGCATTTGATCTGAGAGATCTTACTCAAGCGCGCAATACC 704
Qy 631 CACAGTTCTCCAGCTTTGAGAGAGAGATCTTCACTTGGGCGGAGTTGAATTA 690
Db 705 CACAGTTCTCCAGCTTTGAGAGAGAGATCTTCACTTGGGCGGAGTTGAATTA 764
Qy 691 CAAGCTGCTCTTCTGTTGTGCAAGTGAAGCAAGCAAGTATCCAGAGTT 750
Db 765 CAAGCTGCTCTTCTGTTGTGCAAGTGAAGCAAGCAAGTATCCAGAGTT 824
Qy 751 GGCTTCTCATCTTTTGGCTTACTCAACTCTGA 783
Db 825 GGCTTCTCATCTTTTGGCTTACTCAACTCTGA 857

Search completed: March 9, 2003, 04:46:06
Job time : 35.5164 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: March 8, 2003, 18:35:23 ; Search time 2040.79 Seconds
(without alignments)
11166.008 Million cell updates/sec

Title: US-08-982-272-3

Perfect score: 783
Sequence: 1 ATGATCGAACAATCAACCA.....TTGGCTTACTCAACTCTGA 783

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl.*
1: gb_ba.*
2: gb_hlg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
21: em_or.*
22: em_ov.*
23: em_pat.*
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30: em_hlg_hum.*
31: em_hlg_inv.*
32: em_hlg_other.*
33: em_hlg_mus.*
34: em_hlg_pln.*
35: em_hlg_rod.*
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37: em_hlg_vtc.*
38: em_sy.*
39: em_hlgo_hum.*
40: em_hlgo_mus.*
41: em_hlgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	751	95.9	818	6	AR044778
2	751	95.9	818	6	AR171646
3	751	95.9	1250	6	AX208160
4	749.4	95.7	783	6	AR076918
5	749.4	95.7	783	6	AR078308
6	749.4	95.7	783	6	AR085411
7	749.4	95.7	783	6	AR103367
8	749.4	95.7	783	6	AR169224
9	749.4	95.7	783	6	187865
10	749.4	95.7	1250	10	MMCD40
11	688.6	87.5	783	10	AF013985
12	688.4	87.5	783	10	AF116582
13	631.4	80.6	878	6	AR076933
14	631.4	80.6	878	6	AR078323
15	631.4	80.6	878	6	AR085426
16	631.4	80.6	878	6	AR103382
17	631.4	80.6	878	6	AR169239
18	592.4	75.7	786	6	187864
19	592.4	75.7	840	6	AR044779
20	592.4	75.7	840	6	AR076926
21	592.4	75.7	840	6	AR078316
22	592.4	75.7	840	6	AR085419
23	592.4	75.7	840	6	AR103375
24	592.4	75.7	840	6	AR106246
25	592.4	75.7	840	6	AR169232
26	592.4	75.7	840	6	AR169232
27	592.4	75.7	840	6	AR171647
28	592.4	75.7	840	6	123893
29	592.4	75.7	840	6	127345
30	592.4	75.7	840	6	167828
31	592.4	75.7	879	6	AX090039
32	592.4	75.7	879	6	HSGP39MR
33	592.4	75.7	1803	9	HSCD40
34	592.4	75.7	1816	9	HOMCD40L
35	580.8	75.5	1822	9	HSTRAPA
36	582.8	74.4	1058	9	AF344859
37	577.2	73.7	839	9	HACD40L
38	576.4	73.6	974	9	AF344860
39	573.2	73.2	975	9	AF344844
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42	528.6	67.5	786	4	AB040443
43	467.6	59.7	904	9	AF086711
44	467.6	59.7	904	9	AF344853
45	446.2	57.0	1425	6	AR076929

ALIGNMENTS

RESULT 1
AR044778
LOCUS AR044778 818 bp DNA
DEFINITION Sequence 1 from patent US 5817516.
ACCESSION AR044778
VERSION AR044778.1 GI:5966243
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 818)
AUTHORS Kehry M. and Castle B.
TITLES Methods for proliferating and differentiating B cells with high density membrane CD40 ligand
JOURNAL Patent: US 5817516-A 1 06-OCT-1998;

FEATURES
Source Location/Qualifiers
1..818
/organism="unknown"
BASE COUNT 249 a 170 c 186 g 213 t
ORIGIN

Query Match 95.9%; Score 751; DB 6; Length 818;
Best Local Similarity 97.4%; Pred. No. 1.9e-187;
Matches 763; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ATGATGAAACATACACCAAACTTCCCGATCTGCGGCACTGACCTCCATCAGC 60
DB 13 ATGATGAAACATACACCAAACTTCCCGATCTGCGGCACTGACCTCCATCAGC 72
QY 61 ATGAAATTTTATGATTTTACTCTGTTTCTTATCAACCAAGATGATGATGATG 120
DB 73 ATGAAATTTTATGATTTTACTCTGTTTCTTATCAACCAAGATGATGATGATG 132
QY 121 CTTTTCCTGATCTTCAATGATGATGATGATGATGATGATGATGATGATGATG 180
DB 133 CTTTTCCTGATCTTCAATGATGATGATGATGATGATGATGATGATGATGATG 192
QY 181 GAAGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATG 240
DB 193 GAAGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATG 252
QY 241 TTGCTGAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 300
DB 253 TTGCTGAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 312
QY 301 AACAAAG 360
DB 313 AACAAAG 372
QY 361 ATTGAGACACGTTGTAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 420
DB 373 ATTGAGACACGTTGTAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 432
QY 421 AAGAAAGATTTATGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATG 480
DB 433 AAGAAAGATTTATGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATG 492
QY 481 ACGGTTAAAG 540
DB 493 ACGGTTAAAG 552
QY 541 GAGCCTTGAGTCAAGCCCACTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
DB 553 GAGCCTTGAGTCAAGCCCACTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 612
QY 601 GAGAGATCTTACTCAAGGCGGCAATACCAAGTTCTCCCAAGTTTCCGAGCAGAG 660
DB 613 GAGAGATCTTACTCAAGGCGGCAATACCAAGTTCTCCCAAGTTTCCGAGCAGAG 672
QY 661 TCTGTTCACTTGGGCGAGTGTGTAATTAACAGCTGGGCTTCTGCTGCTGCTGCTG 720
DB 673 TCTGTTCACTTGGGCGAGTGTGTAATTAACAGCTGGGCTTCTGCTGCTGCTGCTG 732
QY 721 ACTGAAGCAAGCAAGTATTCACAGAGTGGCTTCTCATCTTTGGCTTAAGTCAATC 780
DB 733 ACTGAAGCAAGCAAGTATTCACAGAGTGGCTTCTCATCTTTGGCTTAAGTCAATC 792
QY 781 TGA 783
DB 793 TGA 795

RESULT 2
AR171646 818 bp DNA linear PAT 17-DEC-2001
LOCUS AR171646
DEFINITION Sequence 1 from patent US 6297052.
ACCESSION AR171646
VERSION AR171646.1 GI:17910596

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 818)
AUTHORS Kehr, M. and Castle, B.
TITLE B cell culture system comprising high density membrane bound CD40 ligand
JOURNAL Patent: US 6297052-A 1 02-OCT-2001;
FEATURES
Source Location/Qualifiers
1..818
/organism="unknown"
BASE COUNT 249 a 170 c 186 g 213 t
ORIGIN

Query Match 95.9%; Score 751; DB 6; Length 818;
Best Local Similarity 97.4%; Pred. No. 1.9e-187;
Matches 763; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ATGATGAAACATACACCAAACTTCCCGATCTGCGGCACTGACCTCCATCAGC 60
DB 13 ATGATGAAACATACACCAAACTTCCCGATCTGCGGCACTGACCTCCATCAGC 72
QY 61 ATGAAATTTTATGATTTTACTCTGTTTCTTATCAACCAAGATGATGATGATGATG 120
DB 73 ATGAAATTTTATGATTTTACTCTGTTTCTTATCAACCAAGATGATGATGATGATG 132
QY 121 CTTTTCCTGATCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATG 180
DB 133 CTTTTCCTGATCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATG 192
QY 181 GAAGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATG 240
DB 193 GAAGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATG 252
QY 241 TTGCTGAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 300
DB 253 TTGCTGAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 312
QY 301 AACAAAG 360
DB 313 AACAAAG 372
QY 361 ATTGAGACACGTTGTAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 420
DB 373 ATTGAGACACGTTGTAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 432
QY 421 AAGAAAGATTTATGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATG 480
DB 433 AAGAAAGATTTATGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATG 492
QY 481 ACGGTTAAAG 540
DB 493 ACGGTTAAAG 552
QY 541 GAGCCTTGAGTCAAGCCCACTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
DB 553 GAGCCTTGAGTCAAGCCCACTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 612
QY 601 GAGAGATCTTACTCAAGGCGGCAATACCAAGTTCTCCCAAGTTTCCGAGCAGAG 660
DB 613 GAGAGATCTTACTCAAGGCGGCAATACCAAGTTCTCCCAAGTTTCCGAGCAGAG 672
QY 661 TCTGTTCACTTGGGCGAGTGTGTAATTAACAGCTGGGCTTCTGCTGCTGCTGCTG 720
DB 673 TCTGTTCACTTGGGCGAGTGTGTAATTAACAGCTGGGCTTCTGCTGCTGCTGCTG 732
QY 721 ACTGAAGCAAGCAAGTATTCACAGAGTGGCTTCTCATCTTTGGCTTAAGTCAATC 780
DB 733 ACTGAAGCAAGCAAGTATTCACAGAGTGGCTTCTCATCTTTGGCTTAAGTCAATC 792
QY 781 TGA 783
DB 793 TGA 795

Db 793 TGA 795

RESULT 3
LOCUS AX208160 1250 bp DNA linear PAT 31-AUG-2001
DEFINITION Sequence 1 from Patent WO0156602.
ACCESSION AX208160
VERSION AX208160.1 GI:15422583
KEYWORDS
SOURCE Mus sp.
ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS Tripp, R.A., Anderson, L.J., and Brown, M.P.
TITLE Cda0 ligand adjuvant for respiratory syncytial virus
JOURNAL Patent: WO 0156602-A 1 09-AUG-2001;
The Secretary, Department of Health and Human Services (US)

FEATURES
source Location/Qualifiers
1..1250
/organism="Mus sp."
/db_xref="taxon:10095"

BASE COUNT 379 a 273 c 285 g 313 t

ORIGIN

Query Match 95.9%; Score 751; DB 6; Length 1250;
Best Local Similarity 97.4%; Pred. No. 2e-187;
Matches 763; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

1 ATGATCGAAACATACACAACTCTCCCGATCTGGGCACTGAGCTGCCATCAGC 60
13 ATGATGAAACATACAGCCAACTCCCGATCTGGGCACTGAGCTGCCATCAGC 72

61 ATGAAAATTTTAT 120
73 ATGAAATTTTAT 132

121 CTTTGTGCTGTATCTTCATAGAGATTGATAGTTCGAAAGAGAACTTTCAT 180
133 CTTTGTGCTGTATCTTCATAGAGATTGATAGTTCGAAAGAGAACTTTCAT 192

181 GAAGATTTTGTAT 240
193 GAAGATTTTGTAT 252

241 TTGCTGAACCTGTAGAGATGAGAGCAATTTGAAGACCTTGTCAAGATTAACGTTA 300
253 TTGCTGAACCTGTAGAGATGAGAGCAATTTGAAGACCTTGTCAAGATTAACGTTA 312

301 AACAAAGAAAGAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 360
313 AACAAAGAAAGAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 372

361 ATTGCAGCACACCTGTATAGAGCAAGCAAGTAATGAGCATCCGTTCTACAGTGGGCC 420
373 ATTGCAGCACACCTGTATAGAGCAAGCAAGTAATGAGCATCCGTTCTACAGTGGGCC 432

421 AAGAAAGAT 480
433 AAGAAAGAT 492

481 ACGGTTAAAGAGAGAGATCTATATATATATATATATATATATATATATATAT 540
493 ACGGTTAAAGAGAGAGATCTATATATATATATATATATATATATATATATAT 552

541 GAGCCTTGAAGTCAAGCCCATATGATGAGCTGGCTGGAAGCCAGCAATGATCT 600
553 GAGCCTTGAAGTCAAGCCCATATGATGAGCTGGCTGGAAGCCAGCAATGATCT 612

601 GAGAGATTTTACTCAAGGCGGCAATATACCAAGTTCTCTCCAGCTTTGCGAGCAG 660
613 GAGAGATTTTACTCAAGGCGGCAATATACCAAGTTCTCTCCAGCTTTGCGAGCAG 672

661 TCTGTCTACTTGGGCGAGGTGTGAAATTAACAGCTGAGCTTCTGTGTTTTCACAGCTG 720
673 TCTGTCTACTTGGGCGAGGTGTGAAATTAACAGCTGAGCTTCTGTGTTTTCACAGCTG 732

721 ACTGAGAGAGCCCAAGTATCCACAGAGTTGGCTCTCATCTTTTGGCTTACCAACTC 780
733 ACTGAGAGAGCCCAAGTATCCACAGAGTTGGCTCTCATCTTTTGGCTTACCAACTC 792

781 TGA 783
793 TGA 795

RESULT 4
LOCUS AR076918 783 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 1 from patent US 5961974.
ACCESSION AR076918
VERSION AR076918.1 GI:10003664
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
1 (bases 1 to 783)

REFERENCE
AUTHORS Armitage, R.J., Fanslow, M.C. and Spriggs, M.K.
TITLE Monoclonal antibodies to CD40 ligand, pharmaceutical composition comprising the same and hybridomas producing the same
JOURNAL Patent: US 5961974-A 1 05-OCT-1999;
Location/Qualifiers

FEATURES
source 1..783
/organism="unknown"

BASE COUNT 243 a 159 c 178 g 203 t

ORIGIN

Query Match 95.7%; Score 749.4; DB 6; Length 783;
Best Local Similarity 97.3%; Pred. No. 5.2e-187;
Matches 762; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

1 ATGATCGAAACATACACAACTCTCCCGATCTGGGCACTGAGCTGCCATCAGC 60
1 ATGATGAAACATACAGCCAACTCCCGATCTGGGCACTGAGCTGCCATCAGC 60

61 ATGAAAATTTTAT 120
61 ATGAAATTTTAT 120

121 CTTTGTGCTGTATCTTCATAGAGATTGATAGTTCGAAAGAGAACTTTCAT 180
121 CTTTGTGCTGTATCTTCATAGAGATTGATAGTTCGAAAGAGAACTTTCAT 180

181 GAAGATTTTGTAT 240
181 GAAGATTTTGTAT 240

241 TTGCTGAACCTGTAGAGATGAGAGCAATTTGAAGACCTTGTCAAGATTAACGTTA 300
241 TTGCTGAACCTGTAGAGATGAGAGCAATTTGAAGACCTTGTCAAGATTAACGTTA 300

301 AACAAAGAAAGAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 360
301 AACAAAGAAAGAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 360

361 ATTGCAGCACACCTGTATAGAGCAAGCAAGTAATGAGCATCCGTTCTACAGTGGGCC 420
361 ATTGCAGCACACCTGTATAGAGCAAGCAAGTAATGAGCATCCGTTCTACAGTGGGCC 420

421 AAGAAAGAT 480
421 AAGAAAGAT 480

481 ACGGTTAAAGAGAGATCTATATATATATATATATATATATATATATATAT 540
481 ACGGTTAAAGAGAGATCTATATATATATATATATATATATATATATATAT 540

Db	481	ACGGTTAAAAAGAGAGACTGATTATTATGCTACATCAATCACTCTTGCTCTAATCGG	540
Qy	541	GAGCCTTGAGTCAACGCCATTATGTCTGGCCTTGCGTTGAAGCCAGCATGGATCT	600
Db	541	GAGCCTTGAGTCAACGCCATTATGTCTGGCCTTGCGTTGAAGCCAGCATGGATCT	600
Qy	601	GAGAGAAATCTTACTCAAGGCGGCAAAATACCACAGTTCTCCACGCTTGGGAGCAGCAG	660
Db	601	GAGAGAAATCTTACTCAAGGCGGCAAAATACCACAGTTCTCCACGCTTGGGAGCAGCAG	660
Qy	661	TCTGATCACTTGGCGGAGTCTTTGAAATTACAAAGTGGTCTTCTGTGTTGTTCAACTGG	720
Db	661	TCTGATCACTTGGCGGAGTCTTTGAAATTACAAAGTGGTCTTCTGTGTTGTTCAACTGG	720
Qy	721	ACTGAAGCAAGCCAAAGTATCCACAGAGTTGGCTTTCATCTTTGGCTTACTCAAACTTC	780
Db	721	ACTGAAGCAAGCCAAAGTATCCACAGAGTTGGCTTTCATCTTTGGCTTACTCAAACTTC	780
Qy	781	TGA	783
Db	781	TGA	783

RESULT 5				
LOCUS	AR078308	783 bp	DNA	linear
DEFINITION	Sequence 1 from patent US 5962406.			PAT 31-AUG-2000
ACCESSION	AR078308			
VERSION	AR078308.1	GI:1005054		
KEYWORDS				
SOURCE	Unknown.			
ORGANISM	Unknown.			

REFERENCE	TITLE	JOURNAL	FEATURES
1 (bases 1 to 783)			
Armitage, R.J., Fanslow, W.C., Springs, M.K., Srinivasan, S., Gibson, M.G., Morris, A.E. and McGraw, J.T.	Recombinant soluble Cx40 ligand polypeptide and pharmaceutical composition containing the same	Patent: US 5963406-A 1 05-Oct-1999;	
		Location/Qualifiers	
		1 783	

	/organism="unknown"			
BASE COUNT	243 a	159 c	178 g	203 t
ORIGIN				

Query Match	95.7%	Score 749.4	DB 6	Length 783
Best Local Similarity	97.3%	Pred. No. 5.2e-187		
Matches 762; Conservative	0	Mismatches 21	Indels 0	Gaps 0

QY	1	ATGATCGAAACATACAAACCAACTTTCCCGCATCTGGGCGCATGGACTCGCCATCAAC	60
Db	1	ATGATCGAAACATACGACCAACTTCCCCAGATCGGCGCAACTGGACTCTCCACGAGC	60
QY	61	ATGAAATTTTATATGATTTACTACTGTTTTCTTATCACCAGATGGTGGTACGA	120
Db	61	ATGAAATTTTATATGATTTACTACTGTTTTCTTATCACCAGATGGATCTGTG	120
QY	121	CTTTTGGCTGATCTTATATGAAAGTGGATGAGGTGAGAGAAATGAACCTTAT	180
Db	121	CTTTTGGCTGATCTTATATGAAAGTGGATGAGGTGAGAGAAATGAACCTTAT	180
QY	181	GAAAGTTTGTATTCATTAATAAAGCTAAAGATGCAACAAAGAGAGATCTTATCC	240
Db	181	GAAAGTTTGTATTCATTAATAAAGCTAAAGATGCAACAAAGAGAGATCTTATCC	240
QY	241	TTGCTGAAGTGTAGAGAGATGAGAGCAATTTGAAGACTTTGCAAGATATTAACGTGA	300
Db	241	TTGCTGAAGTGTAGAGAGATGAGAGCAATTTGAAGACTTTGCAAGATATTAACGTGA	300
QY	301	AACCAAGAGAGAAAAAGAAAAAGCTTTGAAATGCAAAAGATATGAGATCTTCAA	360
Db	301	AACCAAGAGAGAAAAAGAAAAAGCTTTGAAATGCAAAAGATATGAGATCTTCAA	360

Qy	361	ATTGACGACACGTTGTAAGGAAAGCCACAGTAATGCAAGATCCGTTCTACAGTGGGC	420
Db	361	ATTGACGACACGTTGTAAGGAAAGCCACAGTAATGCAAGATCCGTTCTACAGTGGGC	420
Qy	421	AAGAAAGGATTTATACCATGAAAGCACTTGGTAATGCTGAAATGSGAAACAGCTG	480
Db	421	AAGAAAGGATTTATACCATGAAAGCACTTGGTAATGCTGAAATGSGAAACAGCTG	480
Qy	481	ACGGTAAAGAGAAAGAGCTGTATATATGTTACCTCAAGTCACTTGTGCTTAATGGG	540
Db	481	ACGGTAAAGAGAAAGAGCTGTATATATGTTACCTCAAGTCACTTGTGCTTAATGGG	540
Qy	541	GAGCCTTGAGTCAAGGCCATTTCATCGTGGGCTCTGGGTGAAGCCAGACATTTGGATCT	600
Db	541	GAGCCTTGAGTCAAGGCCATTTCATCGTGGGCTCTGGGTGAAGCCAGACATTTGGATCT	600
Qy	601	GAGAAATCTTAACTCAAGGCGGCAATATCCCAAGTTCCTCCAGCTTTGCGAGCAGAG	660
Db	601	GAGAAATCTTAACTCAAGGCGGCAATATCCCAAGTTCCTCCAGCTTTGCGAGCAGAG	660
Qy	661	TCGTGTCACTTGGGCGGAGTGTGTAATTAACAACCTGGGCTTCGTGGTTTGTCAACCTG	720
Db	661	TCGTGTCACTTGGGCGGAGTGTGTAATTAACAACCTGGGCTTCGTGGTTTGTCAACCTG	720
Qy	721	ACTGAAGCAAGCCAGATGATCCAAGAGTTGGCTTCACTCTTTTGGCTTAACCTCAATC	780
Db	721	ACTGAAGCAAGCCAGATGATCCAAGAGTTGGCTTCACTCTTTTGGCTTAACCTCAATC	780
Qy	781	TGA TGC	
Db	781	TGA TGC	

RESULT	6
AR085411	
LOCUS	783 bp DNA
DEFINITION	Sequence 1 from patent US 5981724.
ACCSSION	AR085411
VERSION	AR085411.1 GI:10012180
PAT	01-SEP-2000

SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
	1 (bases 1 to 783)

AUTHORS Armitage, R.J., Fanslow, W.C., Spriggs, M.K., Srinivasan, S., Gibson, M.G., Morris, A.E. and McGrew, J.T.

FEATURES	Location/Qualifiers
SOURCE	1. .783
BASE COUNT	/organism="unknown"
ORIGIN	243 a 159 c 178 g 203 t

Query Match	95.7%;	Score 749.4;	DB 6;	Length 763;
Best Local Similarity	97.3%;	Pred. No. 5.2e-187;		
Matches 762;	Conservative	0;	Mismatches 21;	Indels 0;
				Gaps 0;

Qy	1	ATGATCGAAACATACACCAACCTTCTCCCGACTGGGCACTGGATCCCATCAGC	60
Db	1	ATGATAGAAACATACAGCCACTTCCCGAGTCGGAGCACTGGACTTCCAGGAGC	60
Qy	61	ATGAAAATTTTATGATTTACTTACGTCTTTCTTATCACCAGATGATGGGTACGA	120
Db	61	ATGAAAGATTTTATGATTTACTTACGTCTTTCTTATCACCAGAAATGGATCTGTG	120
Qy	121	CTTTTGGTGGATCTTCATAGAAATTCGATTAAGGTGGAAGCAAGTAAACCTTAT	180
Db	121	CTTTTGGTGGATCTTCATAGAAATTCGATTAAGGTGGAAGCAAGTAAACCTTAT	180
Qy	181	GAGATTTTGTATTCATAAAAAGCTAAAGATGCAACAAGAGCAAGATCTTATCC	240
Db	181	GAGATTTTGTATTCATAAAAAGCTAAAGATGCAACAAGAGCAAGATCTTATCC	240

QY 241 TTGCTGAACGTGAGAGATGAGAGCAATTTGAGAACCTTGTCAAGATATTAAGTTA 300
DB 241 TTGCTGAACGTGAGAGATGAGAGCAATTTGAGAACCTTGTCAAGATATTAAGTTA 300
QY 301 AACAAAG 360
DB 301 AACAAAG 360
QY 361 ATTGAG 420
DB 361 ATTGAG 420
QY 421 AAGAAAGATATTAATACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
DB 421 AAGAAAGATATTAATACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
QY 481 ACGGTTAAAG 540
DB 481 ACGGTTAAAG 540
QY 541 GAGCCTTGAG 600
DB 541 GAGCCTTGAG 600
QY 601 GAG 660
DB 601 GAG 660
QY 661 TCTGTTCACTTGAG 720
DB 661 TCTGTTCACTTGAG 720
QY 721 ACTGAG 780
DB 721 ACTGAG 780
QY 781 TGA 783
DB 781 TGA 783
RESULT 7
ARI03367 783 bp DNA linear PAT 14-FEB-2001
LOCUS Sequence 1 from patent US 6087329.
ACCESSION ARI03367
VERSION ARI03367.1 GI:12814955
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 783)
AUTHORS Armitage,R.O., Fanslow,W.C. and Spriggs,M.K.
TITLE CD40 ligand polypeptide
JOURNAL Patent: US 6087329-A 1 11-JUL-2000;
FEATURES Location/Qualifiers
source 1..783
BASE COUNT 243 a 159 c 178 g 203 t
ORIGIN
Query Match 95.7%; Score 749.4; DB 6; Length 783;
Best Local Similarity 97.3%; Pred. No. 5,2e-187;
Matches 762; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
QY 1 ATGATGAG 60
DB 1 ATGATGAG 60
QY 61 ATGAAATTTTATGATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 120
DB 61 ATGAAATTTTATGATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 120

QY 121 CTTTGTGCTGATATCTTATGAGAGATTTGAGATTTGAGAGAGAGAGAGAGAGAGAG 180
DB 121 CTTTGTGCTGATATCTTATGAGAGATTTGAGATTTGAGAGAGAGAGAGAGAGAGAG 180
QY 181 GAGATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 240
DB 181 GAGATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 240
QY 241 TTGCTGAACGTGAG 300
DB 241 TTGCTGAACGTGAG 300
QY 301 AACAAAG 360
DB 301 AACAAAG 360
QY 361 ATTGAG 420
DB 361 ATTGAG 420
QY 421 AAGAAAGATATTAATACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
DB 421 AAGAAAGATATTAATACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
QY 481 ACGGTTAAAG 540
DB 481 ACGGTTAAAG 540
QY 541 GAGCCTTGAG 600
DB 541 GAGCCTTGAG 600
QY 601 GAG 660
DB 601 GAG 660
QY 661 TCTGTTCACTTGAG 720
DB 661 TCTGTTCACTTGAG 720
QY 721 ACTGAG 780
DB 721 ACTGAG 780
QY 781 TGA 783
DB 781 TGA 783
RESULT 8
ARI69224 783 bp DNA linear PAT 17-DEC-2001
LOCUS Sequence 1 from patent US 6290972.
ACCESSION ARI69224
VERSION ARI69224.1 GI:17907035
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 783)
AUTHORS Armitage,R.O., Fanslow,W.C., Spriggs,M.K., Srinivasan,S. and
Gibson,M.G.
TITLE Method of augmenting a vaccine response by administering CD40
JOURNAL Patent: US 6290972-A 1 18-SEP-2001;
FEATURES Location/Qualifiers
source 1..783
BASE COUNT 243 a 159 c 178 g 203 t
ORIGIN
Query Match 95.7%; Score 749.4; DB 6; Length 783;

Best Local Similarity 97.3%; Pred. No. 5,2e-187;
Matches 762; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACCAACCACTTCCCGGCTGGGCGCCATCGACATCCAGC 60
Db 1 ATGATGAAACATACCAACCACTTCCCGGCGCCATCGACATCCAGC 60
QY 61 ATGAAATTTTATATGATTTACTTACTGTTTTCTTATACCCAGATGATGGGTACGA 120
Db 61 ATGAAATTTTATATGATTTACTTACTGTTTTCTTATACCCAGATGATGGGTACGTG 120
QY 121 CTTTGGCTGTATCTTATCATGAAAGTGGATTAAGCTGGAAGGAAATCCCTCAT 180
Db 121 CTTTGGCTGTATCTTATCATGAAAGTGGATTAAGCTGGAAGGAAATCCCTCAT 180
QY 181 GAAGATTTTGTATTCATTAATAAGCTAAAGATGCAACAAAGAAAGATCTTATCC 240
Db 181 GAAGATTTTGTATTCATTAATAAGCTAAAGATGCAACAAAGAAAGATCTTATCC 240
QY 241 TTGCTGAACGTGAGAGATGAAAGCAATTTGAAGACCTTGTCAAGATATTAAGTTA 300
Db 241 TTGCTGAACGTGAGAGATGAAAGCAATTTGAAGACCTTGTCAAGATATTAAGTTA 300
QY 301 AACAAAG 360
Db 301 AACAAAG 360
QY 361 ATTGAGACACGCTGTGTAAGCAAGCCAGATGAGAGAGAGAGAGAGAGAGAGAGAG 420
Db 361 ATTGAGACACGCTGTGTAAGCAAGCCAGATGAGAGAGAGAGAGAGAGAGAGAGAG 420
QY 421 AAGAAAGATATTAATCACTGAAAGCACTTGTGAATGCTTGAATGGAAGAGAGCTG 480
Db 421 AAGAAAGATATTAATCACTGAAAGCACTTGTGAATGCTTGAATGGAAGAGAGCTG 480
QY 481 ACGGTTAAAG 540
Db 481 ACGGTTAAAG 540
QY 541 GAGCCTTGAGTCAAGCCCATTCATGCTGCGCTGCGAGAGAGAGAGAGAGAGAGAG 600
Db 541 GAGCCTTGAGTCAAGCCCATTCATGCTGCGCTGCGAGAGAGAGAGAGAGAGAGAG 600
QY 601 GAGAGATCTTACTCAAGGCGGCAATACCAAGTCTCTCCAGCTTTCGAGAGAGAG 660
Db 601 GAGAGATCTTACTCAAGGCGGCAATACCAAGTCTCTCCAGCTTTCGAGAGAGAG 660
QY 661 TCTGTTCACTTGGCGGAGATGTTGAATTAACAAGCTGCTTCTGTTGTCAACGTG 720
Db 661 TCTGTTCACTTGGCGGAGATGTTGAATTAACAAGCTGCTTCTGTTGTCAACGTG 720
QY 721 ACTGAAGCAAGCAAGTGAATCCAGAGATGGCTTCTCATCTTTTGGCTTACTCAATC 780
Db 721 ACTGAAGCAAGCAAGTGAATCCAGAGATGGCTTCTCATCTTTTGGCTTACTCAATC 780
QY 781 TGA 783
Db 781 TGA 783

RESULT 9
LOCUS 187865 783 bp DNA linear PAT 10-AUG-1998
DEFINITION Sequence 5 from patent US 5716805.
ACCESSION 187865
VERSION 187865.1 GI:3407805
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 783)
AUTHORS Srinivasan, S. and Spriggs, M. K.
TITLE Methods of preparing soluble, oligomeric proteins

JOURNAL Patent: US 5716805-A 5 10-FEB-1998;
FEATURES Location/Qualifiers
source 1..783 /organism="unknown"
BASE COUNT 243 a 159 c 178 g 203 t
ORIGIN

Query Match 95.7%; Score 749.4; DB 6; Length 783;
Best Local Similarity 97.3%; Pred. No. 5,2e-187;
Matches 762; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACCAACCACTTCCCGGCTGGGCGCCATCGACATCCAGC 60
Db 1 ATGATGAAACATACCAACCACTTCCCGGCGCCATCGACATCCAGC 60
QY 61 ATGAAATTTTATATGATTTACTTACTGTTTTCTTATACCCAGATGATGGGTACGA 120
Db 61 ATGAAATTTTATATGATTTACTTACTGTTTTCTTATACCCAGATGATGGGTACGTG 120
QY 121 CTTTGGCTGTATCTTATCATGAAAGTGGATTAAGCTGGAAGGAAATCCCTCAT 180
Db 121 CTTTGGCTGTATCTTATCATGAAAGTGGATTAAGCTGGAAGGAAATCCCTCAT 180
QY 181 GAAGATTTTGTATTCATTAATAAGCTAAAGATGCAACAAAGAAAGATCTTATCC 240
Db 181 GAAGATTTTGTATTCATTAATAAGCTAAAGATGCAACAAAGAAAGATCTTATCC 240
QY 241 TTGCTGAACGTGAGAGATGAAAGCAATTTGAAGACCTTGTCAAGATATTAAGTTA 300
Db 241 TTGCTGAACGTGAGAGATGAAAGCAATTTGAAGACCTTGTCAAGATATTAAGTTA 300
QY 301 AACAAAG 360
Db 301 AACAAAG 360
QY 361 ATTGAGACACGCTGTGTAAGCAAGCCAGATGAGAGAGAGAGAGAGAGAGAGAGAG 420
Db 361 ATTGAGACACGCTGTGTAAGCAAGCCAGATGAGAGAGAGAGAGAGAGAGAGAGAG 420
QY 421 AAGAAAGATATTAATCACTGAAAGCACTTGTGAATGCTTGAATGGAAGAGAGCTG 480
Db 421 AAGAAAGATATTAATCACTGAAAGCACTTGTGAATGCTTGAATGGAAGAGAGCTG 480
QY 481 ACGGTTAAAG 540
Db 481 ACGGTTAAAG 540
QY 541 GAGCCTTGAGTCAAGCCCATTCATGCTGCGCTGCGAGAGAGAGAGAGAGAGAGAG 600
Db 541 GAGCCTTGAGTCAAGCCCATTCATGCTGCGCTGCGAGAGAGAGAGAGAGAGAGAG 600
QY 601 GAGAGATCTTACTCAAGGCGGCAATACCAAGTCTCTCCAGCTTTCGAGAGAGAG 660
Db 601 GAGAGATCTTACTCAAGGCGGCAATACCAAGTCTCTCCAGCTTTCGAGAGAGAG 660
QY 661 TCTGTTCACTTGGCGGAGATGTTGAATTAACAAGCTGCTTCTGTTGTCAACGTG 720
Db 661 TCTGTTCACTTGGCGGAGATGTTGAATTAACAAGCTGCTTCTGTTGTCAACGTG 720
QY 721 ACTGAAGCAAGCAAGTGAATCCAGAGATGGCTTCTCATCTTTTGGCTTACTCAATC 780
Db 721 ACTGAAGCAAGCAAGTGAATCCAGAGATGGCTTCTCATCTTTTGGCTTACTCAATC 780
QY 781 TGA 783
Db 781 TGA 783

RESULT 10
LOCUS MIMCD40 1250 bp mRNA linear ROD 26-APR-2001
DEFINITION M. musculus mRNA for CD40 ligand.
ACCESSION X65453

/db xref="GI:4102614"
 /translation="MIETYSPSPRSVATGLPASKMIPLYLITVLIOMIGSVFPAV
 YLHRRLDVBEASLHEDFVFKLKRCKNKGSLSLNCEMRROFEDVLDISLNK
 EEKKEKSPENKXGDEDEPOIAHVVSANASVLOWAKKGYTMKSNLVLENROL
 TYKREGIYVYTOVTFCSNREPLSOPRPYISLWIKXSSESLILRAANTHSSKICE
 QOSIHGVSFELQASVFNVTESOVHIGIFSGLKLK"

BASE COUNT 236 a 152 c 189 g 206 t
 ORIGIN
 Query Match 87.9%; Score 688.6; DB 10; Length 783;
 Best Local Similarity 92.5%; Pred. No. 5.9e-171;
 Matches 724; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACCAACCACTTCCCGCATCTGCGGCGCATCGACCTCCATCAGC 60
 DB 1 ATGATGAGAAACATACCAACCACTTCCCGCATCTGCGGCGCATCGACCTCCATCAGC 60
 QY 61 ATGAAAATTTTATGATTTACTTACTTCTTCTTATCACCAGATGATGGGTCAACA 120
 DB 61 ATGAAAATTTTATGATTTACTTACTTCTTCTTATCACCAGATGATGGGTCAACA 120
 QY 121 CTTTGTGCTGTATCTTATGAAAGATGATGAGAGAGAACTTATCAT 180
 DB 121 CTTTGTGCTGTATCTTATGAAAGATGATGAGAGAGAACTTATCAT 180
 QY 181 GAGATTTTGTATTCATTAATAAAGCTAAAGATGCAACAAAGAGAGATCTTATCC 240
 DB 181 GAGATTTTGTATTCATTAATAAAGCTAAAGATGCAACAAAGAGAGATCTTATCC 240
 QY 241 TTGCTGAACCTGTAGAGAGATGAAAGCATTTGAAAGCTTGTCAAGATATACGTTA 300
 DB 241 TTGCTGAACCTGTAGAGAGATGAAAGCATTTGAAAGCTTGTCAAGATATACGTTA 300
 QY 301 AACAAAG 360
 DB 301 AACAAAG 360
 QY 361 ATTGAGAGACGTTGTAG 420
 DB 361 ATTGAGAGACGTTGTAG 420
 QY 421 AAGAAAGATATATACATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
 DB 421 AAGAAAGATATATACATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
 QY 481 ACGGTAAAG 540
 DB 481 ACGGTAAAG 540
 QY 541 GAGCCTTCGAGTCAAGCCCATTCATGCTGCGCTCTGCTGAAAGCCAGATGGATCT 600
 DB 541 GAGCCTTCGAGTCAAGCCCATTCATGCTGCGCTCTGCTGAAAGCCAGATGGATCT 600
 QY 601 GAGAGATCTTACTCAAGGCGGCAATACCAAGATCTCTCCAGCTTCCGAGAGAGAG 660
 DB 601 GAGAGATCTTACTCAAGGCGGCAATACCAAGATCTCTCCAGCTTCCGAGAGAGAG 660
 QY 661 TCTGTCACTTGGCGGAGTGTGAATTAACAAGTGTGCTTCTGTGTTGTCAACGTG 720
 DB 661 TCTGTCACTTGGCGGAGTGTGAATTAACAAGTGTGCTTCTGTGTTGTCAACGTG 720
 QY 721 ACTGAAG 780
 DB 721 ACTGAAG 780
 QY 781 TGA 783
 DB 781 TGA 783
 RESULT 12
 AF116582
 LOCUS AF116582 783 bp mRNA linear ROD 12-JUL-2000

DEFINITION Rattus norvegicus CD40 ligand mRNA, complete cds.
 ACCESSION AF116582
 VERSION AF116582.1 GI:4545249
 KEYWORDS
 SOURCE Rattus norvegicus.
 ORGANISM Rattus norvegicus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 REFERENCE 1 (bases 1 to 783)
 AUTHORS Hallett,K.M. and Oaks,M.K.
 TITLE Nucleotide sequence of the rat CD40 ligand
 JOURNAL DNA Seq. 10 (6), 405-406 (2000)
 MEDLINE 20284949
 PUBMED 10826698
 REFERENCE 2 (bases 1 to 783)
 AUTHORS Hallett,K.M. and Oaks,M.K.
 TITLE Direct Submission
 JOURNAL Submitted (24-DEC-1998) Transplant Research, St. Luke's Medical
 Center, 2900 W. Oklahoma Ave., Milwaukee, WI 53215, USA
 FEATURES
 source
 1..783
 /organism="Rattus norvegicus"
 /strain="Sprague Dawley"
 /db_xref="taxon:10116"
 /cell_type="splenocyte"
 1..783
 /codon_start=1
 /product="CD40 ligand"
 /protein_id="AND2460.1"
 /db_xref="GI:4545250"
 /translation="MIETYSPSPRSVATGLPASKMIPLYLITVLIOMIGSVFPAV
 YLHRRLDVBEASLHEDFVFKLKRCKNKGSLSLNCEMRROFEDVLDISLNK
 EEKKEKSPENKXGDEDEPOIAHVVSANASVLOWAKKGYTMKSNLVLENROL
 TYKREGIYVYTOVTFCSNREPLSOPRPYISLWIKXSSESLILRAANTHSSKICE
 QOSIHGVSFELQASVFNVTESOVHIGIFSGLKLK"

BASE COUNT 237 a 153 c 189 g 204 t
 ORIGIN

Query Match 87.5%; Score 685.4; DB 10; Length 783;
 Best Local Similarity 92.2%; Pred. No. 4.1e-170;
 Matches 722; Conservative 0; Mismatches 61; Indels 0;
 QY 1 ATGATGAAACATACCAACCACTTCCCGCATCTGCGGCGCATCGACCTCCATCAGC 60
 DB 1 ATGATGAAACATACCAACCACTTCCCGCATCTGCGGCGCATCGACCTCCATCAGC 60
 QY 61 ATGAAAATTTTATGATTTACTTACTTCTTCTTATCACCAGATGATGGGTCAACA 120
 DB 61 ATGAAAATTTTATGATTTACTTACTTCTTCTTATCACCAGATGATGGGTCAACA 120
 QY 121 CTTTGTGCTGTATCTTATGAAAGATGATGAGAGAGAACTTATCAT 180
 DB 121 CTTTGTGCTGTATCTTATGAAAGATGATGAGAGAGAACTTATCAT 180
 QY 181 GAGATTTTGTATTCATTAATAAAGCTAAAGATGCAACAAAGAGAGATCTTATCC 240
 DB 181 GAGATTTTGTATTCATTAATAAAGCTAAAGATGCAACAAAGAGAGATCTTATCC 240
 QY 241 TTGCTGAACCTGTAGAGAGATGAAAGCATTTGAAAGCTTGTCAAGATATACGTTA 300
 DB 241 TTGCTGAACCTGTAGAGAGATGAAAGCATTTGAAAGCTTGTCAAGATATACGTTA 300
 QY 301 AACAAAG 360
 DB 301 AACAAAG 360
 QY 361 ATTGAGAGACGTTGTAG 420
 DB 361 ATTGAGAGACGTTGTAG 420
 QY 421 AAGAAAGATATATACATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
 DB 421 AAGAAAGATATATACATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480

Dh 421 AAGAAAGATATTAACATGAAAACCACTTGAGTGTGAGAAAGGAGAACACTG 480
Qy 481 AGGTTAAAG 540
Dh 481 AGGTTAAAG 540
Qy 541 GAGCTTTCAG 600
Dh 541 GAGCTTTCAG 600
Qy 601 GAGAGATCTTACAG 660
Dh 601 GAGAGATCTTACAG 660
Qy 661 TCTGTTCACTTGGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Dh 661 TCTGTTCACTTGGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Qy 721 ACTGAAAG 780
Dh 721 ACTGAAAG 780
Qy 781 TGA 783
Dh 781 TGA 783

RESULT 13

AR076933

LOCUS AR076933 878 bp DNA linear PAT 31-AUG-2000

DEFINITION Sequence 22 from patent US 5961974.

ACCESSION AR076933

VERSION AR076933.1 GI:10003679

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 878)

AUTHORS Armitage,R.J., Fanslow,W.C. and Spriggs,M.K.

TITLE Monoclonal antibodies to CD40 ligand, pharmaceutical composition

JOURNAL Patent: US 5961974-A 22 05-OCT-1999;

FEATURES Location/Qualifiers

source 1..878

BASE COUNT 277 a 178 c 203 g 220 t

ORIGIN

Query Match 80.6%; Score 631.4; DB 6; Length 878;

Best Local Similarity 99.8%; Pred. No. 7.5e-156;

Matches 632; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 151 GATAGGTCGAG 210
Dh 225 GATAGGTCGAG 284
Qy 211 AGATGCAACAAAG 270
Dh 285 AGATGCAACAAAG 344
Qy 271 TTGAAAGCCTTGCAAGAGATTAACGTTAAACAAAGAGAGAGAGAGAGAGAGAGAG 330
Dh 345 TTGAAAGCCTTGCAAGAGATTAACGTTAAACAAAGAGAGAGAGAGAGAGAGAGAG 404
Qy 331 GAAATGCAAAAG 390
Dh 405 GAAATGCAAAAG 464
Qy 391 AGTAATGAG 450
Dh 465 AGTAATGAG 524
Qy 451 TTGTAATGCTTGAAG 510

Dh 525 TTGTAATGCTTGAAG 584
Qy 511 TAACTCAAGTCACTTCTGCTTAATCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 570
Dh 585 TAACTCAAGTCACTTCTGCTTAATCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 644
Qy 571 GGCCTTCGAG 630
Dh 645 GGCCTTCGAG 704
Qy 631 CACAGTCTCCAGCTTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 690
Dh 705 CACAGTCTCCAGCTTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 764
Qy 691 CAGAGTGTCTCTGCTTGTGTTGTAACGTAAGAGAGAGAGAGAGAGAGAGAGAGAG 750
Dh 765 CAGAGTGTCTCTGCTTGTGTTGTAACGTAAGAGAGAGAGAGAGAGAGAGAGAGAG 824
Qy 751 GGCCTTCATCTTTCGCTTTCGCTTACTCAAGCTCTGA 783
Dh 825 GGCCTTCATCTTTCGCTTTCGCTTACTCAAGCTCTGA 857

RESULT 14

AR078323

LOCUS AR078323 878 bp DNA linear PAT 31-AUG-2000

DEFINITION Sequence 22 from patent US 5962406.

ACCESSION AR078323

VERSION AR078323.1 GI:10005069

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 878)

AUTHORS Armitage,R.J., Fanslow,W.C., Spriggs,M.K., Srinivasan,S.,

TITLE Recombinant soluble CD40 ligand and polypeptide and pharmaceutical

JOURNAL composition containing the same

Patent: US 5962406-A 22 05-OCT-1999;

FEATURES Location/Qualifiers

source 1..878

BASE COUNT 277 a 178 c 203 g 220 t

ORIGIN

Query Match 80.6%; Score 631.4; DB 6; Length 878;

Best Local Similarity 99.8%; Pred. No. 7.5e-156;

Matches 632; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 151 GATAGGTCGAG 210
Dh 225 GATAGGTCGAG 284
Qy 211 AGATGCAACAAAG 270
Dh 285 AGATGCAACAAAG 344
Qy 271 TTGAAAGCCTTGCAAGAGATTAACGTTAAACAAAGAGAGAGAGAGAGAGAGAGAG 330
Dh 345 TTGAAAGCCTTGCAAGAGATTAACGTTAAACAAAGAGAGAGAGAGAGAGAGAGAG 404
Qy 331 GAAATGCAAAAG 390
Dh 405 GAAATGCAAAAG 464
Qy 391 AGTAATGAG 450
Dh 465 AGTAATGAG 524
Qy 451 TTGTAATGCTTGAAG 510
Dh 525 TTGTAATGCTTGAAG 584

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QY 511 TACACTCAAGTCACTTCTGCTTAATCGGAGCCTTGGAGTCAAGCCCATTCATCGTC 570
DB 585 TACACTCAAGTCACTTCTGCTTAATCGGAGCCTTGGAGTCAAGCCCATTCATCGTC 644
QY 571 GGCTCTGGCTGAAGCCGAGCATTTGATCTGAGAGATCTTACTCAAGCGGCAAAATACC 630
DB 645 GGCTCTGGCTGAAGCCGAGCATTTGATCTGAGAGATCTTACTCAAGCGGCAAAATACC 704
QY 631 CACAGTTCCTCCAGCTTTGGAGAGAGCTGCTTCACTTGGGCGGAGTGTGAATTA 690
DB 705 CACAGTTCCTCCAGCTTTGGAGAGAGCTGCTTCACTTGGGCGGAGTGTGAATTA 764
QY 691 CACAGTTCCTCCAGCTTTGGAGAGAGCTGCTTCACTTGGGCGGAGTGTGAATTA 750
DB 765 CACAGTTCCTCCAGCTTTGGAGAGAGCTGCTTCACTTGGGCGGAGTGTGAATTA 824
QY 751 GGCTTCATCTTTGGCTTACTCAAACTCTGA 783
DB 825 GGCTTCATCTTTGGCTTACTCAAACTCTGA 857

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```

RESULT 15
AR085426 878 bp DNA linear PAT 01-SEP-2000
LOCUS AR085426
DEFINITION Sequence 22 from patent US 5981724.
ACCESSION AR085426
VERSION AR085426.1 GI:10012195
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 878)
AUTHORS Armitage,R.J., Fanslow,W.C., Spriggs,M.K., Srinivasan,S.,
Gibson,W.G., Morris,A.E. and McGraw,J.T.
TITLE DNA encoding CD40 ligand, a cytokine that binds CD40
JOURNAL Patent: US 5981724-A 22 09-NOV-1999;
FEATURES
location/Qualifiers
source 1..878
BASE COUNT 277 a 178 c 203 g 220 t
ORIGIN

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Query Match 80.6%; Score 631.4; DB 6; Length 878;
Best Local Similarity 99.8%; Pred. No. 7,5e-156;
Matches 632; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 151 GATAAGGTCAAGAGAGAAAGTAAACCTTCATGAAGATTTGTATTCATAAAAAGCTAAAG 210
DB 225 GATAAGGTCAAGAGAGAAAGTAAACCTTCATGAAGATTTGTATTCATAAAAAGCTAAAG 284
QY 211 AGATGCAACAAAGAGAGAGATCTTATCTGCTGAACCTGAGAGATGAGAGGCA 270
DB 285 AGATGCAACAAAGAGAGAGATCTTATCTGCTGAACCTGAGAGATGAGAGGCA 344
QY 271 TTGGAAGCCTTGTCAAGAGATTAACGTTAAACAAAGAAAGAAAAAGAAACAGCTTT 330
DB 345 TTGGAAGCCTTGTCAAGAGATTAACGTTAAACAAAGAAAGAAAAAGAAACAGCTTT 404
QY 331 GAAATGCAAAAGAGTATGAGATCTTCAAAATTCAGACACAGTTGTAAAGGCAAC 390
DB 405 GAAATGCAAAAGAGTATGAGATCTTCAAAATTCAGACACAGTTGTAAAGGCAAC 464
QY 391 AGTAATGACAGATCCGTTTACAGTGGCCAGAAAGATATTATACATGAAAGCAAC 450
DB 465 AGTAATGACAGATCCGTTTACAGTGGCCAGAAAGATATTATACATGAAAGCAAC 524
QY 451 TTGGAATGCTTGAAGAAATGAGAAACAGCTGACGTTTAAAGAGAGAGCTTATATGTC 510
DB 525 TTGGAATGCTTGAAGAAATGAGAAACAGCTGACGTTTAAAGAGAGAGCTTATATGTC 584
QY 511 TACACTCAAGTCACTTCTGCTTAATCGGAGCCTTGGAGTCAAGCCCATTCATCGTC 570
DB 585 TACACTCAAGTCACTTCTGCTTAATCGGAGCCTTGGAGTCAAGCCCATTCATCGTC 644

```

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DB 585 TACACTCAAGTCACTTCTGCTTAATCGGAGCCTTGGAGTCAAGCCCATTCATCGTC 644
QY 571 GGCTCTGGCTGAAGCCGAGCATTTGATCTGAGAGATCTTACTCAAGCGGCAAAATACC 630
DB 645 GGCTCTGGCTGAAGCCGAGCATTTGATCTGAGAGATCTTACTCAAGCGGCAAAATACC 704
QY 631 CACAGTTCCTCCAGCTTTGGAGAGAGCTGCTTCACTTGGGCGGAGTGTGAATTA 690
DB 705 CACAGTTCCTCCAGCTTTGGAGAGAGCTGCTTCACTTGGGCGGAGTGTGAATTA 764
QY 691 CACAGTTCCTCCAGCTTTGGAGAGAGCTGCTTCACTTGGGCGGAGTGTGAATTA 750
DB 765 CACAGTTCCTCCAGCTTTGGAGAGAGCTGCTTCACTTGGGCGGAGTGTGAATTA 824
QY 751 GGCTTCATCTTTGGCTTACTCAAACTCTGA 783
DB 825 GGCTTCATCTTTGGCTTACTCAAACTCTGA 857

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Search completed: March 9, 2003, 02:11:26
Job time : 2042.79 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 8, 2003, 21:32:03 ; Search time 1286.6 Seconds
(without alignments)
9856.249 Million cell updates/sec

Title: US-08-982-272-3
Perfect score: 783
Sequence: 1 ATGATCGAATCACTCAACCA.....TTGGCTTACTCAACTCTGA 783

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1_0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	312.2	39.9	492	12	BF599437 263218 MAR
2	254.8	32.5	398	10	AM486605 75217 MAR
3	72.8	9.3	638	9	AI982044 pat.pK007
4	55.8	7.1	997	17	CNS0057E
5	52.8	6.7	797	9	AL534423
6	49.8	6.4	878	17	CNS0187R

Result No.	Score	Query Match	Length	ID	Description
7	49.6	6.3	1043	17	CNS0145P
8	48.8	6.2	1101	17	CNS0039G
9	47.8	6.1	1038	17	CNS0108N
10	46.4	5.9	920	17	AZ691914
11	46.4	5.9	1101	17	CNS0181N
12	45.6	5.8	828	17	CNS011TX
13	45.2	5.8	458	9	AL514085
14	45.2	5.8	559	17	A0373239
15	44.6	5.7	529	9	AL514657
16	44.6	5.7	611	13	B1389827
17	44.4	5.7	807	17	CNS0119V
18	44.4	5.7	814	17	AZ203738
19	44.2	5.6	938	17	CNS0067U
20	44	5.6	802	17	CNS0033B
21	43.8	5.6	329	9	AL513719
22	43.8	5.6	799	17	CNS011SA
23	43.8	5.6	1101	17	CNS0182P
24	43.6	5.6	458	9	AL514085
25	43.6	5.6	588	17	AQ451757
26	43.6	5.6	828	17	CNS018FA
27	43.6	5.6	1039	17	CNS02ADN
28	43.6	5.6	1101	17	CNS0000D1
29	43.4	5.5	1201	17	CNS0168L
30	43.2	5.5	889	17	CNS006MT
31	43	5.5	642	13	B1096268
32	42.8	5.5	534	17	CNS003HB
33	42.8	5.5	597	9	AL514721
34	42.8	5.5	1101	17	CNS001LD
35	42.6	5.4	307	17	CNS00A3W
36	42.6	5.4	415	14	R41111
37	42.6	5.4	595	17	AQ521025
38	42.6	5.4	633	9	AL513979
39	42.6	5.4	744	17	AG044338
40	42.6	5.4	805	9	A1557564
41	42.6	5.4	959	17	CNS00655
42	42.6	5.4	1007	17	CNS06X9S
43	42.6	5.4	1101	17	CNS0039L
44	42.6	5.4	1101	17	CNS0100X
45	42.2	5.4	330	9	AL513817

ALIGNMENTS

RESULT 1
LOCUS BF599437 492 bp mRNA linear EST 25-APR-2001
DEFINITION 263218 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BF599437
VERSION BF599437.1 GI:11695919
KEYWORDS EST.
SOURCE BOV.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.

REFERENCE
AUTHORS Smith,T.P.L., Grose,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
1 (bases 1 to 492)
Caese,E., Wray,J.E., White,J., Cho,J., Fahrrenkrug,S.C., Bennett,
G.L., Heaton,M.P., Laegreid,W.M., Kohner,G.A., Chitko-Hckom,C.G.,
Petra,G., Holt,I., Karaycheva,S., Liang,F., Quackenbush,J. and
Keele,J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
21180013

TITLE
JOURNAL
MEDLINE
COMMENT

Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred

v0.980904.e. Vector identified by cross_match with the -minscore 18 and -mismatch 12 options.

PCR Primers
FORWARD: AGGAAACAGCTATGACCT
BACKWARD: GTTTCAGCTACAGC
Plate: 33 row: N column: 5
Seq primer: ATTAGTGACACTATAG.

FEATURES

Location/Qualifiers
1..492
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 380V"
/tissue_type="pooled"
/lab_host="DH10B"

/note="Vector: PCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendinosus muscle, and fetal
longissimus muscle."

BASE COUNT 163 a 103 c 104 g 122 t

ORIGIN

Query Match 39.9%; Score 312.2; DB 12; Length 492;
Best Local Similarity 82.9%; Pred. No. 56-58;
Matches 369; Conservative 0; Mismatches 73; Indels 3; Gaps 1;

QY 1 ATGATCGAAACATACACCAACCTTCCCGATCGCGCAGCTGACCTGCCATCAGC 60
DB 46 ATGATCGAAACATACACCAACCTTCCCGATCGCGCAGCTGACCTGCCATCAGT 105
QY 61 ATGAAATTTTATGATTTTACTTACTTCTTATCACCAGATGATGGGTGACGA 120
DB 106 ATGAAATTTTATGATTTTACTTACTTCTTATCACCAGATGATGGGTGACGG 165
QY 121 CTTTTCGTGTATCTTATCAGATGATGATGATGATGATGATGATGATGATGAT 180
DB 166 CTTTTCGTGTATCTTATCAGATGATGATGATGATGATGATGATGATGATGAT 225
QY 181 GAAATTTTGTATCTTATCAGATGATGATGATGATGATGATGATGATGATGAT 240
DB 226 GAAATTTTGTATCTTATCAGATGATGATGATGATGATGATGATGATGATGAT 285
QY 241 TTGCTGACTGTAGAGATGAGAGCAATTTGAAAGCTTGTCAAGATATTAAGTTA 300
DB 286 TTACTGAAGCTGTAGAGATGAGAGCAATTTGAAAGCTTGTCAAGATATTAAGTTA 345
QY 301 AACAAAGAG--AGAAAAAGAAAAAGCACTTTGAAAGCAAGAGTATGAGATCT 357
DB 346 AACAAAGAGTAAAGAGAAAAAGCACTTTGAAAGTATGAGATGAGAGCTT 405
QY 358 CAAATTCAGACACCTTGTAAAGCAAGCAAGTATGAGATGAGATGAGATGAGAT 417
DB 406 CAGATAGCGGCATGTCATGATGAGGCGCAGATGATGATGATGATGATGATGAT 465
QY 418 GCCAAGAAAGATATTAATCAATGA 442
DB 466 GCCCCCAAGATATTAATCAATGA 490

RESULT 2

AM486605 398 bp mRNA linear EST 25-Apr-2001
LOCUS 75217 MARC 180V Bos taurus cDNA 5', mRNA sequence.
DEFINITION AM486605
ACCESSION AM486605.1 GI:7056711
VERSION
KEYWORDS EST.
SOURCE
ORGANISM Bos taurus
Cow.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.

REFERENCE

1 (bases 1 to 398)
Smith,T.P.L., Grobse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Caas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett

G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,
Petter,G., Holt,I., Karamycheva,S., Lang,F., Quackenbush,J. and
Keele,J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)

COMMENT

Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4365
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Baes called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 20
and -mismatch 12 options.

PCR Primers
FORWARD: AGGAAACAGCTATGACCT
BACKWARD: GTTTCAGCTACAGCAGC
Plate: 34 row: F column: 23
Seq primer: ATTAGTGACACTATAG.

FEATURES

Location/Qualifiers
1..398
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 180V"
/tissue_type="pooled"
/lab_host="DH10B"

/note="Vector: PCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from lymph node, ovary,
fat, hypothalamus, and pituitary."

BASE COUNT 134 a 77 c 82 g 105 t

ORIGIN

Query Match 32.5%; Score 254.8; DB 10; Length 398;
Best Local Similarity 85.5%; Pred. No. 1,7e-45;
Matches 296; Conservative 0; Mismatches 47; Indels 3; Gaps 1;

QY 1 ATGATGAAACATACACCAACCTTCCCGATCGCGCAGCTGACCTGCCATCAGC 60
DB 53 ATGATGAAACATACACCAACCTTCCCGATCGCGCAGCTGACCTGCCATCAGT 112
QY 61 ATGAAATTTTATGATTTTACTTACTTCTTATCACCAGATGATGGGTGACGA 120
DB 113 ATGAAATTTTATGATTTTACTTACTTCTTATCACCAGATGATGGGTGACGG 172
QY 121 CTTTTCGTGTATCTTATCAGATGATGATGATGATGATGATGATGATGATGAT 180
DB 173 CTTTTCGTGTATCTTATCAGATGATGATGATGATGATGATGATGATGATGAT 232
QY 181 GAAATTTTGTATCTTATCAGATGATGATGATGATGATGATGATGATGATGAT 240
DB 233 GAAATTTTGTATCTTATCAGATGATGATGATGATGATGATGATGATGATGAT 292
QY 241 TTGCTGACTGTAGAGATGAGAGCAATTTGAAAGCTTGTCAAGATATTAAGTTA 300
DB 293 TTACTGAAGCTGTAGAGATGAGAGCAATTTGAAAGCTTGTCAAGATATTAAGTTA 352
QY 301 AACAAAGAG--AGAAAAAGAAAAAGCACTTTGAAAGCAAGAGTATGAGATCT 343
DB 353 AACAAAGAGTAAAGAGAAAAAGCACTTTGAAAGTATGAGATGAGAGCTT 398

RESULT 3

AI982044 638 bp mRNA linear EST 07-MAY-2001
LOCUS 1A1982044
DEFINITION pat.pK0072.c9.f chicken activated T cell cDNA Gallus gallus cDNA
clone pat.pK0072.c9.f 5' similar to CD40 ligand, mRNA sequence.
ACCESSION AI982044
VERSION AI982044.1 GI:5885072
KEYWORDS EST.
SOURCE
ORGANISM Gallus gallus

d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Rayan. It has been constructed in the vector pBelobAC11.

FEATURES

source

Location/Qualifiers
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/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="BACN03101"
/clone_lib="DrosBAC"
/plasmid="pBelobAC11"
/note="end : 596"
BASE COUNT 372 a 6 c 119 g 219 t 322 others
ORIGIN

Query Match 6.1%; Score 47.8; DB 17; Length 1038;
Best Local Similarity 34.6%; Pred. No. 1.7;
Matches 155; Conservative 20; Mismatches 273; Indels 0; Gaps 0;

72 TATGATTTACTTCTGCTTTTCTTATACCCAGATGATGGGTGACACTTTTGTCTGT 131
Db TTTTNNNTTTNNNNNTTTTGTGTMNNAACVTTTATTTTATTTTATTTTATTTTAA 96
Qy 132 GTATCTTCATGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 191
Db 97 TTAATAAAGYRCANCANCTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 156
Qy 192 ATTCATTAAGGATGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 251
Db 157 TTTTNTTTTATTTNN 216
Qy 252 TGAGAGATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 311
Db 217 NNNNTNNTTAAANNAATTTATTAATTAATTAATTAATTAATTAATTAATTAATTA 276
Qy 312 GAAAAAGAAAAAGCTTTGAAATGCAAGAGCTGATGAGATCTCTCAATGCGACACA 371
Db 277 AAAAAAGAAAAAGCTTTGAAATGCAAGAGCTGATGAGATCTCTCAATGCGACACA 336
Qy 372 CGTTGAAGCAAGCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 431
Db 337 AAAAAAGAAAAAGCTTTGAAATGCAAGAGCTGATGAGATCTCTCAATGCGACACA 396
Qy 432 TTATACATGAAGCACTGTTGAAATGCAAGAGCTGATGAGATCTCTCAATGCGACACA 491
Db 397 TATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 456
Qy 492 AGAAGACTTATTTATGCTTCACTCAA 519
Db 457 ADWDAAAAAAATWDTGKKAASAAAA 484

RESULT 10
AZ691914 920 bp DNA linear GSS 14-DEC-2000
LOCUS ENTM26TR Entamoeba histolytica Sheared DNA Entamoeba histolytica
DEFINITION genomic, DNA sequence.
ACCESSION AZ691914
VERSION AZ691914.1 GI:11829180
KEYWORDS GSS.
SOURCE Entamoeba histolytica.
ORGANISM Entamoeba histolytica.
REFERENCE 1 (bases 1 to 920)
Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HML:IMSS sheared DNA library
Unpublished (2000)
JOURNAL Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208

Fax: 301 838 3543
Email: bjoftus@igf.org
Clones are derived from the Entamoeba histolytica HML:IMSS sheared DNA library
Seq primer: M13-Reverse
Class: shotgun
High quality sequence start: 15
High quality sequence stop: 330.
Location/Qualifiers
1..920
/organism="Entamoeba histolytica"
/strain="HML:IMSS"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pBOS1; Site: 1; Bst I: Constructed at The Institute for Genomic Research (IGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (~2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaubin and B. Barrell, Oxford University Press, 1999)."

FEATURES

source

BASE COUNT 354 a 54 c 131 g 381 t
ORIGIN
Query Match 5.9%; Score 46.4; DB 17; Length 920;
Best Local Similarity 54.8%; Pred. No. 3.6;
Matches 92; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

Qy 186 TTTTGTATCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 245
Db 687 TTTTGTATCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 746
Qy 246 GAACGTGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAG 305
Db 747 TTATGG 806
Qy 306 AGAAGAAAAAGAAAAAGCACTTTGAAATGCAAGAGCTGATGAGATCTCTCAATGCGAC 353
Db 807 AAAAAAGATGAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAA 854

RESULT 11
CNS0181N 1101 bp DNA linear GSS 26-JUL-1999
LOCUS Drosophila melanogaster genome survey sequence Spe end of BAC
DEFINITION BACN37P10 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION AL108773.1 GI:5629077
VERSION AL108773
KEYWORDS GSS.
SOURCE Drosophila melanogaster.
ORGANISM Drosophila melanogaster.
REFERENCE 1 (bases 1 to 1101)
Genoscope.
Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail: seqreg@genoscope.cns.fr - Web: www.genoscope.cns.fr)
Determination of this BAC end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billand at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton

1

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: March 8, 2003, 18:30:53 ; Search time 163.589 Seconds
(without alignments)
10778.963 Million cell updates/sec

Title: US-08-982-272-3
Perfect score: 783
Sequence: 1 ATGATCGAAACATACACCA.....TTGGCTTACTCAACTCTGA 783

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 112599159 residues
Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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24: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	783	100.0	783	19	AAV38999
2	773.4	98.8	783	19	AAV39001
3	751	95.9	783	19	AAV38998
4	751	95.9	818	19	AAV61062
5	749.4	95.7	783	15	AAO63960
6	749.4	95.7	783	19	AAV12853
7	749.4	95.7	783	20	AAZ27524
8	745.2	95.2	782	14	AAQ41507
9	648.6	82.8	783	19	AAV42184

10	645.2	82.4	1477	22	AAH25527	Nucleotide sequence
11	632.6	80.8	818	16	AAH05762	Murine CD40 ligand
12	631.4	80.6	878	20	AAZ27538	Mouse trimeric CD4
13	592.4	75.7	786	15	AAO63959	Human CD40-L type
14	592.4	75.7	786	19	AAV38997	CD40 ligand gene u
15	592.4	75.7	786	19	AAV12852	CD40 ligand coding
16	592.4	75.7	840	14	AAQ41506	CD40-L DNA. Homo
17	592.4	75.7	840	16	AAO67123	CD40 ligand gene.
18	592.4	75.7	840	16	AAO57633	Human CD40 ligand
19	592.4	75.7	840	18	AAV93782	CDNA of CD40L, a n
20	592.4	75.7	840	19	AAV61063	Human CD40-L codin
21	592.4	75.7	840	20	AAZ27525	Nucleotide sequence
22	592.4	75.7	879	22	AAZ55539	Human CD40 ligand
23	592.4	75.7	1816	21	AAAS1745	Human CD40L mtein
24	592.4	75.7	1816	23	AAH86571	Human CD40L mtein
25	591	75.5	840	15	AAV58122	Genomic sequence o
26	589.2	75.2	840	15	AAO57984	Human CD40-L CDNA.
27	587.6	75.0	840	16	AAO94091	Human CD40-L CDNA.
28	582.8	72.8	786	19	AAV39000	Exemplary CD40 lig
29	570	71.6	786	19	AAV39003	Exemplary CD40 lig
30	560.4	69.1	864	19	AAV39004	CD40 ligand gene u
31	541.2	69.1	885	21	AAZ55540	Feline CD154 CDNA.
32	535	68.3	885	21	AAZ55541	Feline CD154 CDNA
33	535	68.3	885	21	AAZ55542	Feline CD154 CDNA
34	532	67.9	780	21	AAZ55543	Feline CD154 CDNA
35	532	67.9	780	21	AAZ55544	Canine CD154 CDNA
36	527	67.3	1878	21	AAZ55545	Canine CD154 CDNA
37	527	67.3	1878	21	AAZ55546	Canine CD154 CDNA
38	524	66.9	780	21	AAZ55547	Canine CD154 CDNA
39	524	66.9	780	21	AAZ55548	Canine CD154 CDNA
40	454.6	58.1	1532	22	AAH25535	Nucleotide sequence
41	449.2	57.4	865	22	AAH2933	HIV-1 gp120 V3 100
42	449.2	57.4	906	22	AAH2932	HIV-1 gp120 V3 100
43	449.2	57.4	2209	22	AAH2929	HIV-1 gp120-human
44	449.2	57.4	2252	22	AAH2928	HIV-1 gp120-human
45	446.2	57.0	1425	14	AAQ41516	Human CD40-L/Fc fu

ALIGNMENTS

RESULT 1	AAV38999	standard; DNA; 783 BP.
ID	AAV38999	
AC	AAV38999	
XX		
DT	23-SEP-1998	(first entry)
XX		
DE	Exemplary CD40 ligand gene used in the course of the invention.	
XX		
KW	CD40 ligand; alteration; immunoreactivity; human cell;	
KW	accessory molecule; ligand; AMI; gene therapy; treatment; neoplasia;	
KW	autoimmune disorder; rheumatoid arthritis; vaccine; chimera; ss.	
OS	Chimeric - Mus sp.	
OS	Chimeric - Homo sapiens.	
XX		
PN	WO9826061-A2.	
XX		
PD	18-JUN-1998.	
XX		
FE	08-DEC-1997;	97MO-US22740.
XX		
PR	01-DEC-1997;	97US-0982272.
PR	09-DEC-1996;	96US-0032145.
XX		
PA	(REGC) UNIV CALIFORNIA.	
XX		
PI	Cantwell M, Kipps TJ, Sharma S;	
XX		
DR	WPI; 1998-348521/30.	
XX		

PT Vectors containing accessory molecule ligand genes - used for
 PT altering immunoreactivity of cells, particularly for treatment of
 PT neoplasia or autoimmune disorders, e.g. rheumatoid arthritis
 XX
 XX Disclosure, Page 105; 167pp; English.

XX The present sequence represents an exemplary CD40 ligand gene,
 CC comprising nucleotides encoding the extracellular domains (Domains III
 CC and IV) of the murine CD40 ligand gene (AAV38997) operatively linked to
 CC nucleotides encoding the extracellular domains (domains III and IV) and
 CC transmembrane domain (Domain II) of human CD40 ligand gene (AAV38998).
 CC The sequence is used to exemplify the method of the invention. The
 CC specification describes a method for altering the immunoreactivity of
 CC human cells which comprises introducing a gene encoding an accessory
 CC molecule ligand (AML) into the cells so that the AML is expressed on the
 CC surface of the cells. Vectors containing the AML genes can be used in
 CC gene therapy for treating neoplasia or autoimmune disorders such as
 CC rheumatoid arthritis. They can also be used for vaccination to produce
 CC immunity against a virus cell, bacteria, protein, fungus or neoplasia.
 XX
 XX Sequence 783 BP; 243 A; 161 C; 175 G; 204 T; 0 other;

Query Match 100.0%; Score 783; DB 19; Length 783;
 Best Local Similarity 100.0%; Pred. No. 5e-210;
 Matches 783; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGATGAACATACACCAACTTCCCGATCTGCGGCACTGGACCTGCCATCAGC 60
 Db 1 ATGATGAACATACACCAACTTCCCGATCTGCGGCACTGGACCTGCCATCAGC 60
 Qy 61 ATGAAATTTTATGATTTTACTCTGTTTCTTATCCACCAAGATGAGGTGACGA 120
 Db 61 ATGAAATTTTATGATTTTACTCTGTTTCTTATCCACCAAGATGAGGTGACGA 120
 Qy 121 CTTTGTGCTGTATCTTCAAGAGATTGATGAGTGAAGAGAGAGAGTAACTTCAAT 180
 Db 121 CTTTGTGCTGTATCTTCAAGAGATTGATGAGTGAAGAGAGAGAGTAACTTCAAT 180
 Qy 181 GAAGATTTTATTCATTAATAAAGCTTAAAGATGACCAAGAGAGAGATCTTATCC 240
 Db 181 GAAGATTTTATTCATTAATAAAGCTTAAAGATGACCAAGAGAGAGATCTTATCC 240
 Qy 241 TTGCTGAACCTGTGAGAGATGAGAGCAATTTGAAGACCTTGTCAAGATATTAAGCTTA 300
 Db 241 TTGCTGAACCTGTGAGAGATGAGAGCAATTTGAAGACCTTGTCAAGATATTAAGCTTA 300
 Qy 301 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATCTTCA 360
 Db 301 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATCTTCA 360
 Qy 361 ATTGACAGACAGCTTGTAAAGCAAGCAAGTATGACAGATCCGTTCTACAGTGGGCC 420
 Db 361 ATTGACAGACAGCTTGTAAAGCAAGCAAGTATGACAGATCCGTTCTACAGTGGGCC 420
 Qy 421 AAGAAAGATTTATTCATTAATAAAGCTTAAAGATGACCAAGAGAGAGATCTTCA 480
 Db 421 AAGAAAGATTTATTCATTAATAAAGCTTAAAGATGACCAAGAGAGAGATCTTCA 480
 Qy 481 ACGTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATCTTCA 540
 Db 481 ACGTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATCTTCA 540
 Qy 541 GAGCTTGAAGTCAAGGCCATTCATGCTGGGCTGTGCTGGAAGCCACATTTGATCT 600
 Db 541 GAGCTTGAAGTCAAGGCCATTCATGCTGGGCTGTGCTGGAAGCCACATTTGATCT 600
 Qy 601 GAGAGATCTTACTCAAGCGGCAATACCAAGTTCCTCCAGCTTTGCGAGAGAG 660
 Db 601 GAGAGATCTTACTCAAGCGGCAATACCAAGTTCCTCCAGCTTTGCGAGAGAG 660
 Qy 661 TCTGTTCACTGGGCGAGTGTGATTAACAGCTGGTGTCTGTGTTTGTCAAGCTG 720
 Db 661 TCTGTTCACTGGGCGAGTGTGATTAACAGCTGGTGTCTGTGTTTGTCAAGCTG 720

Qy 721 ACTGAAGCAAGCCAGATGATCCAGAGTGGCTTCTCATCTTTGGCTTACTCAATC 780
 Db 721 ACTGAAGCAAGCCAGATGATCCAGAGTGGCTTCTCATCTTTGGCTTACTCAATC 780
 Qy 781 TGA 783
 Db 781 TGA 783

RESULT 2
 ID AAV39001 standard; DNA; 783 BP.
 XX AAV39001;
 AC AAV39001;
 XX
 DT 23-SEP-1998 (first entry)
 XX
 DE Exemplary CD40 ligand gene used in the course of the invention.
 XX
 KW CD40 ligand; alteration; immunoreactivity; human cell;
 KW accessory molecule ligand; AML; gene therapy; treatment; neoplasia;
 KW autoimmune disorder; rheumatoid arthritis; vaccine; chimera; ss.
 XX
 OS Chimeric - Mus sp.
 OS Chimeric - Homo sapiens.
 XX
 PN W09826061-A2.
 XX
 PD 18-JUN-1998.
 PF 08-DEC-1997; 97WO-US22740.
 XX
 PR 01-DEC-1997; 97US-0982272.
 PR 09-DEC-1996; 96US-0032145.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Cantwell M, Kipps TJ, Sharma S;
 XX
 DR WPI, 1998-348521/30.
 XX
 PT Vectors containing accessory molecule ligand genes - used for
 PT altering immunoreactivity of cells, particularly for treatment of
 PT neoplasia or autoimmune disorders, e.g. rheumatoid arthritis
 XX
 XX Disclosure, Page 106; 167pp; English.
 XX The present sequence represents an exemplary CD40 ligand gene,
 CC comprising nucleotides encoding the extracellular domains (Domains III
 CC and IV) and transmembrane domain (Domain II) of the murine CD40 ligand gene
 CC (AAV38997) operatively linked to nucleotides encoding the cytoplasmic
 CC domain of the human CD40 ligand gene (AAV38998). The sequence is used to
 CC exemplify the method of the invention. The specification describes a
 CC method for altering the immunoreactivity of human cells which comprises
 CC introducing a gene encoding an accessory molecule ligand (AML) into the
 CC cells so that the AML is expressed on the surface of the cells. Vectors
 CC containing the AML genes can be used in gene therapy for treating
 CC neoplasia or autoimmune disorders such as rheumatoid arthritis. They can
 CC also be used for vaccination to produce immunity against a virus cell,
 CC bacteria, protein, fungus or neoplasia.
 XX
 XX Sequence 783 BP; 243 A; 161 C; 174 G; 205 T; 0 other;

Query Match 98.8%; Score 773.4; DB 19; Length 783;
 Best Local Similarity 99.2%; Pred. No. 2.5e-207;
 Matches 777; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ATGATGAACATACACCAACTTCCCGATCTGCGGCACTGGACCTGCCATCAGC 60
 Db 1 ATGATGAACATACACCAACTTCCCGATCTGCGGCACTGGACCTGCCATCAGC 60
 Qy 61 ATGAAATTTTATGATTTTACTCTGTTTCTTATCCACCAAGATGAGGTGACGA 120

Db	61	ATGAAATTTTATGATTTACTACTGTTTCTCTTATCACCCAATGATGGATCTGTG	120
Qy	121	CTTTTTCGTGTATCTTCAATGAAAGTTGGATTAAGTGAAGGAAGTAACTTAT	180
Db	121	CTTTTTCGTGTATCTTCAATGAAAGTTGGATTAAGTGAAGGAAGTAACTTAT	180
Qy	181	GAGATTTTGTATTCATAAAAAGCTAAAGATGCAACAAAGAGAGATCTTATCC	240
Db	181	GAGATTTTGTATTCATAAAAAGCTAAAGATGCAACAAAGAGAGATCTTATCC	240
Qy	241	TTCGTGAACCTGAGGAGATGGAAGGCAATTGGAACCTTTCACGATTAACGTTA	300
Db	241	TTCGTGAACCTGAGGAGATGGAAGGCAATTGGAACCTTTCACGATTAACGTTA	300
Qy	301	AACAAGAGAGAAAAAAGAAAAAGCTTTGAATCAAGAGGTGATGAGATCTCA	360
Db	301	AACAAGAGAGAAAAAAGAAAAAGCTTTGAATCAAGAGGTGATGAGATCTCA	360
Qy	361	ATTGCAAGACGTTGTAAGCGCAAGCAACGTAAATGCAAGATCCGTTCAAGTGGCC	420
Db	361	ATTGCAAGACGTTGTAAGCGCAAGCAACGTAAATGCAAGATCCGTTCAAGTGGCC	420
Qy	421	AGAAAAGATATTATACATGAAAAAGCACTTGTATCTTGAATAAGGAAACAGCTG	480
Db	421	AGAAAAGATATTATACATGAAAAAGCACTTGTATCTTGAATAAGGAAACAGCTG	480
Qy	481	ACGGTTAAAAAGAGGACATTAATGTCGACATCAAGTCACTTCCTGCTTAATGG	540
Db	481	ACGGTTAAAAAGAGGACATTAATGTCGACATCAAGTCACTTCCTGCTTAATGG	540
Qy	541	GAGCTTGAATCAAGCCCATTCATGCTGGGCTCTGGCTGAAGCCACAGATTGATCT	600
Db	541	GAGCTTGAATCAAGCCCATTCATGCTGGGCTCTGGCTGAAGCCACAGATTGATCT	600
Qy	601	GAGAGATCTTACTCAAGCGGCAATTAACCAAGTTCCTCCACGTTTGCAGAGAG	660
Db	601	GAGAGATCTTACTCAAGCGGCAATTAACCAAGTTCCTCCACGTTTGCAGAGAG	660
Qy	661	TCTGTTCACTTGGCGGAGTGTGAATTACAGCTGAGTCTCTGTGTGTCAAGTG	720
Db	661	TCTGTTCACTTGGCGGAGTGTGAATTACAGCTGAGTCTCTGTGTGTCAAGTG	720
Qy	721	ACTGAAGCAACCAAGGATCCACAGAGTTGGCTCTCATCTTTTGGCTTACCAATC	780
Db	721	ACTGAAGCAACCAAGGATCCACAGAGTTGGCTCTCATCTTTTGGCTTACCAATC	780
Qy	781	TGA 783	
Db	781	TGA 783	

	RESULT 3
AAV38998	
ID	AAV38998 standard; DNA; 783 BP.
XX	
AC	AAV38998;
XX	
DT	23-SEP-1998 (first entry)
XX	
DE	CPd40 ligand gene used in the course of the invention.
XX	
XX	
KM	CPd40 ligand; alteration; immunoreactivity; human cell;
KM	accessory molecule ligand; AML; gene therapy; treatment; neoplasia;
KM	autoimmune disorder; rheumatoid arthritis; vaccine; ss.
XX	
OS	Homo sapiens.
XX	
PM	MO9826061-A2.
XX	
PD	18-JUN-1998.
XX	
PF	08-DEC-1997; 97WO-US22740.

PR	01-DEC-1997;	97US-0982272.
PR	09-DEC-1996;	96US-0032145.
XX		
PA	(REGC) UNIV CALIFORNIA.	
XX		
PI	Cantwell M, Kipps TJ, Sharma S;	
DR	MP1; 1998-348521/30.	
XX		
FT	Vectors containing accessory molecule ligand genes - used for	
FT	altering immunoreactivity of cells, particularly for treatment of	
FT	neoplasia or autoimmune disorders, e.g. rheumatoid arthritis	
XX		
PS	Disclosure; Pages 104-105; 167p; English.	
XX		
CC	The present sequence represents a CD40 ligand gene. The sequence is	
CC	used to exemplify the method of the invention. The specification	
CC	describes a method for altering the immunoreactivity of human cells	
CC	which comprises introducing a gene encoding an accessory molecule	
CC	ligand (AML) into the cells so that the AML is expressed on the surface	
CC	of the cells. Vectors containing the AML genes can be used in gene	
CC	therapy for treating neoplasia or autoimmune disorders such as rheumatoid	
CC	arthritis. They can also be used for vaccination to produce immunity	
CC	against a virus cell, bacteria, protein, fungus or neoplasia.	
XX		
SO	Sequence 783 BP; 243 A; 159 C; 177 G; 204 T; 0 other:	
	Query Match	95.9%; Score 751; DB 19; Length 783;
	Best Local Similarity	97.4%; Pred. No. 5e-201;
	Matches 763; Conservative	0; Mismatches 20; Indels 0; Gaps
Oy	1	ATGATCGAATCATACAAACCACTTCCTCCGATCTGCGGACATGACATCGCCATCAGC 60
Ds	1	ATGATATAAACAATACAGCAACTTCCCAAGATCGGTGCAATGACATCTCCAGCAGC 60
Oy	61	ATGAAAATTTTATGATTTTACTTACTGTTTTCTTATACCCAGATGATGGGTGACGA 120
Ds	61	ATGAAGATTTTATGATTTTACTTACTGTTTTCTTATACCCAAATGATTTGATCTGTG 120
Oy	121	CTTTTTCCTGTGATCTTCAATAGAAATGGATGGATGGTGAAGAGAAATCCTTCAAT 180
Ds	121	CTTTTTCCTGTGATCTTCAATATAAATTTGATAGGTGGAAGAGAAATGAACTTCAAT 180
Oy	181	GAAATTTTGTATTCATATAAAGCTAAAGATGACAAAGAGAGATCTTTATCC 240
Ds	181	GAAATTTTGTATTCATATAAAGCTAAAGATGACAAAGAGAGATCTTTATCC 240
Oy	241	TTGCTGAACGTGAGAGATGAGAAAGCAATTTCAAGACCTTGTCAGATATATACGTTA 300
Ds	241	TTGCTGAACGTGAGAGATGAGAAAGCAATTTCAAGACCTTGTCAGATATATACGTTA 300
Oy	301	AACAAAGAGAGAAAAAGAAAACAGCTTTGAAATGCAAGAGGTATGAGATCTTCAA 360
Ds	301	AACAAAGAGAGAAAAAGAAAACAGCTTTGAAATGCAAGAGGTATGAGATCTTCAA 360
Oy	361	ATTGACACACAGTTGTATGAGAGCAACAGTATATGACATCGTTTCAACAGTGGGCC 420
Ds	361	ATTGACACACAGTTGTATGAGAGCAACAGTATATGACATCGTTTCAACAGTGGGCC 420
Oy	421	AAGAAAGATATTTATACATGAAAGCACTTGATATGCTTGAATGGGAAACAGCTG 480
Ds	421	AAGAAAGATATTTATACATGAAAGCACTTGATATGCTTGAATGGGAAACAGCTG 480
Oy	481	ACGGTATTAAGAGAGACTCTTATATGCTACACTCAAGTCACTTCTCTTATCGG 540
Ds	481	ACGGTATTAAGAGAGACTCTTATATGCTACACTCAAGTCACTTCTCTTATCGG 540
Oy	541	GAGCCTTCAGATCAACGCCATTCATCGTGGCTCTGGCTGAGACCCAGATGGAATCT 600
Ds	541	GAGCCTTCAGATCAACGCCATTCATCGTGGCTCTGGCTGAGACCCAGATGGAATCT 600
Oy	601	GAGGATCTTACTCAAGGCGGCAATACCAACAGTTCTCTCCAGCTTTGCGAGGAGG 660

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Db 601 GAGAGAACTTCTAAGCGGCGAAATATACCAAGTCTCCAGCTTTGCGAGGAGCAG 660
Qy 661 TCTGTTCACTTGGGCGAGTGTGATTAACAGCTGCTTCTGCTTTGTCAAAGCTG 720
Db 661 TCTGTTCACTTGGGCGAGTGTGATTAACAGCTGCTTCTGCTTTGTCAAAGCTG 720
Qy 721 ACTGAGCAAGCCAGTATGATCAAGAGTTGGCTTCTGCTTTGCTTACTCAACTC 780
Db 721 ACTGAGCAAGCCAGTATGATCAAGAGTTGGCTTCTGCTTTGCTTACTCAACTC 780
Qy 781 TGA 783
Db 781 TGA 783

RESULT 4
AAV61062
ID AAV61062 standard; DNA; 818 BP.
XX
AC AAV61062;
XX
DT 08-DEC-1998 (first entry)
XX
DE Murine CD40 ligand encoding DNA sequence.
XX
KM Murine; mouse; CD40 ligand; TNF receptor family; activated T cell;
KM type 2 membrane glycoprotein; cell proliferation; differentiation;
KM B cell; ds.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 13..795
FT /tag= a
FT /product= "CD40 ligand"
XX
PN US5817516-A.
XX
PD 06-OCT-1998.
XX
PF 28-APR-1995; 95US-0431055.
XX
PR 28-APR-1995; 95US-0431055.
PR 28-APR-1994; 94US-0234580.
XX
PA (BOEH ) BOEHRINGER INGELHEIM PHARM INC.
XX
PI Caetle B, Kehry M;
XX
DR WPI, 1998-556393/47.
DR P-PsDB; AAW71750.
XX
XX
PT Increased proliferation of B cells in culture - by incubating them
PT in the presence of membrane-bound CD40 ligand
XX
PS Example 2; Fig 1; 37pp; English.
XX
CC The present sequence encodes murine CD40 ligand which is used in the
CC method of the invention. The method has been developed for proliferating
CC B cells to increase their number at least 100-fold. The method
CC comprises: (a) providing high density, membrane bound CD40 ligand; and
CC (b) culturing one or more B cells in the presence of this ligand. The
CC culture results in a proliferation in the number of B cells of at least
CC 100 fold. Also described is a method as above where the B cells are
CC induced to differentiate into antibody-producing cells in the presence
CC of one or more cytokines. The method can be used for stimulating B-cell
CC proliferation in vitro or in vivo, e.g. for treating conditions in which
CC B-cell proliferation and activation is suppressed. Eight rounds of
CC division over six days can be achieved, corresponding to a 256-fold
CC increase in cell numbers, which is a vast increase compared to previous
CC culturing methods.
XX

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SQ Sequence 818 BP; 249 A; 170 C; 186 G; 213 T; 0 other;
Query Match 95.9%; Score 751; DB 19; Length 818;
Best Local Similarity 97.4%; Pred. No. 5,1e-201;
Matches 763; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
Qy 1 ATGATGAAACATACACCAACTTCTCCGATCTGCGGCACTGAGCTGCCATAGC 60
Db 13 ATGATGAAACATACACCAACTTCTCCGATCTGCGGCACTGAGCTGCCATAGC 72
Qy 61 ATGAAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 120
Db 73 ATGAAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 132
Qy 121 CTTTTCCTGCTGATCTTCAATGAGATTTGATGATGATGATGATGATGATGATGAT 180
Db 133 CTTTTCCTGCTGATCTTCAATGAGATTTGATGATGATGATGATGATGATGATGAT 192
Qy 181 GAAGATTTTGTATTCATTAATAAAGCTTAAAGATGCAACAAAGAGAGATCTTTATCC 240
Db 193 GAAGATTTTGTATTCATTAATAAAGCTTAAAGATGCAACAAAGAGAGATCTTTATCC 252
Qy 241 TTGCTGAATCTGTAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
Db 253 TTGCTGAATCTGTAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 312
Qy 301 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Db 313 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 372
Qy 361 ATTGACGACAGCTTTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Db 373 ATTGACGACAGCTTTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 432
Qy 421 AAGAAAGATATTAATCAATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Db 433 AAGAAAGATATTAATCAATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 492
Qy 481 ACGGTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Db 493 ACGGTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 552
Qy 541 GAGCTTCGAGTCAACGCGCATTCATCGTGGGCTCTGAGTGAAGCCAGAGATGATCT 600
Db 553 GAGCTTCGAGTCAACGCGCATTCATCGTGGGCTCTGAGTGAAGCCAGAGATGATCT 612
Qy 601 GAGAGATCTTACTCAAGGCGGCAATTAACCAAGCTTCTCCAGCTTTGGAGACAGC 660
Db 613 GAGAGATCTTACTCAAGGCGGCAATTAACCAAGCTTCTCCAGCTTTGGAGACAGC 672
Qy 661 TCTGTTCACTTGGGCGAGTGTGATTAACAGCTGCTTCTGCTTTGTCAAAGCTG 720
Db 673 TCTGTTCACTTGGGCGAGTGTGATTAACAGCTGCTTCTGCTTTGTCAAAGCTG 732
Qy 721 ACTGAGCAAGCCAGTATGATCAAGAGTTGGCTTCTGCTTTGCTTACTCAACTC 780
Db 733 ACTGAGCAAGCCAGTATGATCAAGAGTTGGCTTCTGCTTTGCTTACTCAACTC 792
Qy 781 TGA 783
Db 793 TGA 795

RESULT 5
AAQ63960
ID AAQ63960 standard; cDNA to mRNA; 783 BP.
XX
AC AAQ63960;
XX
DT 12-JAN-1995 (first entry)
XX
DM Mouse CD40-L type II transmembrane protein coding sequence.
XX

```

KM Leucine zipper; trimerisation; trimeric CD40-L; fusion protein;
 KM hetero-oligomer; homo-oligomer; type II transmembrane protein;
 KM soluble CD40-L; tumour necrosis factor family; ss.
 OS Mus musculus.

XX Key Location/Qualifiers
 FH CDS 1..783
 FT /*tag= a
 FT /product= mouse CD40-L
 FT /note= "nucleotides 148-780 code for the
 extracellular region (amino acids 50-260)"

MO9410308-A.

11-MAY-1994.

20-OCT-1993; 93MO-US10034.

23-OCT-1992; 92US-0969703.

13-AUG-1993; 93US-0107353.

(IMMV) IMMUNEX CORP.

Spriggs MK, Srinivasan S;

WPI; 1994-167465/20.

P-PSDB; AARS3970.

Prepn. of soluble oligomeric mammalian proteins - using host
 cells to express a fusion protein comprising a leucine zipper
 domain and a heterologous mammalian protein

Example 1; Page 25-26; 35pp; English.

XX A DNA fragment encoding the extracellular (soluble) region of mouse
 CC CD40-L was ligated to a synthetic oligonucleotide sequence coding
 CC for a leader peptide, a 33 amino acid leucine zipper sequence
 CC (AARS3968) and the Flag (RTM) linker sequence. Cells expressing the
 CC fusion construct are grown to accumulate oligomeric, soluble CD40-L
 CC in the supernatant. The leucine zipper sequence spontaneously
 CC trimerises in solution and fusion proteins comprising
 CC the sequence fused to a heterologous mammalian protein also form
 CC oligomers.

SQ Sequence 783 BP; 243 A; 159 C; 178 G; 203 T; 0 other;

Query Match 95.7%; Score 749.4; DB 15; Length 783;

Best Local Similarity 97.3%; Pred. No. 1.4e-200;

Matches 762; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 ATGATGGAACATACACCAACCTCTCCCGATCTGCGGCACTGGACCTGCCATCAGC 60
 DB 1 ATGATGGAACATACACCAACCTCTCCCGATCTGCGGCACTGGACCTGCCATCAGC 60
 QY 61 ATGAAATTTTATGATTTTACTTACTGTTTTCTTATCAACCAATGATGATCTGTC 120
 DB 61 ATGAAATTTTATGATTTTACTTACTGTTTTCTTATCAACCAATGATGATCTGTC 120
 QY 121 CTTTGGCTGTATCTTCAATAGATTTGATTAAGTTCAGAGAGAGATTAACCTTCA 180
 DB 121 CTTTGGCTGTATCTTCAATAGATTTGATTAAGTTCAGAGAGAGATTAACCTTCA 180
 QY 181 GAAGATTTTGTATTCATTAAGAGATGCAACAAAGAGAGATCTTTATCC 240
 DB 181 GAAGATTTTGTATTCATTAAGAGATGCAACAAAGAGAGATCTTTATCC 240
 QY 241 TTGCTGAACGTGAGAGATGAGAGCAATTGGAAGCTTGTCAAGATTAACCTTA 300
 DB 241 TTGCTGAACGTGAGAGATGAGAGCAATTGGAAGCTTGTCAAGATTAACCTTA 300
 QY 301 AACAAAG 360

DB 301 AACAAAG 360
 QY 361 ATTGAGAGACAGCTGTATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
 DB 361 ATTGAGAGACAGCTGTATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
 QY 421 AAGAAAGATATTTATCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
 DB 421 AAGAAAGATATTTATCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
 QY 481 AAGGATTAAG 540
 DB 481 AAGGATTAAG 540
 QY 541 GAGCCTTGAGTCAAG 600
 DB 541 GAGCCTTGAGTCAAG 600
 QY 601 GAGAGATCTTACTCAAG 660
 DB 601 GAGAGATCTTACTCAAG 660
 QY 661 TCTGTTCACTTGGCGAG 720
 DB 661 TCTGTTCACTTGGCGAG 720
 QY 721 ACTGAAG 780
 DB 721 ACTGAAG 780
 QY 781 TGA 783
 DB 781 TGA 783

RESULT 6
 AAV12853
 ID AAV12853 standard; cDNA to mRNA; 783 BP.
 AC AAV12853;
 XX 13-MAY-1998 (first entry)
 DE CD40 ligand coding sequence.
 XX Leucine zipper; fusion protein production; soluble oligomeric protein;
 KM heterologous mammalian type II transmembrane protein; activated T cell;
 KM heterologous mammalian type I transmembrane protein; antibody production;
 KM CD40-L; B-cell proliferation; CD27-L; lymphocyte antigen; ss.
 OS Mus sp.
 XX Key Location/Qualifiers
 FH CDS 1..783
 FT /*tag= a
 FT /product= a
 FT /note= "nucleotides 148-780 code for the
 extracellular region (amino acids 50-260)"

18-MAY-1995; 95US-0446922.
 18-MAY-1995; 95US-0446922.
 25-OCT-1991; 91US-0783707.
 05-DEC-1991; 91US-0805723.
 23-OCT-1992; 92US-0969703.
 13-AUG-1993; 93US-0107353.
 (IMMV) IMMUNEX CORP.
 Spriggs MK, Srinivasan S;
 WPI; 1998-144799/13.

Db	541	GAGCCTTGAGTCAACGCCCATTCATCGTGGCCTGTGGCTGAAAGCCACAGATG99ATCT	600
Qy	601	GAGAGATCTTATCTCAAGAGGGGCAATATCCACAGTCTCTCCACGCTTTGGAGCAGCAG	660
Db	601	GAGAGATCTTATCTCAAGAGGGGCAATATCCACAGTCTCTCCACGCTTTGGAGCAGCAG	660
Qy	661	TCTGTTCACCTGGGCGGAGTGTGTAATTAACAAGCTGAGTCTTGCTGTGTTGACAAGCG	720
Db	661	TCTGTTCACCTGGGCGGAGTGTGTAATTAACAAGCTGAGTCTTGCTGTGTTGACAAGCG	720
Qy	721	ACTGAAGCAACCAAGTATCAACAGAGTTGGCTTCATCTTTTGGCTTACTCAAACTC	780
Db	721	ACTGAAGCAACCAAGTATCAACAGAGTTGGCTTCATCTTTTGGCTTACTCAAACTC	780
Qy	781	TG 782	
Db	781	TG 782	

CC membrane-bound (hmb) CD40 ligand (AAR5485) that induces long-term
 CC proliferation of B-cells in culture. These proliferating B-cells
 CC can be induced to differentiate into antibody-prod. cells. The
 CC nucleotide sequence is incorporated into a baculovirus vector that
 CC is used to transfect Sf9 insect cells for prodn. of recombinant
 CC hmbCD40.

XX Sequence 818 BP; 237 A; 182 C; 188 G; 211 T; 0 other;

Query Match 80.8%; Score 632.6; DB 16; Length 818;

Best Local Similarity 88.0%; Pred. No. 16-167; Matches 689; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACACCAACCTTCTCCGATCTGCGGCACTGACCTCCATCAC 60
 DB 13 ATGATGAAACATACACCAACCTTCCCGATCTGCGGCACTGACCTCCATCAC 72
 QY 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCAGATGATGGGTGACA 120
 DB 73 ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCAGATGATGGGTGACA 132
 QY 121 TTTTGGCTGTATCTTATGAAAGATGATGATGATGATGATGATGATGATGAT 180
 DB 133 TTTTGGCTGTATCTTATGAAAGATGATGATGATGATGATGATGATGATGAT 192
 QY 181 GAAATTTTGTATCTTATGAAAGATGATGATGATGATGATGATGATGATGAT 240
 DB 193 GAAATTTTGTATCTTATGAAAGATGATGATGATGATGATGATGATGATGAT 252
 QY 241 TTTGCTGATCTGTGAGAGATGAAAGCAATTTGAAGCTTGTCAAGATATACGTTA 300
 DB 253 TTTGCTGATCTGTGAGAGATGAAAGCAATTTGAAGCTTGTCAAGATATACGTTA 312
 QY 301 AACAAAG 360
 DB 313 AACAAAG 372
 QY 361 ATTGCAACACCTGTTAAGCAAGCAACATGATGATGATGATGATGATGATGAT 420
 DB 373 ATTGCAACACCTGTTAAGCAAGCAACATGATGATGATGATGATGATGATGAT 432
 QY 421 AAGAAGATTTATACATGATGAAAGCACTTGATATGCTTGAAGAGAGAGAGAG 480
 DB 433 CTAAAGCGGGAATATACCAAGTTCCTCCAGCTTGGAGAGAGAGAGAGAGAG 492
 QY 481 ACGTTAAAG 540
 DB 493 ACGTTAAAG 552
 QY 541 GAGCTTGAAGTCAAGCCATTCATGCTGAGGCTCTGAGTGAAGCCAGCATTTGAT 600
 DB 553 GAGCTTGAAGTCAAGCCATTCATGCTGAGGCTCTGAGTGAAGCCAGCATTTGAT 612
 QY 601 GAGAGATCTTACTCAAGCGGCAATACCAAGTTCCTCCAGCTTGGAGAGAGAG 660
 DB 613 GAGAGATCTTACTCAAGCGGCAATACCAAGTTCCTCCAGCTTGGAGAGAGAG 672
 QY 661 TCTGTTCACTTGGCGAGAGTGTGAATTAAGCTGAGTCTGCTGTTTGAAGAG 720
 DB 673 TCTGTTCACTTGGCGAGAGTGTGAATTAAGCTGAGTCTGCTGTTTGAAGAG 732
 QY 721 ACTGAAGCAAGCAAGTGTATCAAGAGTGGCTTCTCATCTTTGGCTTACTCAAG 780
 DB 733 ACTGAAGCAAGCAAGTGTATCAAGAGTGGCTTCTCATCTTTGGCTTACTCAAG 792
 QY 781 TGA 783
 DB 793 TGA 795

RESULT 12
 AA227538
 ID AA227538 standard; cDNA; 878 BP.

XX AA227538;
 AC 13-DEC-1999 (first entry)
 DT
 XX
 DE Mouse trimeric CD40-L coding sequence.

XX CD40-L; CD40 receptor ligand; anti-human CD40-L monoclonal antibody;
 KW binding inhibitor; trimeric CD40-L; anti-immunoglobulin M;
 KW peripheral blood B cell; proliferation inhibitor; ss.

XX Mus sp.

XX US961974-A.

XX 05-OCT-1999.

XX 24-MAY-1994; 94US-0249189.

XX 25-OCT-1991; 91US-0783707.

XX 05-DEC-1991; 91US-0805723.

XX 23-OCT-1992; 92US-0969703.

XX (IMMUNEX CORP.

XX Spriggs MK, Fanslow WC, Armitage RJ;

XX WPI; 1999-579604/49.

XX P-PSDB; AAY39941.

XX Anti-human CD40-Ligand monoclonal antibodies -

XX Example 17; Column 69-72; 59pp; English.

XX This sequence encodes the mouse trimeric CD40 receptor ligand (CD40-L).

XX The invention relates to anti-human CD40-L monoclonal antibodies M90

XX secreted by hybridoma hCD40L-M90 (ATCC HB-12055) and M91 secreted by

XX hybridoma hCD40L-M91 (ATCC HB-12056). M90 and M91 inhibit CD40-L binding

XX to CD40 and the ability of trimeric CD40-L and anti-immunoglobulin M to

XX induce proliferation of peripheral blood B cells.

XX Sequence 878 BP; 277 A; 178 C; 203 G; 220 T; 0 other;

QY Query Match 80.6%; Score 631.4; DB 20; Length 878;

QY Best Local Similarity 99.8%; Pred. No. 2-3e-167; Matches 632; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 151 GATAGGTGAAG 210

QY 225 GATAGGTGAAG 284

QY 211 AGATGCAACAAAG 270

QY 285 AGATGCAACAAAG 344

QY 271 TTTGAAGACCTTGTCAAGATATACGTTAAACAAAGAGAGAGAGAGAGAGAGAG 330

QY 345 TTTGAAGACCTTGTCAAGATATACGTTAAACAAAGAGAGAGAGAGAGAGAGAG 404

QY 331 GAAATGCAAG 390

QY 405 GAAATGCAAG 464

QY 391 AGTAATGAGCATCCGTTCTTACAGTGGGCAAGAGAGATATATACATGAAAGCAAC 450

QY 465 AGTAATGAGCATCCGTTCTTACAGTGGGCAAGAGAGATATATACATGAAAGCAAC 510

QY 451 TTGGTATGCTTGAAG 564

QY 525 TTGGTATGCTTGAAG 570

Db 585 TACAGTCAAGTACCTTCTGCTCTAATGAGGAGCTTCGAGTCAAGCCATTCATGTC 644
 Qy 571 GGCCTTGGCTGAAGCCGACGATGGATCTGAAGATCTTACTCAAGCGGCAATATCC 630
 Db 645 GGCCTTGGCTGAAGCCGACGATGGATCTGAAGATCTTACTCAAGCGGCAATATCC 704
 Qy 631 CACAGTTCCTCCAGCTTTCGAGAGAGTCTTCACTTGGGCGAGTGTGAATTA 690
 Db 705 CACAGTTCCTCCAGCTTTCGAGAGAGTCTTCACTTGGGCGAGTGTGAATTA 764
 Qy 691 CAGCTGGTCTTCTGT 750
 Db 765 CAGCTGGTCTTCTGT 824
 Qy 751 GGCCTTCATCTTTGGCTTACTCAAACTCTGA 783
 Db 825 GGCCTTCATCTTTGGCTTACTCAAACTCTGA 857

RESULT 13

AA063959
 ID AA063959 standard; cDNA to mRNA; 786 BP.

AC AA063959;

DT 11-JAN-1995 (first entry)

XX Human CD40-L type II transmembrane protein coding sequence.

XX Leucine zipper; trimerisation; trimeric CD40-L; fusion protein;

KW hetero-oligomer; homo-oligomer; type II transmembrane protein;

XX soluble CD40-L; tumour necrosis factor family; ss.

OS Homo sapiens.

XX Key

FT CDS

FT 1..786

FT /product= human CD40-L

FT /tag= a

FT /note= "nucleotides 148-783 code for the

PR 23-OCT-1993; 93MO-US10034.

PR 13-AUG-1993; 93US-0107353.

XX (IMMV) IMMUNEX CORP.

XX Spriggs MK, Strinivasan S;

XX WPI; 1994-167465/20.

XX P-RSDB; AARS3969.

XX Prep. of soluble oligomeric mammalian proteins - using host

XX cells to express a fusion protein comprising a leucine zipper

XX domain and a heterologous mammalian protein

XX Example 1; Page 22-23; 35pp; English.

CC A DNA fragment encoding the extracellular (soluble) region of human
 CC CD40-L was ligated to a synthetic oligonucleotide sequence coding
 CC for a leader peptide, a 33 amino acid leucine zipper sequence
 CC (AARS3968) and the Flag (RTM) linker sequence. Cells expressing the
 CC fusion construct are grown to accumulate oligomeric, soluble CD40-L
 CC in the supernatant. The leucine zipper sequence spontaneously
 CC trimerises in solution and fusion proteins comprising
 CC the sequence fused to a heterologous mammalian protein also form
 CC oligomers.

XX SQ Sequence 786 BP; 250 A; 168 C; 168 G; 200 T; 0 other;

Query Match 75.7%; Score 592.4; DB 15; Length 786;

Best Local Similarity 85.5%; Pred. No. 2e-156;

Matches 672; Conservative 0; Mismatches 111; Indels 3; Gaps 1;

Qy 1 ATGATCGAAACATACCAACAACTTCCCGGATCGGCGGCACTGGACATCCATCAGC 60
 Db 1 ATGATCGAAACATACCAACAACTTCCCGGATCGGCGGCACTGGACATCCATCAGC 60
 Qy 61 ATGAAATTTTATGATTTTACTTACTGTTTTTTCTTATCCAGATGATGGGTACGA 120
 Db 61 ATGAAATTTTATGATTTTACTTACTGTTTTTTCTTATCCAGATGATGGGTACGA 120
 Qy 121 CTTTGTGCTGTATCTTATGAAAGATGGAAGGCACTTGTCAAGATATTAACCTTAT 180
 Db 121 CTTTGTGCTGTATCTTATGAAAGATGGAAGGCACTTGTCAAGATATTAACCTTAT 180
 Qy 181 GAAATTTTGTATTCATTAAGAGATGCAAGAGAGAGAGATCTTTATCC 240
 Db 181 GAAATTTTGTATTCATTAAGAGATGCAAGAGAGAGAGATCTTTATCC 240
 Qy 241 TTGCTGAACCTGTAGAGATGGAAGGCACTTGTCAAGATATTAACCTTAT 300
 Db 241 TTGCTGAACCTGTAGAGATGGAAGGCACTTGTCAAGATATTAACCTTAT 300
 Qy 301 AACAAAGAGA--GAAAAAGAAAAAGCTTTGAAATGCAAGAGTATGAGATCCT 357
 Db 301 AACAAAGAGA--GAAAAAGAAAAAGCTTTGAAATGCAAGAGTATGAGATCCT 357
 Qy 358 CAAATGTAGACACAGCTTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 417
 Db 358 CAAATGTAGACACAGCTTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 417
 Qy 418 GCGAAGAAAGATATTATACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 477
 Db 418 GCGAAGAAAGATATTATACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 477
 Qy 478 CTGACGCTTAAAG 537
 Db 478 CTGACGCTTAAAG 537
 Qy 538 CCGAGAGCTTGAAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 597
 Db 538 CCGAGAGCTTGAAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 597
 Qy 598 TCTGAGAGATCTTACTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 657
 Db 598 TCTGAGAGATCTTACTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 657
 Qy 601 TTGAGAGAGATCTTACTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
 Db 601 TTGAGAGAGATCTTACTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
 Qy 658 CAGTCTGTCACTTGGAG 717
 Db 658 CAGTCTGTCACTTGGAG 717
 Qy 718 GTGAG 777
 Db 718 GTGAG 777
 Qy 778 CTCTGA 783
 Db 781 CTCTGA 786

RESULT 14

AAV38997
 ID AAV38997 standard; DNA; 786 BP.

AC AAV38997;

XX 23-SEP-1998 (first entry)

DE CD40 ligand gene used in the course of the invention.

XX CD40 ligand; alteration; immunoreactivity; human cell;
 KM accessory molecule ligand; AML; gene therapy; treatment; neoplasia;
 KM autoimmune disorder; rheumatoid arthritis; vaccine; ss.
 XX Mus sp.
 OS WO9826061-A2.
 XX PN 18-JUN-1998.
 XX PD 08-DEC-1997; 97WO-US22740.
 XX PF 01-DEC-1997; 97US-0982272.
 XX PR 09-DEC-1996; 96US-0032145.
 XX PA (REGC) UNIV CALIFORNIA.
 XX PI Cantwell M, Kipps TJ, Sharma S;
 XX MPI; 1998-348521/30.
 XX DR Vectors containing accessory molecule ligand genes - used for
 XX PT altering immunoreactivity of cells, particularly for treatment of
 XX neoplasia or autoimmune disorders, e.g. rheumatoid arthritis
 XX PS Disclosure; Page 104; 167pp; English.
 XX
 CC The present sequence represents the CD40 ligand gene. The sequence is
 CC used to exemplify the method of the invention. The specification
 CC describes a method for altering the immunoreactivity of human cells
 CC which comprises introducing a gene encoding an accessory molecule
 CC ligand (AML) into the cells so that the AML is expressed on the surface
 CC of the cells. Vectors containing the AML genes can be used in gene
 CC therapy for treating neoplasia or autoimmune disorders such as rheumatoid
 CC arthritis. They can also be used for vaccination to produce immunity
 CC against a virus cell, bacteria, protein, fungus or neoplasia.
 CC XX
 SQ Sequence 786 BP; 250 A; 168 C; 168 G; 200 T; 0 other;
 Query Match 75.7%; Score 592.4; DB 19; Length 786;
 Best Local Similarity 85.5%; Pred. No. 2e-156;
 Matches 672; Conservative 0; Mismatches 111; Indels 3; Gaps 1;
 QY 1 ATGATCGAACAATACATCAACCACTCTCCCGATCGCGGACGACGACCCATCAGC 60
 DB 1 ATGATCGAACAATACATCAACCACTCTCCCGATCGCGGACGACGACCCATCAGC 60
 QY 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATACCCAGATGATGGGTGACA 120
 DB 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATACCCAGATGATGGGTGACA 120
 QY 121 CTTTGGCTGTATCTTCATGAAGATGATGATGATGATGATGATGATGATGATGAT 180
 DB 121 CTTTGGCTGTATCTTCATGAAGATGATGATGATGATGATGATGATGATGATGAT 180
 QY 181 GAAGATTTTGTATCTTAATAAAGCTAAAGATGCAACAAAGAGAGATTTATCC 240
 DB 181 GAAGATTTTGTATCTTAATAAAGCTAAAGATGCAACAAAGAGAGATTTATCC 240
 QY 241 TTGCTGAACGTGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATG 300
 DB 241 TTGCTGAACGTGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATG 300
 QY 301 AACAAAG 357
 DB 301 AACAAAG 357
 QY 358 CAATTTGAG 417
 DB 358 CAATTTGAG 417
 QY 418 GCGAAG 477
 DB 418 GCGAAG 477

DB 421 GCTGAAG 480
 QY 478 CTGACGCTTAAAG 537
 DB 481 CTGACGCTTAAAG 540
 QY 538 CGGAGAGCTTGAAG 597
 DB 541 CGGAGAGCTTGAAG 600
 QY 598 TCTGAGAGATCTTCAAG 657
 DB 601 TTGAGAGAGATCTTCAAG 660
 QY 658 CAGTCTGTCTTCAAG 717
 DB 661 CAATCTCTTCAAG 720
 QY 718 GTGACTGAAG 777
 DB 721 GTGACTGAAG 780
 QY 778 CTCTGA 783
 DB 781 CTCTGA 786
 RESULT 15
 ID AAV12852 standard; CDNA to mRNA; 786 BP.
 XX AAV12852;
 AC AAV12852;
 AC 13-MAY-1998 (first entry)
 DT 13-MAY-1998 (first entry)
 XX CD40 ligand coding sequence.
 DE
 XX Leucine zipper; fusion protein production; soluble oligomeric protein;
 KM heterologous mammalian type II transmembrane protein; activated T cell;
 KM heterologous mammalian type I transmembrane protein; antibody production;
 KM CD40-L; B-cell proliferation; CD27-L; lymphocyte antigen; ss.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FT CDS 1..786
 FT /*tag= a
 XX US5716805-A.
 XX 10-FEB-1998.
 PD 18-MAY-1995; 95US-0446922.
 PF 18-MAY-1995; 95US-0446922.
 XX 18-MAY-1995; 95US-0446922.
 PR 25-OCT-1991; 91US-0783707.
 PR 05-DEC-1991; 91US-0805723.
 PR 23-OCT-1992; 92US-0969703.
 PR 13-AUG-1993; 93US-0107353.
 XX (IMNV) IMMUNEX CORP.
 PA Spriggs MK, Srinivasan S;
 PI WPI; 1998-144799/13.
 DR P-PSDB; AAW41178.
 DR Soluble oligomeric fusion proteins - comprising leucine zipper fused
 PT to extracellular region of transmembrane protein
 XX Example 1; column 19-20; 21pp; English.
 PS

CC This sequence is the coding sequence for the human CD40 ligand (CD40-L).
CC The encoded protein can be used in a fusion protein produced using the
CC method of the invention. The method is for preparing soluble oligomeric
CC protein by culturing a host cell transfected with a vector for the
CC fusion protein. The soluble oligomeric proteins comprise a leucine zipper
CC fused to the N terminus of the extracellular region of a heterologous
CC mammalian type II transmembrane protein or to the C terminus of the
CC extracellular region of a heterologous mammalian type I transmembrane
CC protein, where the leucine zipper is a peptide comprising at least part
CC of AAW41171 or AAW41172, optionally with conservative amino acid
CC substitutions, provided that the peptide trimerizes in solution. A
CC soluble fusion protein comprising the leucine zipper of AAW41171 linked
CC to the extracellular region of CD40-L (a type II transmembrane protein
CC that is found on activated T cells and acts as a ligand for the B-cell
CC antigen CD40) stimulates B-cell proliferation and antibody production in
CC a similar manner to membrane-bound CD40-L. A soluble fusion protein
CC comprising the leucine zipper of AAW41172 linked to the extracellular
CC region of CD27-L (a type II transmembrane protein that binds to the
CC lymphocyte antigen CD27) inhibits binding of CD27c (a fusion protein
CC to EBV-transformed B cells expressing CD27-L).

XX Sequence 786 BP; 250 A; 168 C; 168 G; 200 T; 0 other;

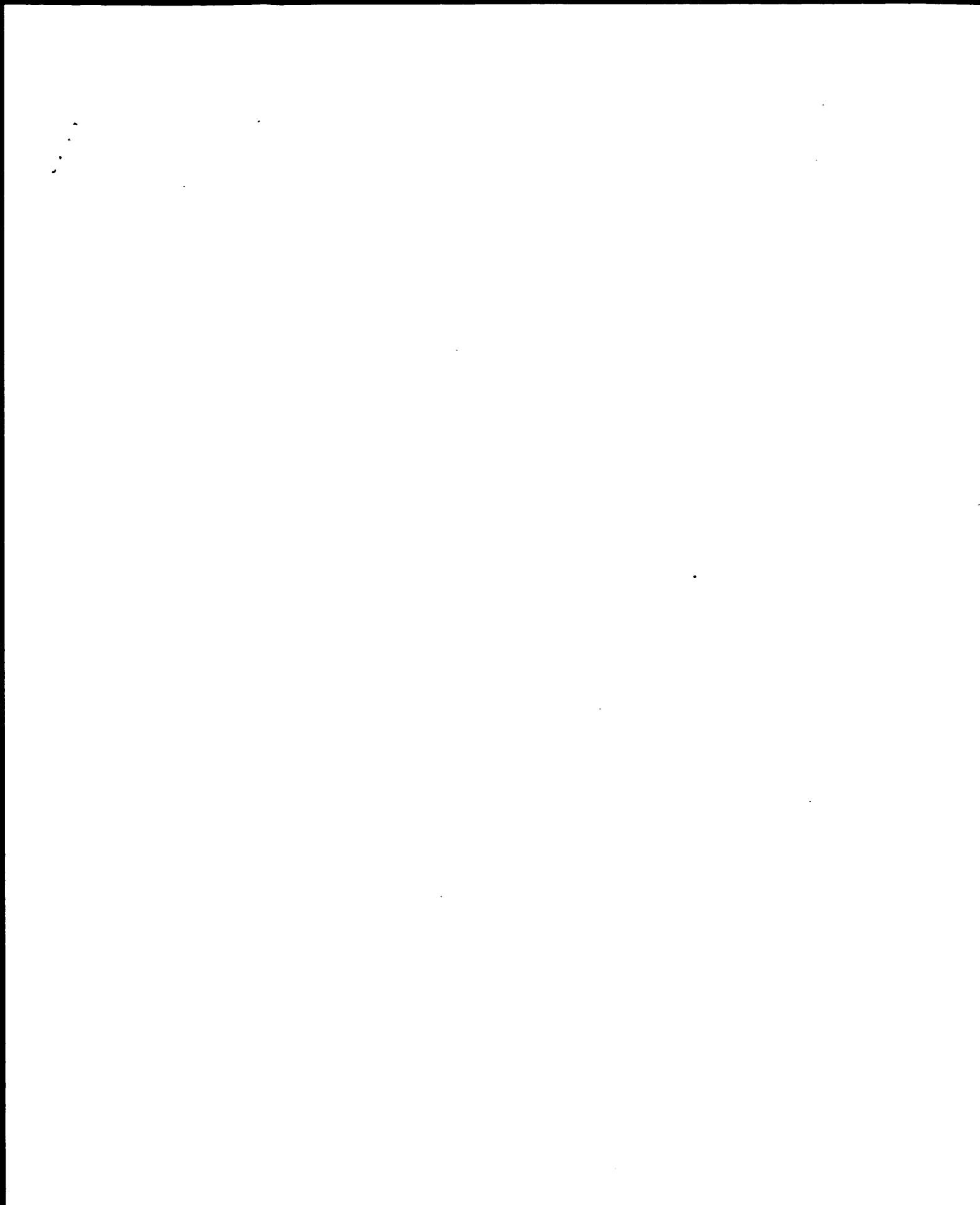
Query Match 75.7%; Score 592.4; DB 19; Length 786;

Best Local Similarity 85.5%; Pred. No. 26-156;
Matches 672; Conservative 0; Mismatches 111; Indels 3; Gaps 1;

QY 1 ATGATGAAACATCAACCACTTCCCGATCTGGGCACTGACCTGCCATCAGC 60
DB 1 ATGATGAAACATCAACCACTTCCCGATCTGGGCACTGACCTGCCATCAGC 60
QY 61 ATGAAATTTTATGATTTACTCTGTTTCTTATCACCAGATGATGGGTCAGCA 120
DB 61 ATGAAATTTTATGATTTACTCTGTTTCTTATCACCAGATGATGGGTCAGCA 120
QY 121 CTTTGGCTGCTATCTTCATAGAGATTGATAGGTGAAAGAAATTAACCTTCAT 180
DB 121 CTTTGGCTGCTATCTTCATAGAGATTGATAGGTGAAAGAAATTAACCTTCAT 180
QY 181 GAAGATTTTATTCATTAAGAAAGCTAAAGATGCAACAAAGAGAGATCTTTATCC 240
DB 181 GAAGATTTTATTCATTAAGAAAGCTAAAGATGCAACAAAGAGAGATCTTTATCC 240
QY 241 TTGCTGAACCTGAGAGAGAGAGAGCAATTGAAACCTTGTCAAGATATTAAGTTA 300
DB 241 TTGCTGAACCTGAGAGAGAGAGAGCAATTGAAACCTTGTCAAGATATTAAGTTA 300
QY 301 AACAAAGAGA---GAAAAAGAAAAGCTTGAATGCAAGAGATGATGATCTCT 357
DB 301 AACAAAGAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATCTCT 357
QY 358 CAAATTTGAG 417
DB 358 CAAATTTGAG 417
QY 418 GCCAAGAAAGAGATTTATCAATGAAAGCACTTGATGCTTGAAGATGAGAAACAG 477
DB 418 GCCAAGAAAGAGATTTATCAATGAAAGCACTTGATGCTTGAAGATGAGAAACAG 477
QY 478 GTGAAAGAGATTTATCAATGAAAGCACTTGATGCTTGAAGATGAGAAACAG 480
DB 478 GTGAAAGAGATTTATCAATGAAAGCACTTGATGCTTGAAGATGAGAAACAG 480
QY 481 CTGACGTTTAAAG 540
DB 481 CTGACGTTTAAAG 540
QY 538 CGGAGACCTTGAAGTCAACCCATTCATCTGCGCTCTGCTGAGAGCCAGATTTGA 597
DB 538 CGGAGACCTTGAAGTCAACCCATTCATCTGCGCTCTGCTGAGAGCCAGATTTGA 597
QY 541 CGGAGACCTTGAAGTCAACCCATTCATCTGCGCTCTGCTGAGAGCCAGATTTGA 600
DB 541 CGGAGACCTTGAAGTCAACCCATTCATCTGCGCTCTGCTGAGAGCCAGATTTGA 600
QY 598 TCTGAGAGATCTTACTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 657
DB 598 TCTGAGAGATCTTACTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 657
QY 601 TTGAGAGAGATCTTACTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
DB 601 TTGAGAGAGATCTTACTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
QY 658 CAGTCTTTCACTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 717
DB 658 CAGTCTTTCACTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 717

DB 661 CAAATCAATTCATCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY 718 GTGACTGAAGCAAGCCAAAGTATCCACAGAGTTGGCTTCTCATCTTTGGCTTACTCAA 777
DB 721 GTGACTGAATCCAAAGCCAAAGTATCCACAGAGTTGGCTTCTCATCTTTGGCTTACTCAA 780
QY 778 CTCTGA 783
DB 781 CTCTGA 786

Search completed: March 8, 2003, 22:12:44
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	751	95.9	1250	9 US-10-182-093-1	Sequence 1, Appl1
2	155.8	19.9	2395	9 US-09-875-453-9	Sequence 9, Appl1
3	46	5.9	9121	10 US-09-070-927A-221	Sequence 221, App
4	44	5.6	2220	10 US-09-897-214-15	Sequence 15, Appl1
5	40.4	5.2	176373	9 US-10-095-407-17	Sequence 17, Appl1
6	37	4.7	1758	12 US-10-071-751-29	Sequence 29, Appl1
7	36.2	4.6	262	10 US-09-919-580-896	Sequence 896, App
8	36.2	4.6	2430	9 US-10-105-695-1	Sequence 1, Appl1
9	36.2	4.6	2430	9 US-10-105-694-1	Sequence 1, Appl1
10	36.2	4.6	2430	10 US-09-747-521-1	Sequence 1, Appl1
11	36.2	4.6	2430	10 US-10-106-014-1	Sequence 1, Appl1
12	36	4.6	544	10 US-09-864-761-7124	Sequence 7124, App
13	35.6	4.5	736	10 US-09-772-134B-31	Sequence 31, Appl1
14	35.6	4.5	23632	10 US-09-764-878-262	Sequence 262, App
15	35.6	4.5	23632	10 US-09-764-860-941	Sequence 941, App
16	35.6	4.5	24768	10 US-09-764-887-602	Sequence 602, App
17	35.4	4.5	424	10 US-09-960-352-11218	Sequence 11218, A
18	35.4	4.5	1352	9 US-09-938-842A-3149	Sequence 3149, App
19	35.4	4.5	1352	9 US-09-938-842A-5264	Sequence 5264, App

20	35.2	4.5	4956	10 US-09-070-927A-291	Sequence 291, App
21	35.2	4.5	33593	9 US-09-754-853A-2	Sequence 2, Appl1
22	35.2	4.5	33593	9 US-09-754-853A-3	Sequence 3, Appl1
23	35	4.5	2272	10 US-09-873-438-1	Sequence 1, Appl1
24	34.8	4.4	312	10 US-09-960-352-8414	Sequence 8414, App
25	34.8	4.4	337	10 US-09-960-352-14222	Sequence 14222, A
26	34.8	4.4	391	10 US-09-813-358-196	Sequence 196, App
27	34.8	4.4	399	10 US-09-960-352-14574	Sequence 14574, A
28	34.8	4.4	404	10 US-09-960-352-9259	Sequence 9259, App
29	34.8	4.4	420	10 US-09-960-352-7144	Sequence 7144, App
30	34.8	4.4	431	10 US-09-960-352-5558	Sequence 5558, App
31	34.8	4.4	433	10 US-09-960-352-1058	Sequence 1058, App
32	34.8	4.4	555	9 US-09-736-457-380	Sequence 380, App
33	34.8	4.4	555	9 US-09-802-941-380	Sequence 380, App
34	34.8	4.4	555	9 US-09-849-626-380	Sequence 380, App
35	34.8	4.4	3303	10 US-09-833-790-421	Sequence 421, App
36	34.8	4.4	465237	10 US-09-933-267A-1	Sequence 1, Appl1
37	34.6	4.4	725	10 US-09-910-943-232	Sequence 232, App
38	34.2	4.4	341	10 US-09-960-352-12302	Sequence 12302, A
39	34.2	4.4	422	10 US-09-764-864-675	Sequence 675, App
40	34.2	4.4	20561	10 US-09-070-927A-292	Sequence 292, App
41	34	4.3	1710	9 US-10-078-770-137	Sequence 137, App
42	34	4.3	1744	10 US-09-804-682-78	Sequence 78, Appl1
43	34	4.3	23626	10 US-09-764-878-261	Sequence 261, App
44	34	4.3	23626	10 US-09-764-860-940	Sequence 940, App
45	33.6	4.3	170	10 US-09-867-701-9094	Sequence 9094, App

ALIGNMENTS

RESULT 1
US-10-182-093-1
Sequence 1, Application US/10182093
Publication No. US20030021808A1
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as represented by
APPLICANT: c/o Center for Disease Control and Human Services,
APPLICANT: Timp, Ralph
APPLICANT: Jones, Les
APPLICANT: Anderson, Larry
APPLICANT: Brown, Michael
TITLE OF INVENTION: CD40 Ligand Adjuvant for Respiratory
FILE REFERENCE: 14114.030102
CURRENT APPLICATION NUMBER: US/10/182.093
CURRENT FILING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: 60/179,905
PRIOR FILING DATE: 2000-02-02
NUMBER OF SEQ ID NOS: 1
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1250
TYPE: DNA
ORGANISM: Murine
US-10-182-093-1
Query Match: 95.9%; Score 751; DB 9; Length 1250;
Best Local Similarity: 97.4%; Pred. No. 1.4e-195;
Matches 763; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
1 ATGATGAAACATACCAACTTCTCCCGATCTGCGGCACTGACATGATCCCATCAGC 60
13 ATGATGAAACATACCAACTTCTCCCGATCTGCGGCACTGACATGATCCCATCAGC 72
61 ATGAAATTTTATGATTTTATCTTCTTTTCTTATCACCAGATGATGGTGCAGCA 120
73 ATGAAATTTTATGATTTTATCTTCTTTTCTTATCACCAGATGATGGTGCAGCA 132
121 CTTTTCCTGCTGATCTTCTTATGAAAGATTGATGAGTGAAGAGAGAACTTTCAT 180
133 CTTTTCCTGCTGATCTTCTTATGAAAGATTGATGAGTGAAGAGAGAACTTTCAT 192

Query Match 5.9%; Score 46; DB 10; Length 9121;
Best Local Similarity 52.6%; Pred. No. 0.022; Indels 0; Gaps 0;
Matches 100; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

Qy 161 AAGAGAAAGTAACCTTCATGAGATTTTGTATTCATMAAAAGCTAAAGATGACACA 220
Db 8754 AAGAAAAAGCAAAAAAATTCAGTATTTTGAAGAGAAAAACAATGAAATTTTATA 8813

Qy 221 AAGGAGAGATCTTTCCTGCGAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 280
Db 8814 AATGAAAGACCTTATTTTGCATTAATGCTGCTTAAGTGAAGAAAAACAATTTAAAC 8873

Qy 281 TTGTCAAGATATTAACCTTAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 340
Db 8874 TTACAGAGATTTGTTTGGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 8933

Qy 341 GAGTGATGA 350
Db 8934 CAATGATGA 8943

RESULT 4
US-09-897-214-15/c
Sequence 15, Application US/09897214
Patent No. US20020076779A1
GENERAL INFORMATION:
APPLICANT: Thayer, Edward C.
APPLICANT: Sheppard, Paul O.
APPLICANT: Preenell, Scott R.
TITLE OF INVENTION: Leucine-Rich Repeat Proteins, Zlrr7,
TITLE OF INVENTION: Zlrr8, and Zlrr9
FILE REFERENCE: 01-27
CURRENT APPLICATION NUMBER: US/09/897,214
CURRENT FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: 60/215,446
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 15
LENGTH: 2220
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:
NAME/KEY: misc.feature
LOCATION: (1)...(2220)
OTHER INFORMATION: n = A,T,C or G
US-09-897-214-15

Query Match 5.6%; Score 44; DB 10; Length 2220;
Best Local Similarity 25.3%; Pred. No. 0.039;
Matches 96; Conservative 70; Mismatches 212; Indels 1; Gaps 1;

Qy 262 AGAGGCAATTTGAAGACCTTCTCAAGATATTAACGTTAAACAAGAGAGAGAGAGAG 321
Db 925 AATARTTATNSMNRNACGTGNSMNSMPTCNARNGTCANAGNGRANSMNSMART 866

Qy 322 AACGCTTGAATGCAAGAGGTGATGAGATCTCAAAATGACAGACCT-TGTAG 380
Db 865 TTRCARTTGTGAAANRNRNACGTGNAARRGTGNGAGTCTCTGAADARTNGNGNMA 806

Qy 381 CGAAGCCACAGTAATGCAATCCGTTCTACAGTGGGCCAAGAGAGATTTATACAT 440
Db 805 CNSWNGCNAANGONGNSMRTCTYGCARCACARVYGTGNARRTTNGNGIDATYTTTRA 746

Qy 441 GAAAGCACTTGATGATGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGACT 500
Db 745 ADATRTCCCTGNAANGTNGTNAANGGACATTTTCNARRTANRNSMNGNART 686

Qy 501 CTATTATGCTACACTCAAGTCACTTCTGCTTAATCGGAGAGCTTCAAGTCAAGGCC 560
Db 685 TNGNARTCNCKDATCCANCCNSWYTCNACNCKYTCNARRAANGTNCNSMNRARTCNA 626

Qy 561 ATTATGTCGCGCTTGAGTGAAGCCACAGATGATGAGAGATCTTACAGAGC 620
Db 625 KACACTCNAANGTNAANGNANGNCCRTCTTCNCCNGCNAANGNCGTTCNGDANNC 566

Qy 621 GGCNAATACCCACAGTTCC 639
Db 565 CNCCYTGNCCNCCNCC 547

RESULT 5
US-10-095-407-17
Sequence 17, Application US/10095407
Patent No. US2002016430A1
GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/10/095,407
CURRENT FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/091,650
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: US 60/054,646
PRIOR FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 17
LENGTH: 176373
TYPE: DNA
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: misc.feature
LOCATION: (1)...(176373)
OTHER INFORMATION: n = A,T,C or G
US-10-095-407-17

Query Match 5.2%; Score 40.4; DB 9; Length 176373;
Best Local Similarity 48.3%; Pred. No. 3;
Matches 113; Conservative 0; Mismatches 121; Indels 0; Gaps 0;

Qy 213 ATGCAACAAAGAGAGATCTTATCTCTGTAAGTGTGAGAGATGAGAGCAATT 272
Db 114639 ATAAABAAATGAAATGAGATATTAATCTGAAACATCAAGGAAAAATGGAATA 114698

Qy 273 TGAAGCTTGTCAAGATATTAACGTTAAACAAGAGAGAGAGAGAGAGAGAGAGAG 332
Db 114699 AGAAAACTGACCAAAAAACATCTCAGTCATCAAAAAAAGAGAGAGAGAGAG 114758

Qy 333 AATGCAAGAGATGATGAGATCTCAATTTGACAGACAGCTTGAAGCAAGCAG 392
Db 114759 TTGCGAAGAGAGAGAGATGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 114818

Qy 393 TAATGACATCTGTTTACAGTGGCCAGAGAGAGATTTTATACATGAAAAAG 446
Db 114819 GTTGAAGAGAGAGAGTCCAGAAATATCATCTAGTCATCAATCAACATTAAGAG 114872

RESULT 6
US-10-071-751-29
Sequence 29, Application US/10071751
Patent No. US2002014232A1
GENERAL INFORMATION:
APPLICANT: Hunter, Shirley Wu
APPLICANT: Sim, Gek-kee
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA PROTEINS AND APPARATUS TO COLLECT SUCH PROTEINS
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: SHERIDAN ROSS P. C.
STREET: 1560 BROADWAY, SUITE 1200
CITY: DENVER

STATE: CO
COUNTRY: U.S.A.
ZIP: 80202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/071,751
FILING DATE: 07-Feb-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/171,156
FILING DATE: 1998-10-09
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-17-C4-PUS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303/863-9700
TELEFAX: 303/863-0223
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 1758 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1...1758
NAME/KEY: W = A or T
LOCATION: 1136
SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-10-071-751-29

Query Match
Best Local Similarity 4.7%; Score 37; DB 12; Length 1758;
Matches 109; Conservative 1; Mismatches 121; Indels 0; Gaps 0;

QY 155 AGGTGGAAGAGAGATTAACCTTCATGAGATTTTGTATTCATTAAGGCTAAAGAGAT 214
DB 1043 AAGATGTAGAGATTTGAAGAGCATAGTCTCTGAGAAACCAAGAGATGAGATTA 1102
QY 215 GCAACAAAGAGAGATCTTATCTTCTGCTGAACTGTGAGAGATGAGAGCAATTTG 274
DB 1103 AAGAACTTAAGAGAGCTCAAGATTTGTAAGAGGTTAAAGATGATTAAGAAATGG 1162
QY 275 AAGACCTTGTCAAGATATTAAGTTAAACAAAGAGAGAAAGAAAGAGCTTTGAAA 334
DB 1163 ATACTGTTGTACAAAGAAATTTGAAGCAAAAGATCTGAGAAAGCCAAACATTCGCC 1222
QY 335 TGCAGAGAGGTGATGAGATCTCAATTTGACAGCACTTTGTAAGGAG 385
DB 1223 TTGAAGCTCTTAGAGGCTACTGAACTCAAGATTAAGTATTAAGGAAAG 1273

RESULT 7
US-09-919-580-896
Sequence 896, Application US/09919580
Patent No. US20020110832A1
GENERAL INFORMATION:
APPLICANT: Fyle, Ruth
APPLICANT: Xu, Jiangchun
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121, 552
CURRENT APPLICATION NUMBER: US/09/919,580
CURRENT FILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 934

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 896
LENGTH: 262
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: 58, 132, 133, 139, 140, 147, 262
OTHER INFORMATION: n = A,T,C or G
US-09-919-580-896

Query Match
Best Local Similarity 4.6%; Score 36.2; DB 10; Length 262;
Matches 92; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 135 TCTTCATAGAGATTGATGATTAAGTCGAGAGAGAAACCTTCATGAGATTTGTAAT 194
DB 56 TTTTCTTATAGCTGCTCATATTAAATGAAATGATTTAAAGATCTGCAACT 115
QY 195 CATTAAGAGCTTAAGAGATGCAACAAAGAGAGATCTTTATCTTGTGTAAGTGA 254
DB 116 ACTATCCAACTTATATNNCTGCTNNCAAGTNAAGATCTTTATAGTTCATTA 175
QY 255 GGAAGATGAGAGCAATTTGAAAGACTTGTCAAGGATTAACGTTAAACAAAGAGAA 314
DB 176 ATATTAAGCAAGATTAATTAATTTGCTTTTGTAAAGAAAAA 235
QY 315 AAAAGAAACA 325
DB 236 AAAAAAAAAA 246

RESULT 8
US-10-105-695-1
Sequence 1, Application US/10105695
Publication No. US20020197272A1
GENERAL INFORMATION:
APPLICANT: Gallows, Darrel R.
APPLICANT: Mateczun, Alfred J.
TITLE OF INVENTION: Methods for Protection Against Lethal Infection with Bacillus
FILE REFERENCE: 22727/04115
CURRENT APPLICATION NUMBER: US/10/105,695
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER: US 09/747,521
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patent in version 3.1
SEQ ID NO 1
LENGTH: 2430
TYPE: DNA
ORGANISM: Bacillus anthracis
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(2430)
OTHER INFORMATION:
US-10-105-695-1

Query Match
Best Local Similarity 4.6%; Score 36.2; DB 9; Length 2430;
Matches 89; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 158 TCGAAGAGAGTAACCTTCATGAGATTTTGTATTCATTAAGGCTAAAGAGATGCA 217
DB 1053 TCTTAAGAGATTAACAAATTTGATGATTTTATCTACGAGAGAAAGAGTTT 1112
QY 218 ACAAGAGAGAGATCTTATCTTCTGCTGAACTGTGAGAGAGAGAGCAATTTGAG 277
DB 1113 AAAAAAGCTTAATTTGATTTGCTATTTCTTATCTGAGAGAGAGAGAGCTTTTAA 1172
QY 278 ACCTTGTCAAGATTAACGTTAAACAAAGAGAGAGAGAGAGAGAGAGAGAGAG 334
DB 1173 TAGAATTAAGGTGATGATGATTAATCTTATCTGAGAGAGAGAGAGAGAGAGAG 1229

RESULT 9

US-10-105-694-1
; Sequence 1, Application US/10105694
; Publication No. US20030003109A1
; GENERAL INFORMATION:
; APPLICANT: Galloway, Darrel R.
; APPLICANT: Mateczun, Alfred J.
; TITLE OF INVENTION: Methods for Protection Against Lethal Infection with Bacillus Ant
; FILE REFERENCE: 22727/04116
; CURRENT APPLICATION NUMBER: US/10/105,694
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US 09/747,521
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2430
; TYPE: DNA
; ORGANISM: Bacillus anthracis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2430)
; OTHER INFORMATION:
US-10-105-694-1

Query Match

Best Local Similarity 4.6%; Score 36.2; DB 9; Length 2430;
Matches 89; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 158 TCGAAGAGAAAGTAACTTCATGAGATTTTGTATCTAATAAAGCTTAAGAGATGCA 217
DB 1053 TCTAAAAAGAAATACAAATGATAGTATGATTTTATCTACTGAGAAAAAGGTTTTT 1112
QY 218 ACAAGAGAGAGATCTTATCTGCTGAGAGATGAGAGCAATTGAG 277
DB 1113 AAAAAAGCTCAAAATGATATTCGATCTTATCTGAGAGAAAAAGCTTTTAA 1172
QY 278 ACCTGTCAAGATATTAAGCTTAAACAAAGAGAAAAAGAAACGCTTGAAA 334
DB 1173 TAGAATACAGGTGATAGTATTAATCTTATCTGAAAAAGAAAGGTTTTTAA 1229

RESULT 10

US-09-747-521-1
; Sequence 1, Application US/09747521
; Patent No. US20020051791A1
; GENERAL INFORMATION:
; APPLICANT: Galloway, Darrel
; APPLICANT: Mateczun, Alfred
; TITLE OF INVENTION: Methods for Protection Against Lethal Infection with Bacillus Ant
; FILE REFERENCE: 22727/04079
; CURRENT APPLICATION NUMBER: US/09/747,521
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 2430
; TYPE: DNA
; ORGANISM: Bacillus anthracis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2430)
US-09-747-521-1

Query Match

Best Local Similarity 4.6%; Score 36.2; DB 10; Length 2430;
Matches 89; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 158 TCGAAGAGAGTAACTTCATGAGATTTTGTATCTAATAAAGCTTAAGAGATGCA 217
DB 1053 TCTAAAAAGAAATACAAATGATAGTATGATTTTATCTACTGAGAAAAAGGTTTTT 1112

QY 218 ACAAGAGAGAGATCTTATCTGCTGAGAGATGAGAGCAATTGAG 277

DB 1113 AAAAAAGCTCAAAATGATATTCGATCTTATCTGAGAGAAAAAGCTTTTAA 1172

QY 278 ACCTGTCAAGATATTAAGCTTAAACAAAGAGAAAAAGAAACGCTTGAAA 334

DB 1173 TAGAATACAGGTGATAGTATTAATCTTATCTGAAAAAGAAAGGTTTTTAA 1229

RESULT 11

US-10-106-014-1
; Sequence 1, Application US/10106014
; Patent No. US20020142002A1
; GENERAL INFORMATION:
; APPLICANT: Galloway, Darrel R.
; APPLICANT: Mateczun, Alfred J.
; TITLE OF INVENTION: Methods for Protection Against Lethal Infection with Bacillus
; FILE REFERENCE: 22727/04114
; CURRENT APPLICATION NUMBER: US/10/106,014
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US 09/747,521
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2430
; TYPE: DNA
; ORGANISM: Bacillus anthracis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2430)
; OTHER INFORMATION:
US-10-106-014-1

Query Match

Best Local Similarity 4.6%; Score 36.2; DB 12; Length 2430;
Matches 89; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 158 TCGAAGAGAGTAACTTCATGAGATTTTGTATCTAATAAAGCTTAAGAGATGCA 217
DB 1053 TCTAAAAAGAAATACAAATGATAGTATGATTTTATCTACTGAGAAAAAGGTTTTT 1112
QY 218 ACAAGAGAGAGATCTTATCTGCTGAGAGATGAGAGCAATTGAG 277
DB 1113 AAAAAAGCTCAAAATGATATTCGATCTTATCTGAGAGAAAAAGCTTTTAA 1172
QY 278 ACCTGTCAAGATATTAAGCTTAAACAAAGAGAAAAAGAAACGCTTGAAA 334
DB 1173 TAGAATACAGGTGATAGTATTAATCTTATCTGAAAAAGAAAGGTTTTTAA 1229

RESULT 12

US-09-864-761-7124/C
; Sequence 7124, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David K.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wenheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04

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; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine ver. 1.1
; SEQ ID NO 7124
; LENGTH: 544
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL157405.2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.8
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.2
; US-09-864-761-7124

Query Match          4.6%; Score 36; DB 10; Length 544;
Best Local Similarity 50.0%; Pred. No. 3.1;
Matches 90; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 129 TGTGATCTTCATAGAGATTGATGATGATGAGAGAGAGATTAACCTTCATGAGATT 188
    |||
DB 416 TGTGATCTTCATAGAGATTGATGATGATGAGAGAGATTAACCTTCATGAGATT 357
    |||

QY 189 TGTATTCATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 248
    |||
DB 356 TAGAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 297
    |||

QY 249 CTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 308
    |||
DB 296 GTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 237
    |||

RESULT 13
US-09-772-134B-31/c
; Sequence 31, Application US/09772134B
; Patent No. US20020144310A1
; GENERAL INFORMATION:
; APPLICANT: Southern Illinois University
; APPLICANT: Lightfoot, David
; APPLICANT: Meksem, Khalid
; TITLE OF INVENTION: ISOLATED POLYNUCLEOTIDES AND POLYPEPTIDES RELATING TO LOCI UNDER
; TITLE OF INVENTION: RESISTANCE TO SOYBEAN CYST NEMATODE AND SOYBEAN SUDDEN DEATH SYND
```

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; TITLE OF INVENTION: METHODS EMPLOYING SAME
; FILE REFERENCE: 1268/4/2
; CURRENT APPLICATION NUMBER: US/09/772,134B
; CURRENT FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: 60/178,811
; PRIOR FILING DATE: 2000-01-28
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31
; LENGTH: 736
; TYPE: DNA
; ORGANISM: soybean
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(736)
; OTHER INFORMATION: n is an undetermined nucleotide (dATP, dCTP, dGTP, or dTTP)
; US-09-772-134B-31

Query Match          4.5%; Score 35.6; DB 10; Length 736;
Best Local Similarity 50.3%; Pred. No. 4.6;
Matches 86; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

QY 192 ATTGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 251
    |||
DB 184 ATTGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 125
    |||

QY 252 TGAGGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 311
    |||
DB 124 TTACGAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 65
    |||

QY 312 GAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 362
    |||
DB 64 ATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 14
    |||

RESULT 14
US-09-764-878-262/c
; Sequence 262, Application US/09764878
; Patent No. US20020090615A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA121
; CURRENT APPLICATION NUMBER: US/09/764,878
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PAM or file wrapper
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 262
; LENGTH: 23632
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-764-878-262

Query Match          4.5%; Score 35.6; DB 10; Length 23632;
Best Local Similarity 47.0%; Pred. No. 24;
Matches 110; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

QY 108 GATTGGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 167
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QY 168 AGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 227
    |||
DB 4650 ATTATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4651
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DB 4530 TTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4531
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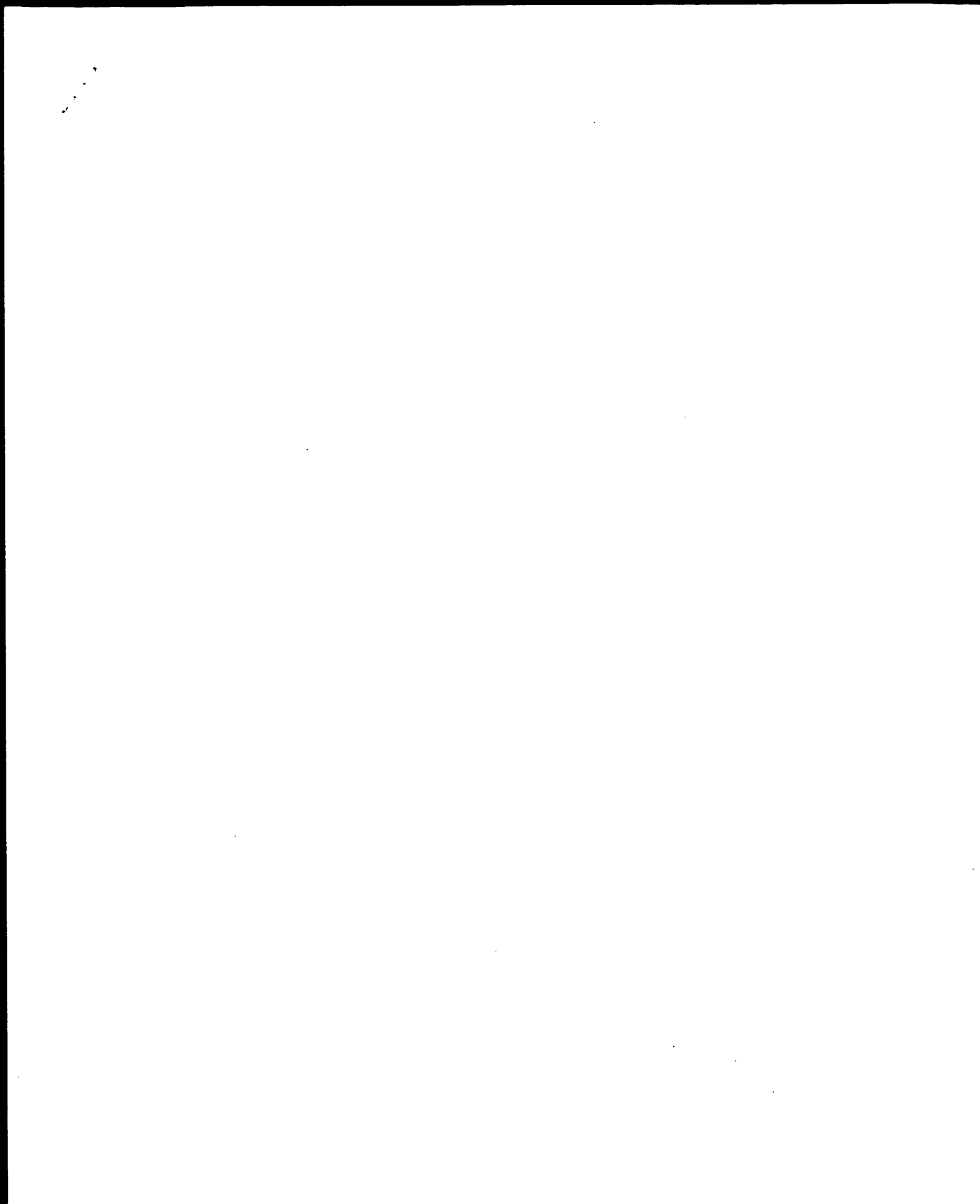
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; Sequence 941, Application US/09764860
; Patent No. US20020094953A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC008
; CURRENT APPLICATION NUMBER: US/09/764,860
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1198
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 941
; LENGTH: 23632
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-860-941

Query Match 4.5%; Score 35.6; DB 10; Length 23632;
Best Local Similarity 47.0%; Pred. No. 24;
Matches 110; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

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QY 228 AGGATCTTTATCTTGGTGAAGTGAAGATGAGAGCAATTGGAAGCCTTGCA 287
DB 4590 TTCAGATCGGCTCCCAACCTATTTGAAGTATATGCGGTTAGAAAATCTTCTHC 4531
QY 288 GGATATAAGCTTAACAAAGAGAGAAAAAGAAACAGCTTGAAATGCAAG 341
DB 4530 AGCAGTCATTTCTCGGGAATTAAGACACACTTACAGACTTCAATGGAAG 4477

Search completed: March 9, 2003, 09:42:06
Job time : 231.054 secs



GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: March 8, 2003, 21:49:58 ; Search time 33.5164 Seconds
(without alignments)
7164.491 Million cell updates/sec

Title: US-08-982-272-3

Perfect score: 783
Sequence: 1 ATATGGAACATCAACCA.....TTGGCTTACTCAAACTCTGA 783

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents, NA.*
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6: /cgn2_6/prodata/2/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	751	95.9	818	1	US-08-431-055-1 Sequence 1, Appl
2	751	95.9	818	1	US-08-858-197-1 Sequence 1, Appl
3	749.4	95.7	783	1	US-08-446-922-5 Sequence 5, Appl
4	749.4	95.7	783	2	US-08-249-189-1 Sequence 1, Appl
5	749.4	95.7	783	2	US-08-484-624-1 Sequence 1, Appl
6	749.4	95.7	783	2	US-08-477-733B-1 Sequence 1, Appl
7	749.4	95.7	783	3	US-09-088-913A-1 Sequence 1, Appl
8	749.4	95.7	783	4	US-08-769-819-1 Sequence 1, Appl
9	749.4	95.7	783	4	US-08-770-981-1 Sequence 1, Appl
10	749.4	95.7	783	4	US-08-770-981-1 Sequence 1, Appl
11	749.4	95.7	783	4	US-08-770-981-1 Sequence 1, Appl
12	749.4	95.7	783	5	PCT-US93-10034-5 Sequence 5, Appl
13	749.4	95.7	783	5	PCT-US93-10034-5 Sequence 5, Appl
14	631.4	80.6	878	2	US-08-249-189-22 Sequence 22, Appl
15	631.4	80.6	878	2	US-08-477-733B-22 Sequence 22, Appl
16	631.4	80.6	878	3	US-09-088-913A-22 Sequence 22, Appl
17	631.4	80.6	878	4	US-08-769-819-22 Sequence 22, Appl
18	631.4	80.6	878	4	US-08-770-981-22 Sequence 22, Appl
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21	592.4	75.7	786	1	US-08-446-922-3 Sequence 3, Appl
22	592.4	75.7	786	5	PCT-US93-10034-3 Sequence 3, Appl
23	592.4	75.7	840	1	US-07-940-605A-1 Sequence 1, Appl
24	592.4	75.7	840	1	US-08-184-422-7 Sequence 7, Appl
25	592.4	75.7	840	1	US-08-360-923A-1 Sequence 3, Appl
26	592.4	75.7	840	1	US-08-431-055-3 Sequence 1, Appl
27	592.4	75.7	840	2	US-08-650-096-1 Sequence 1, Appl

ALIGNMENTS

28	592.4	75.7	840	2	US-08-249-189-11	Sequence 11, Appl
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33	592.4	75.7	840	3	US-08-589-771B-7	Sequence 7, Appl
34	592.4	75.7	840	4	US-08-769-819-11	Sequence 11, Appl
35	592.4	75.7	840	4	US-08-770-974-11	Sequence 11, Appl
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37	592.4	75.7	840	4	US-08-770-981-11	Sequence 11, Appl
38	592.4	75.7	840	4	US-09-399-106-11	Sequence 11, Appl
39	446.2	57.0	1425	2	US-08-249-189-15	Sequence 15, Appl
40	446.2	57.0	1425	2	US-08-484-624A-15	Sequence 15, Appl
41	446.2	57.0	1425	2	US-08-477-733B-15	Sequence 15, Appl
42	446.2	57.0	1425	3	US-09-088-913A-15	Sequence 15, Appl
43	446.2	57.0	1425	4	US-08-769-819-15	Sequence 15, Appl
44	446.2	57.0	1425	4	US-08-770-974-15	Sequence 15, Appl
45	446.2	57.0	1425	4	US-08-770-981-15	Sequence 15, Appl

RESULT 1
US-08-431-055-1
Sequence 1, Application US/08431055
Patent No. 5817516
GENERAL INFORMATION:
APPLICANT: KERRY, MERILYN R
TITLE OF INVENTION: METHODS FOR PROLIFERATING AND
TITLE OF INVENTION: DIFFERENTIATING B CELLS, AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: STERN, KESSLER, GOLDSTEIN & FOX
STREET: 100 NEW YORK AVE. N.W. SUITE 600
CITY: WASHINGTON
STATE: D.C.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,055
FILING DATE: 28-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/234,580
FILING DATE: 28-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: WILDMAN, ROBERT A
REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 1011.1030000/RAM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ. ID NO. 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 818 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 13..795
US-08-431-055-1
Query Match 95.9%, Score 751, DB 1, Length 818;
Best Local Similarity 97.4%, Pred. No. 2.3e-212;
Matches 763, Conservative 0, Mismatches 20, Indels 0, Gaps 0;

QY 1 ATGATCGAAACATACCAACCAACTCTTCCCCGATCTGGCGCCACTGGACCTGCCCATCAGC 60
DB 13 ATGATAGAAACATACCAACCAACTCTTCCCCGATCTGGCGCCACTGGACCTGCCCATCAGC 72
QY 61 ATGAAATATTTTATGATTTTACTTACTGTTTTCTTATACCCCAAGATGATTTGGGTACCA 120
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QY 121 CTTTGTGCTGATCTCTCATATGAAAGATGATTAAGCTGAAAGGAAAGTAAACCTTAT 180
DB 133 CTTTGTGCTGATCTCTCATATGAAAGATGATTAAGCTGAAAGGAAAGTAAACCTTAT 192
QY 181 GAAGATTTTGTATTCTATTAATAAGCTAAAGATGCAACAAAGAGAGATCTTTATCC 240
DB 193 GAAGATTTTGTATTCTATTAATAAGCTAAAGATGCAACAAAGAGAGATCTTTATCC 252
QY 241 TTGCTGAACCTGTAGAGATGAGAGGCAATTTGAAGACCTTGTCAAGATATACGTTA 300
DB 253 TTGCTGAACCTGTAGAGATGAGAGGCAATTTGAAGACCTTGTCAAGATATACGTTA 312
QY 301 AACAAAG 360
DB 313 AACAAAG 372
QY 361 ATTGACGACACGTTGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 373 ATTGACGACACGTTGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 432
QY 421 AAGAAAGATATTAATCACTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
DB 433 AAGAAAGATATTAATCACTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 492
QY 481 ACGTTAAAG 540
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QY 541 GAGCTTGTAGTCAAGCCCATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
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QY 601 GAGAGATCTTACTCAAGGCGGCAATACCAAGTCTCTCCCAAGCTTTCCGAGAGAG 660
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QY 721 ACTGAAG 780
DB 733 ACTGAAG 792
QY 781 TGA 783
DB 793 TGA 795

RESULT 2

US-08-858-197-1

Sequence 1, Application US/08858197

Patent No. 6237052

GENERAL INFORMATION:

APPLICANT: KERRY, MERILYN R

APPLICANT: CASTLE, BRIAN E

TITLE OF INVENTION: METHODS FOR PROLIFERATING AND

TITLE OF INVENTION: DIFFERENTIATING B CELLS, AND USES THEREOF

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX

STREET: 100 NEW YORK AVE. N.W. SUITE 600

CITY: WASHINGTON

STATE: D. C.

ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/858,197
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/234,580
FILING DATE: 28-Apr-1994
ATTORNEY/AGENT INFORMATION:
NAME: MILLMAN, ROBERT A
REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 1011.1030000/RAM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 818 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 13..795
US-08-858-197-1

Query Match 95.4%; Score 751; DB 4; Length 818;
Best Local Similarity 97.4%; Pred. No. 2.3e-112;
Matches 763; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACCAACCAACTCTTCCCCGATCTGGCGCCACTGGACCTGCCCATCAGC 60
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QY 241 TTGCTGAACCTGTAGAGATGAGAGGCAATTTGAAGACCTTGTCAAGATATACGTTA 300
DB 253 TTGCTGAACCTGTAGAGATGAGAGGCAATTTGAAGACCTTGTCAAGATATACGTTA 312
QY 301 AACAAAG 360
DB 313 AACAAAG 372
QY 361 ATTGACGACACGTTGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 373 ATTGACGACACGTTGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 432
QY 421 AAGAAAGATATTAATCACTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
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QY 481 ACGTTAAAG 540
DB 493 ACGTTAAAG 552
QY 541 GAGCTTGTAGTCAAGCCCATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600

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Qy 601 GAGAGATCTTACTCAAGGGGGAATATCCACAGTTCTCCAGCTTTGGAGCAGCG 660
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Db 673 TCTGTTCACCTTGGGCGAGTGTTCGAATTAACAAGCTGTCTGTGTTCGAAGTG 732
Qy 721 ACTGAAGCAAGCCCAAGTATCCACAGAGTGGCTTCTCATCTTTGGCTTACTCAACTC 780
Db 733 ACTGAAGCAAGCCCAAGTATCCACAGAGTGGCTTCTCATCTTTGGCTTACTCAACTC 792
Qy 781 TGA 783
Db 793 TGA 795

RESULT 3
US-08-446-922-5
; Sequence 5, Application US/08446922
; Patent No. 5716805
; GENERAL INFORMATION:
; APPLICANT: Spriggs, Melanie
; TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.1
; SOFTWARE: Microsoft Word for Apple, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,922
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/107,353
; FILING DATE: 08-13-93
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 1003-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 783 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Mouse
; STRAIN: CD40-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..780
; US-08-446-922-5

Query Match 95.7%; Score 749.4; DB 1; Length 783;
Best Local Similarity 97.3%; Pred. No. 6,5e-212;
Matches 762; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
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Db 1 ATGATGAGAAATATACAGCCCACTTCCCGCATGCGGCACTGAGATGCGCATCAGC 60
Qy 61 ATGAAATTTTATGATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 120
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Db 181 GAAATTTTGTATTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTC 240
Qy 241 TTGCTGAACCTGTGAGAGATGAGAGCAATTTGAACCTTGTCAAGATTAACCTTGA 300
Db 241 TTGCTGAACCTGTGAGAGATGAGAGCAATTTGAACCTTGTCAAGATTAACCTTGA 300
Qy 301 ATCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 360
Db 301 ATCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 360
Qy 361 ATTCAGCAGCAGCTGTGAGCAAGCCCAAGTATGAGAGATCGTTCTACAGTGGGCC 420
Db 361 ATTCAGCAGCAGCTGTGAGCAAGCCCAAGTATGAGAGATCGTTCTACAGTGGGCC 420
Qy 421 AAGAAAGATATATATCCATGAAAGCAATGATGATGATGATGATGATGATGATGATG 480
Db 421 AAGAAAGATATATATCCATGAAAGCAATGATGATGATGATGATGATGATGATGATG 480
Qy 481 ACGGTTAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 540
Db 481 ACGGTTAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 540
Qy 541 GAGCCTTCGAGTGAAGCCCAATGATGATGATGATGATGATGATGATGATGATGATG 600
Db 541 GAGCCTTCGAGTGAAGCCCAATGATGATGATGATGATGATGATGATGATGATGATG 600
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Db 661 TCTGTTCACCTTGGGCGAGTGTTCGAATTAACAAGCTGTCTGTGTTCGAAGTG 720
Qy 721 ACTGAAGCAAGCCCAAGTATCCACAGAGTGGCTTCTCATCTTTGGCTTACTCAACTC 780
Db 721 ACTGAAGCAAGCCCAAGTATCCACAGAGTGGCTTCTCATCTTTGGCTTACTCAACTC 780
Qy 781 TGA 783
Db 781 TGA 783
RESULT 4
US-08-249-189-1
; Sequence 1, Application US/08249189
; Patent No. 5961974
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: FANSTLOW, WILIAM
; APPLICANT: SPRIGGS, MELANIE
; APPLICANT: SRINIVASAN, SUBHASHINI
; APPLICANT: GIBSON, MARYLOU
; TITLE OF INVENTION: NOVEL CYTOKINE

NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.1
SOFTWARE: Microsoft Word for Apple, version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/249,189
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,703
FILING DATE: October 23, 1992
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/805,723
FILING DATE: December 5, 1991
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/783,707
FILING DATE: October 25, 1991
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ. ID NO. 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 783 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: MOUSE
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 1..783
US-08-249-189-1
Query Match 95.7%; Score 749.4; DB 2; Length 783;
Best Local Similarity 97.3%; Pred. No. 6,5e-212;
Matches 762; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 ATGATCGAAGACATGACCAAACTTCTCCCGATCGCGCGCACTGAGTCCGCAATCAGC 60
DB 1 ATGATGAGAAACATACGACCACTTCCCGATCGCGCGCACTGAGTCCGCAATCAGC 60
QY 61 ATGAAATTTTATGATTTACTTACTGTTTTCTTATCACCAGATGATGGGTGACA 120
DB 61 ATGAAATTTTATGATTTACTTACTGTTTTCTTATCACCAGATGATGGGTGACTG 120
QY 121 CTTTGGCTGATCTCATAGAAAGTGTGATGAGTGAAGAGAAAGTAACTTCAAT 180
DB 121 CTTTGGCTGATCTCATAGAAAGTGTGATGAGTGAAGAGAAAGTAACTTCAAT 180
QY 181 GAAATTTTGTATCTATTAAGAAAGTAAAGATGCAACAAAGAGAGATCTTTATCC 240
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DB 241 TTGCTGAAGTGTGAGAGATGAGAGGCAATTTGAGACCTTGTCAAGATATATACCTTA 300
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DB 301 AACAAAG 360
QY 361 ATTGCAGCAGAGTTGTGAG 420
DB 361 ATTGCAGCAGAGTTGTGAG 420
QY 421 AAGAAAGATATTTATCCATGAAAGCACTTGTGTAATGCTTGAAGAGAGAGAGAGAG 480
DB 421 AAGAAAGATATTTATCCATGAAAGCACTTGTGTAATGCTTGAAGAGAGAGAGAGAG 480
QY 481 ACGGTAAAG 540
DB 481 ACGGTAAAG 540
QY 541 GAGCCTTGAGTCAAGCCGCTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
DB 541 GAGCCTTGAGTCAAGCCGCTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 601 GAGAGATCTTACTCAAGCGCGCAATACCAAGTTCCTCCAGCTTTGGAGAGAGAG 660
DB 601 GAGAGATCTTACTCAAGCGCGCAATACCAAGTTCCTCCAGCTTTGGAGAGAGAG 660
QY 661 TCGTTCACCTGGCGGAGAGTGTGTAATTAACAGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
DB 661 TCGTTCACCTGGCGGAGAGTGTGTAATTAACAGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
QY 721 ACTGAGCAAGCAAGTATGATCAGAGTGGCTTCTCATCTTTGGCTTACTCAACTC 780
DB 721 ACTGAGCAAGCAAGTATGATCAGAGTGGCTTCTCATCTTTGGCTTACTCAACTC 780
QY 781 TGA 783
DB 781 TGA 783

RESULT 5
US-08-484-624A-1
Sequence 1, Application US/08484624A
Patent No. 5962406
GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: FANSLAW, WILLIAM
APPLICANT: SPRIGGS, MELANIE
APPLICANT: SRINIVASAN, SUBHASHINI
APPLICANT: GIBSON, MARYLOU
APPLICANT: MORRIS, ARVIA E.
APPLICANT: MCCREY, JEFFREY
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,624A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/477,733
FILING DATE: June 07, 1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,703
FILING DATE: October 23, 1992
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/805,723
FILING DATE: December 5, 1991
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/783,707
FILING DATE: October 25, 1991
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 783 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: MOUSE
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 1..783
US-08-484-624A-1

Query Match 95.7%; Score 749.4; DB 2; Length 783;
Best Local Similarity 97.3%; Pred. No. 6.5e-212;
Matches 762; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 ATGATGAAACATACACCACTTCTCCCGCATCTGCGGCACCTGGATGCCATAGC 60
DB 1 ATGATGAAACATACACCACTTCTCCCGCATCTGCGGCACCTGGATGCCATAGC 60
QY 61 ATGAAATTTTATATTTACTTACTGTTTCTTATCAACCAAGATGATGGGTACGA 120
DB 61 ATGAAATTTTATATTTACTTACTGTTTCTTATCAACCAAGATGATGGGTACGA 120
QY 121 CTTTGTGCTGTGATCTTATGAAAGATTTGATAGGTCGAAGAGAAATTAACCTTCAT 180
DB 121 CTTTGTGCTGTGATCTTATGAAAGATTTGATAGGTCGAAGAGAAATTAACCTTCAT 180
QY 181 GAAGATTTTATATTTACTTAAAGCTTAAGAGATGCAACAAGAGAGATCTTATCC 240
DB 181 GAAGATTTTATATTTACTTAAAGCTTAAGAGATGCAACAAGAGAGATCTTATCC 240
QY 241 TTGCTGAACCTGTGAGAGATGAAAGCAATTTGAAGCCTTGCAAGATTAACCTGA 300
DB 241 TTGCTGAACCTGTGAGAGATGAAAGCAATTTGAAGCCTTGCAAGATTAACCTGA 300
QY 301 AACAAAG 360
DB 301 AACAAAG 360
QY 361 ATTGACACACAGCTGTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 361 ATTGACACACAGCTGTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
QY 421 AAGAAAGATATTTATATCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480

DB 421 AAGAAAGATATTTATCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
QY 481 ACGGTTAAAG 540
DB 481 ACGGTTAAAG 540
QY 541 GAGCCTTGAGTCAACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
DB 541 GAGCCTTGAGTCAACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
QY 601 GAGAGATCTTATCTCAAGCGGCAATATCCCAAGTCTCCAGCTTTGCGAGAGAGAG 660
DB 601 GAGAGATCTTATCTCAAGCGGCAATATCCCAAGTCTCCAGCTTTGCGAGAGAGAG 660
QY 661 TCTGTTCACTTGGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
DB 661 TCTGTTCACTTGGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY 721 ACTGAG 780
DB 721 ACTGAG 780
QY 781 TGA 783
DB 781 TGA 783
RESULT 6
US-08-477-733B-1
Sequence 1, Application US/08477733B
Patent No. 5981724
GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: FANSLAW, WILLIAM
APPLICANT: SPRIGGS, MELANIE
APPLICANT: SRINIVASAN, SUBHASHINI
APPLICANT: GIBSON, MARYLOU
APPLICANT: MORRIS, ARVIA E.
APPLICANT: MCGREW, JEFFERY
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: MS word for Apple Power Macintosh, version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,733B
FILING DATE: June 07, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,189
FILING DATE: May 24, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,703
FILING DATE: October 23, 1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/805,723
FILING DATE: December 5, 1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/783,707
FILING DATE: October 25, 1991

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870430
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 783 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: MOUSE
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 1..783
US-08-477-733B-1

Query Match 95.7% Score 749.4; DB 2; Length 783;
Best Local Similarity 97.3%; Pred. No. 6.5e-212;
Matches 762; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATTCACCAAACTTCCCGGATCTGCGGCACTGAGCTGCCATCAGC 60
DB 1 ATGATGAAACATTCACCAAACTTCCCGGATCTGCGGCACTGAGCTGCCATCAGC 60
QY 61 ATGAAATTTTATGATTTATCTTACTCTTCTTTCTTATCACCAGATGATGGGTGAGA 120
DB 61 ATGAAATTTTATGATTTATCTTACTCTTCTTTCTTATCACCAGATGATGGGTGAGA 120
QY 121 CTTTCTGCTGCTATCTTCTTGAAGATTGATGATGAAAGAGAAATTAACCTTCTAT 180
DB 121 CTTTCTGCTGCTATCTTCTTGAAGATTGATGATGAAAGAGAAATTAACCTTCTAT 180
QY 181 GAAGATTTTGTATCATTAATAAGCTTAAGATGCAACAAGAGAGATCTTATCC 240
DB 181 GAAGATTTTGTATCATTAATAAGCTTAAGATGCAACAAGAGAGATCTTATCC 240
QY 241 TTGCTGAACGTGAGAGATGAAAGCAATTTGAAACCTTGTCAAGATATTAAGTTA 300
DB 241 TTGCTGAACGTGAGAGATGAAAGCAATTTGAAACCTTGTCAAGATATTAAGTTA 300
QY 301 AACAAAG 360
DB 301 AACAAAG 360
QY 361 ATTGAGACACGCTGTGTAAGCGAAGCAAGTAAGCAAGTCCGTTCTACAGTGGGCC 420
DB 361 ATTGAGACACGCTGTGTAAGCGAAGCAAGTAAGCAAGTCCGTTCTACAGTGGGCC 420
QY 421 AAGAAAGGATTTATCAATGAAAGCAACTTGGTATCTTGAATAATGGGAAACAGCTG 480
DB 421 AAGAAAGGATTTATCAATGAAAGCAACTTGGTATCTTGAATAATGGGAAACAGCTG 480
QY 481 ACGTTAAAG 540
DB 481 ACGTTAAAG 540
QY 541 GAGCTTGAAGTCAAGCCCATTCATCTGCGGCTCTGGCTGAAGCCAGCATTTGATCT 600
DB 541 GAGCTTGAAGTCAAGCCCATTCATCTGCGGCTCTGGCTGAAGCCAGCATTTGATCT 600
QY 601 GAGAGATCTTACTCAAGGGGCGCAATACCAAGTCTCCCGAGCTTTGGCGAGGAG 660
DB 601 GAGAGATCTTACTCAAGGGGCGCAATACCAAGTCTCCCGAGCTTTGGCGAGGAG 660

QY 661 TCTGTTCACTTGGCGGAGAGTGTGAAATTAAGAGTGTCTGTGTTGTCAAGCTG 720
DB 661 TCTGTTCACTTGGCGGAGAGTGTGAAATTAAGAGTGTCTGTGTTGTCAAGCTG 720
QY 721 ACTGAGCAAGCCCAAGTATCCACAGAGTGTCTGTCACTTTGCTTACCAAGCTC 780
DB 721 ACTGAGCAAGCCCAAGTATCCACAGAGTGTGTCTGTCTCTTGTGCTTACCAAGCTC 780
QY 781 TGA 783
DB 781 TGA 783

RESULT 7
US-09-088-913A-1
Sequence 1, Application US/09088913A
Patent No. 6087329
GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: FANSLAW, WILLIAM
APPLICANT: SPRIGGS, MELANIE
APPLICANT: SRINIVASAN, SUBHASHINI
APPLICANT: GIBSON, MARLOU
APPLICANT: MORRIS, ARVIA E.
APPLICANT: MCGREW, JEFFERY
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/088,913A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484,624
FILING DATE:
APPLICATION NUMBER: 08/477,733
FILING DATE: June 07, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,703
FILING DATE: October 23, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/805,723
FILING DATE: December 5, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/783,707
FILING DATE: October 25, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 783 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO

ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: MOUSE
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 1..783
US-09-088-913A-1

Query Match 95.7%; Score 749.4; DB 3; Length 783;
Best Local Similarity 97.3%; Pred. No. 6.5e-212;
Matches 762; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 ATGATGAAACATACAAACCACTTCCCGATCTGCGGCACTGACCTGCCATCAGC 60
Db 1 ATGATGAAACATACAAACCACTTCCCGATCTGCGGCACTGACCTGCCATCAGC 60
QY 61 ATGAAATTTTATGATTTTATCTTACTGTTTCTTATACCCAGATGATGGGTACGA 120
Db 61 ATGAAATTTTATGATTTTATCTTACTGTTTCTTATACCCAGATGATGGGTACGA 120
QY 121 CTTTTCCTGCTGATCTTCTTACATAGATTTGATAGGTGCGAAGAGATTAACCTTCA 180
Db 121 CTTTTCCTGCTGATCTTCTTACATAGATTTGATAGGTGCGAAGAGATTAACCTTCA 180
QY 181 GAAGATTTGTATCATATAAAAGCTTAAAGATGCAAAAGAGAGATCTTATCC 240
Db 181 GAAGATTTGTATCATATAAAAGCTTAAAGATGCAAAAGAGAGATCTTATCC 240
QY 241 TTGCTGAACGTGAGAGATGAGAAAGCAATTTGAGACCTTGTCAAGATATTAAGCTTA 300
Db 241 TTGCTGAACGTGAGAGATGAGAAAGCAATTTGAGACCTTGTCAAGATATTAAGCTTA 300
QY 301 AACAAAGAAAGAAAGAAAGAAAGCTTTGAATGCAAGAGATGAGAAAGCTTCA 360
Db 301 AACAAAGAAAGAAAGAAAGAAAGCTTTGAATGCAAGAGATGAGAAAGCTTCA 360
QY 361 ATTGAGCAACAGTTGTAAAGCAAGATGATGATGATGATGATGATGATGATGATGATG 420
Db 361 ATTGAGCAACAGTTGTAAAGCAAGATGATGATGATGATGATGATGATGATGATGATG 420
QY 421 AAGAAAGATTTATACATGAAAGAAAGCTTGTATGCTTGAAGAGAGAAAGCTG 480
Db 421 AAGAAAGATTTATACATGAAAGAAAGCTTGTATGCTTGAAGAGAGAAAGCTG 480
QY 481 ACGTTAAAGAAAGAAAGCTTATATGCTTCACTCACTCACTCACTCACTCACTCACTCA 540
Db 481 ACGTTAAAGAAAGAAAGCTTATATGCTTCACTCACTCACTCACTCACTCACTCACTCA 540
QY 541 GAGCCTTGAAGTCAAGCCCATTCATGCTGCGGCTGCGTGAAGCCAGATGATGAT 600
Db 541 GAGCCTTGAAGTCAAGCCCATTCATGCTGCGGCTGCGTGAAGCCAGATGATGAT 600
QY 601 GAGAGATCTTATCTCAAGGCGGCAATACCAAGTCTCCAGCTTTGCGAGCAGAG 660
Db 601 GAGAGATCTTATCTCAAGGCGGCAATACCAAGTCTCCAGCTTTGCGAGCAGAG 660
QY 661 TCTGTTCACTTGGGCGAGGTTTGAATTAAGCTGAGGCTTCTGATGCTTGAAGCTG 720
Db 661 TCTGTTCACTTGGGCGAGGTTTGAATTAAGCTGAGGCTTCTGATGCTTGAAGCTG 720
QY 721 ACTGAAGCAAGCAAGTATCAAGAGTGGCTTCTCATCTTTTGGCTTCACTCAATC 780
Db 721 ACTGAAGCAAGCAAGTATCAAGAGTGGCTTCTCATCTTTTGGCTTCACTCAATC 780
QY 781 TGA 783
Db 781 TGA 783

RESULT 8
US-08-769-819-1

Sequence 1, Application US/08769819
Patent No. 6264951
GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: FANSLAW, WILLIAM
APPLICANT: SPRIGGS, MELANIE
APPLICANT: SRINIVASAN, SUBHASHINI
APPLICANT: GIBSON, MARYLOU
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.1
SOFTWARE: Microsoft Word for Apple, version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/769,819
FILING DATE: 19-DEC-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484,624
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: 08/249,189
FILING DATE: May 24, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,703
FILING DATE: October 23, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/805,723
FILING DATE: December 5, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/783,707
FILING DATE: October 25, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 783 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: MOUSE
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 1..783
US-08-769-819-1

Query Match 95.7%; Score 749.4; DB 4; Length 783;
Best Local Similarity 97.3%; Pred. No. 6.5e-212;
Matches 762; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 ATGATGAAACATACAAACCTTCCCGATCTGCGGCACTGACCTGCCATCAGC 60
Db 1 ATGATGAAACATACAAACCTTCCCGATCTGCGGCACTGACCTGCCATCAGC 60

OY	61	ATGAAAATTATTAGTATTACTCTACTGTTCCTTTCTATACCCAGAAGATTGGTGACA	120
Dd	61	ATGAAGATTTTTTAAGTATTACTACTGTTCCTTCTATACCCAAAGATTGGATCTGTG	120
OY	121	CTTTTTCCTGTGTACTCTCATAGAAAGTTGGATTAAGCTGAAAGAGAAATACTTAT	180
Dd	121	CTTTTTCCTGTGTACTCTCAATGAAAGATTGGATTAAGCTGAAAGAGAAATACTTAT	180
OY	181	GAGATTTTGTATTCATAAAAAAGCTAAGATGCAACAAAGAGAAAGATCTTTATCC	240
Dd	181	GAGATTTTGTATTCATAAAAAAGCTAAGATGCAACAAAGAGAAAGATCTTTATCC	240
OY	241	TTCCTGAACCTGTGAGAGATGAGAAAGC AATTTGAAGCCTTGTCAAAGATTAACCTTA	300
Dd	241	TTCCTGAACCTGTGAGAGATGAGAAAGC AATTTGAAGCCTTGTCAAAGATTAACCTTA	300
OY	301	AACAAAGAAAGAAAAGAAAACGCTTTGAATGC AAAGAGGTGATGAGATCC TCA	360
Dd	301	AACAAAGAAAGAAAAGAAAACGCTTTGAATGC AAAGAGGTGATGAGATCC TCA	360
OY	361	ATTGCAGCACGTTGTAAGCGAAGCCAAACGTATGCGATCCGTTCTACAGTGGGCC	420
Dd	361	ATTGCAGCACGTTGTAAGCGAAGCCAAACGTATGCGATCCGTTCTACAGTGGGCC	420
OY	421	AAGAAAGATTTATTCATGAAAAGCACTGGTATCTTGAAAAATGGGAAACAGCTG	480
Dd	421	AAGAAAGATTTATTCATGAAAAGCACTGGTATCTTGAAAAATGGGAAACAGCTG	480
OY	481	ACGGTTAAAAAGAGAGACTTATTAATGTCTTCACTCAAGTCAACCTTCTGTCTAATCGG	540
Dd	481	ACGGTTAAAAAGAGAGACTTATTAATGTCTTCACTCAAGTCAACCTTCTGTCTAATCGG	540
OY	541	GACCCTTGAGTCAAGGCCCAATTCATCGTGGCCCTGGCTGSAAGCCACAGATGGATCT	600
Dd	541	GACCCTTGAGTCAAGGCCCAATTCATCGTGGCCCTGGCTGSAAGCCACAGATGGATCT	600
OY	601	GAGAGATTCCTTACTCAAGGCGGCAATACCCAAGTTCCTCCAGCTTTGCGAGACAG	660
Dd	601	GAGAGATTCCTTACTCAAGGCGGCAATACCCAAGTTCCTCCAGCTTTGCGAGACAG	660
OY	661	TCGTGTCACCTTGGGCGGAGGTGTTGAATTAAGCTGGTGCCTCGTGTGTCAAACGTG	720
Dd	661	TCGTGTCACCTTGGGCGGAGGTGTTGAATTAAGCTGGTGCCTCGTGTGTCAAACGTG	720
OY	721	ACTGAAGCAAGCCAAAGTATCCACAGAGTTGGCTTCACTTTTGGCTTACTCAATC	780
Dd	721	ACTGAAGCAAGCCAAAGTATCCACAGAGTTGGCTTCACTTTTGGCTTACTCAATC	780
OY	781	TGA TGA	
Dd	781	TGA TGA	

RESULT 9
US-08-770-974-1
Sequence 1, Application US/08770974
Patent No. 6290972
GENERAL INFORMATION:
APPLICANT: ARNITAGE, RICHARD
APPLICANT: FANSLON, WILLIAM
APPLICANT: SPRINGS, MELANIE
APPLICANT: SRINIVASAN, SUBHASHINI
APPLICANT: GIBSON, MARLOU
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:

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1 MEDIUM TYPE: Floppy disk
2 COMPUTER: Apple Macintosh
3 OPERATING SYSTEM: Apple Operating System 7.1
4 SOFTWARE: Microsoft Word for Apple, version 5.1a
5 CURRENT APPLICATION DATA:
6 APPLICATION NUMBER: US/08/770,974
7 FILING DATE: 20-DEC-1996
8 CLASSIFICATION: 435
9 PRIOR APPLICATION DATA:
10 APPLICATION NUMBER: 08/477,733
11 FILING DATE: 02-AUG-1995
12 APPLICATION NUMBER: 08/249,189
13 FILING DATE: May 24, 1994
14 PRIOR APPLICATION DATA:
15 APPLICATION NUMBER: 07/969,703
16 FILING DATE: October 23, 1992
17 PRIOR APPLICATION DATA:
18 APPLICATION NUMBER: 07/805,723
19 FILING DATE: December 5, 1991
20 PRIOR APPLICATION DATA:
21 APPLICATION NUMBER: 07/783,707
22 FILING DATE: October 25, 1991
23 ATTORNEY/AGENT INFORMATION:
24 NAME: Perkins, Patricia A.
25 REGISTRATION NUMBER: 34,693
26 REFERENCE/DOCKET NUMBER: 2802-D
27 TELECOMMUNICATION INFORMATION:
28 TELEPHONE: 2065870430
29 TELEFAX: 2065870606
30 INFORMATION FOR SEQ. ID NO.: 1:
31 SEQUENCE CHARACTERISTICS:
32 LENGTH: 783 base pairs
33 TYPE: nucleic acid
34 STRANDEDNESS: single
35 TOPOLOGY: linear
36 MOLECULE TYPE: cDNA
37 HYPOTHETICAL: NO
38 ANTI-SENSE: NO
39 ORIGINAL SOURCE:
40 ORGANISM: MOUSE
41 IMMEDIATE SOURCE:
42 CLONE: CD40-L
43 FEATURE:
44 NAME/KEY: CDS
45 LOCATION: 1..783
46 US-08-770-974-1

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Query Match      95.7%; Score 749.4; DB 4; Length 783;
Best Local Similarity 97.3%; Seed No. 6,5e-212;
Matches 762; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy      1 ATGATCGAAGCATACAAACCAACTTCTCCCGATCTGGCGGCCATCTGCACTACAGC 60
Db      1 ATGATAGAAACATACAGCCCAACTTCCCGCAGATCGTGCGCACTGCACTTCCACAGAGC 60

Qy      61 ATGAAATTTTATATGATATTACTATCTGTTTTCTTATACCCAGATGATGSGGTCAACA 120
Db      61 ATGAAAGATTTTATATGATATTACTTACTGTGTTTTCTTATACCCAAATGATGATCTGTG 120

Qy      121 CTTTTCCTGCTGATCTTCATATAGAGATTTGATTAAGTGTGAAGAGAACTTTCAT 180
Db      121 CTTTTCCTGCTGATCTTCATATAGAGATTTGATTAAGTGTGAAGAGAACTTTCAT 180

Qy      181 GAAAGATTTTGTATCATATAAAAAGCTTAAAGAGATGCAACAAAGGAGAAGATCTTTATCC 240
Db      181 GAAAGATTTTGTATCATATAAAAAGCTTAAAGAGATGCAACAAAGGAGAAGATCTTTATCC 240

Qy      241 TTGCTGAACGTGAGAGATGAGAGGCAATTTTGAAGACTTGTCAAGATATAACGTTA 300
Db      241 TTGCTGAACGTGAGAGATGAGAGGCAATTTTGAAGACTTGTCAAGATATAACGTTA 300

Qy      301 AACCAAGAGAGAAAAAGAAAACAGCTTTGAATGCAAGGTGATGAGATCTCTAA 360

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QY 541 GAGCTTCGAGTCAACGCCCATTCATCTCGGCTTCGGGCAAGCCGAGTGAATCT 600
 Db 541 GAGCTTCGAGTCAACGCCCATTCATCTCGGCTTCGGGCAAGCCGAGTGAATCT 600
 QY 601 GAGAGATCTTACTCAAGCGCGCAAAATACCCACAGTTCTCCAGCTTTGGGAGAGAG 660
 Db 601 GAGAGATCTTACTCAAGCGCGCAAAATACCCACAGTTCTCCAGCTTTGGGAGAGAG 660
 QY 661 TCTGTTCACTGGGGGAGTGTGTTGAATTACAAGTGTGCTTCTGTTGTCAAGCTG 720
 Db 661 TCTGTTCACTGGGGGAGTGTGTTGAATTACAAGTGTGCTTCTGTTGTCAAGCTG 720
 QY 721 ACTGAAGCAAGCAAGTATCCACAGAGTTGCTTCTGATCTTTGGCTTACTCAATC 780
 Db 721 ACTGAAGCAAGCAAGTATCCACAGAGTTGCTTCTGATCTTTGGCTTACTCAATC 780
 QY 781 TGA 783
 Db 781 TGA 783

RESULT 11

US-09-399-106-1
 ; Sequence 1, Application US/09399106
 ; Patent No. 6410711

GENERAL INFORMATION:

APPLICANT: ARMITAGE, RICHARD
 APPLICANT: PANSLOW, WILLIAM
 APPLICANT: SPRIGGS, MELANIE
 APPLICANT: SRINIVASAN, SUBHASHINI
 APPLICANT: GIBSON, MARYLOU
 APPLICANT: MORRIS, ARVIA E.
 APPLICANT: MCGREW, JEFFERY
 TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: IMMUNEX CORPORATION
 STREET: 51 UNIVERSITY STREET
 CITY: SEATTLE
 STATE: WASHINGTON
 COUNTRY: USA
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: Apple Operating System 7.5.5
 SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/399,106
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/477,733
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/969,703
 FILING DATE: October 23, 1992
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/805,723
 FILING DATE: December 5, 1991
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/783,707
 FILING DATE: October 25, 1991
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Perkins, Patricia A.
 REGISTRATION NUMBER: 34,693
 REFERENCE/DOCKET NUMBER: 2802-D
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 2065870430

TELEFAX: 2065870606
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 783 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHEICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: MOUSE
 IMMEDIATE SOURCE:
 CLONE: CD40-L
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..783
 US-09-399-106-1

Query Match

Best Local Similarity 95.7%; Score 749.4; DB 4; Length 783;
 Best Local Similarity 97.3%; Pred. No. 6,5e-212;
 Matches 762; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 ATGATGAAACATTAACCAACAACTTCTCCGATCTGCGCCACTGAGTCCCATCAGC 60
 Db 1 ATGATGAAACATTAACCAACAACTTCTCCGATCTGCGCCACTGAGTCCCATCAGC 60
 QY 61 ATGAAATTTTATGATTTTACTTCTGTTTCTTATCCACCAAGATGTTGGTCAGCA 120
 Db 61 ATGAAATTTTATGATTTTACTTCTGTTTCTTATCCACCAAGATGTTGGTCAGCA 120
 QY 121 CTTTGTGCTGTGATCTTCTCAATAGATTTGATTAAGTGCAGAGAACTAACTTCAT 180
 Db 121 CTTTGTGCTGTGATCTTCTCAATAGATTTGATTAAGTGCAGAGAACTAACTTCAT 180
 QY 121 CTTTGTGCTGTGATCTTCTCAATAGATTTGATTAAGTGCAGAGAACTAACTTCAT 180
 Db 121 CTTTGTGCTGTGATCTTCTCAATAGATTTGATTAAGTGCAGAGAACTAACTTCAT 180
 QY 181 GAAGATTTTGTATCATTAATAAAGCTAAAGATGCAACAAAGAAAGATCTTTATCC 240
 Db 181 GAAGATTTTGTATCATTAATAAAGCTAAAGATGCAACAAAGAAAGATCTTTATCC 240
 QY 241 TTGCTAACCTGTGAGAGATGAGAGAGCAATTTGAACCTTGTCAAGATATAGCTTA 300
 Db 241 TTGCTAACCTGTGAGAGATGAGAGAGCAATTTGAACCTTGTCAAGATATAGCTTA 300
 QY 241 TTGCTAACCTGTGAGAGATGAGAGAGCAATTTGAACCTTGTCAAGATATAGCTTA 300
 Db 241 TTGCTAACCTGTGAGAGATGAGAGAGCAATTTGAACCTTGTCAAGATATAGCTTA 300
 QY 301 AACAAAG 360
 Db 301 AACAAAG 360
 QY 361 ATTGCAGCACAGCTTTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
 Db 361 ATTGCAGCACAGCTTTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
 QY 361 ATTGCAGCACAGCTTTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
 Db 361 ATTGCAGCACAGCTTTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
 QY 421 AAGAAAGATATTATACCATGAAAGCACTTGTGTAATGCTTGAATAAGGAAACAGCTG 480
 Db 421 AAGAAAGATATTATACCATGAAAGCACTTGTGTAATGCTTGAATAAGGAAACAGCTG 480
 QY 481 ACGTTTAAAG 540
 Db 481 ACGTTTAAAG 540
 QY 481 ACGTTTAAAG 540
 Db 481 ACGTTTAAAG 540
 QY 541 GAGCTTCGAGTCAACGCCCATTCATCTCGGCTTCGGGCAAGCCGAGTGAATCT 600
 Db 541 GAGCTTCGAGTCAACGCCCATTCATCTCGGCTTCGGGCAAGCCGAGTGAATCT 600
 QY 601 GAGAGATCTTACTCAAGCGCGCAAAATACCCACAGTTCTCCAGCTTTGGGAGAGAG 660
 Db 601 GAGAGATCTTACTCAAGCGCGCAAAATACCCACAGTTCTCCAGCTTTGGGAGAGAG 660
 QY 661 TCTGTTCACTGGGGGAGTGTGTTGAATTACAAGTGTGCTTCTGTTGTCAAGCTG 720
 Db 661 TCTGTTCACTGGGGGAGTGTGTTGAATTACAAGTGTGCTTCTGTTGTCAAGCTG 720
 QY 721 ACTGAAGCAAGCAAGTATCCACAGAGTTGCTTCTGATCTTTGGCTTACTCAATC 780
 Db 721 ACTGAAGCAAGCAAGTATCCACAGAGTTGCTTCTGATCTTTGGCTTACTCAATC 780

MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
CLONE: Murine CD40-L trimer
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 15..92
FEATURE:
NAME/KEY: CDS
LOCATION: 15..857
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 93..857
US-08-484-624A-22

Query Match 80.6%; Score 631.4; DB 2; Length 878;
Best Local Similarity 99.8%; Pred. No. 5e-177;
Matches 632; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 151 GATTAAGTGAAGAGAGTAACCTTCAAGTAAGATTTGTATCAATAAAGCTTAAG 210
Db 225 GATTAAGTGAAGAGAGTAACCTTCAAGTAAGATTTGTATCAATAAAGCTTAAG 284
Qy 211 AGATGCAACAAAGAGAGATCTTATCTTGTGAAGTGAAGATGAAGCA 270
Db 285 AGATGCAACAAAGAGAGATCTTATCTTGTGAAGTGAAGATGAAGCA 344
Qy 271 TTTGAAGCTTGTCAAGATTAACGTAAACAAAGAGAGAGAGAGAGAGAGAG 330
Db 345 TTTGAAGCTTGTCAAGATTAACGTAAACAAAGAGAGAGAGAGAGAGAGAG 404
Qy 331 GAAATGCAAGAGAGTGAAGATCTCAAAATTCAGCAACGTTGTAAGCAAGCAAC 390
Db 405 GAAATGCAAGAGAGTGAAGATCTCAAAATTCAGCAACGTTGTAAGCAAGCAAC 464
Qy 391 AGTAATGCAAGATCTTCAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 450
Db 465 AGTAATGCAAGATCTTCAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 524
Qy 451 TTGTAATGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 510
Db 525 TTGTAATGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 584
Qy 511 TACACTCAAGTCAAGTCTTCAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 570
Db 585 TACACTCAAGTCAAGTCTTCAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 644
Qy 571 GGCCTCTGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 630
Db 645 GGCCTCTGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 704
Qy 631 CACAGTCTCTCCAGCTTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 690
Db 705 CACAGTCTCTCCAGCTTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 764
Qy 691 CAACTGAGTCTTCTGTGTTTCAAGTGAAGAGAGAGAGAGAGAGAGAGAGAG 750
Db 765 CAACTGAGTCTTCTGTGTTTCAAGTGAAGAGAGAGAGAGAGAGAGAGAGAG 824
Qy 751 GGCCTCTCATTTTGGCTTAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 783
Db 825 GGCCTCTCATTTTGGCTTAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 857

RESULT 15
US-08-477-733B-22
Sequence 22, Application US/0847733B
Patent No. 5981724
GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: FANSLAW, WILLIAM
APPLICANT: SPRINGS, MELANIE
APPLICANT: SRINIVASAN, SUBHASHINI
APPLICANT: GIBSON, MARYLOU

APPLICANT: MORRIS, ARVIA E.
APPLICANT: MCGREW, JEFFERY
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESS: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,733B
FILING DATE: June 07, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,189
FILING DATE: May 24, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,703
FILING DATE: October 23, 1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/805,723
FILING DATE: December 5, 1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/783,707
FILING DATE: October 25, 1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 878 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
CLONE: Murine CD40-L trimer
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 15..92
FEATURE:
NAME/KEY: CDS
LOCATION: 15..857
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 93..857
US-08-477-733B-22

Query Match 80.6%; Score 631.4; DB 2; Length 878;
Best Local Similarity 99.8%; Pred. No. 5e-177;
Matches 632; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 151 GATTAAGTGAAGAGAGTAACCTTCAAGTAAGATTTGTATCAATAAAGCTTAAG 210
Db 225 GATTAAGTGAAGAGAGTAACCTTCAAGTAAGATTTGTATCAATAAAGCTTAAG 284
Qy 211 AGATGCAACAAAGAGAGATCTTATCTTGTGAAGTGAAGATGAAGCA 270

Db 285 AGATGCAACAAAGGAAAGATCTTTATCTCTGCTGAACCTGTGAGAGATGAAAGGCA 344
Qy 271 TTGAAAGACCTTGTCAAGATATTAACGTTAAACAAAGAGAGAAAAAGAAAAACGCTTT 330
Db 345 TTGAAAGACCTTGTCAAGATATTAACGTTAAACAAAGAGAGAAAAAGAAAAACGCTTT 404
Qy 331 GAATGCAAGAGATGATGAGATCTCAAAATTGACAGACACGTTGTAAGGAAAGCCAAAC 390
Db 405 GAAATGCAAGAGATGATGAGATCTCAAAATTGACAGACACGTTGTAAGGAAAGCCAAAC 464
Qy 391 AGTAATGCAAGATCCGTTCTACAGTGGGCGCAAGAAAGATATTAAACATGAAGCAAC 450
Db 465 AGTAATGCAAGATCCGTTCTACAGTGGGCGCAAGAAAGATATTAAACATGAAGCAAC 524
Qy 451 TTGTTAATGCTTGAAATGGGAAACAGCTGACGTTAAAGAAAGAAAGAAAGAAAGAAAG 510
Db 525 TTGTTAATGCTTGAAATGGGAAACAGCTGACGTTAAAGAAAGAAAGAAAGAAAGAAAG 584
Qy 511 TACACTCAAGTCACTTCTGCTCTTAATCGGAGACCTTCAGTCAACGCCAATTCAATGCTC 570
Db 585 TACACTCAAGTCACTTCTGCTCTTAATCGGAGACCTTCAGTCAACGCCAATTCAATGCTC 644
Qy 571 GGCCCTGAGCTGAAGCCAGCATTTGATCTGAGAGATCTTACTCAAGGGGCAATATAC 630
Db 645 GGCCCTGAGCTGAAGCCAGCATTTGATCTGAGAGATCTTACTCAAGGGGCAATATAC 704
Qy 631 CACAGTTCTCCAGCTTTGGAGAGACAGTCTGTTCACTTGGGCGAGTGTGATTA 690
Db 705 CACAGTTCTCCAGCTTTGGAGAGACAGTCTGTTCACTTGGGCGAGTGTGATTA 764
Qy 691 CAAGCTGAGCTTCTGTTGTTGTCACAGTCAAGCAAGCAAGCAAGCAAGCAAGCAAGT 750
Db 765 CAAGCTGAGCTTCTGTTGTTGTCACAGTCAAGCAAGCAAGCAAGCAAGCAAGT 824
Qy 751 GGCTTCTCATCTTTGGCTTACTCAACTCTGA 783
Db 825 GGCTTCTCATCTTTGGCTTACTCAACTCTGA 857

Search completed: March 9, 2003, 04:46:09
Job time : 36.5164 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: March 8, 2003, 18:35:23 ; Search time 2048.61 Seconds

(without alignments)
11166.008 Million cell updates/sec

Title: US-08-982-272-4

Perfect score: 786
Sequence: 1 ATGATCGAATCACTACACCA.....TTGGCTTACTCAACTCTGA 786Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

GenBank! :
1: gb_da : *
2: gb_hcg : *
3: gb_in : *
4: gb_om : *
5: gb_ov : *
6: gb_pat : *
7: gb_ph : *
8: gb_pl : *
9: gb_pr : *
10: gb_ro : *
11: gb_sts : *
12: gb_sy : *
13: gb_un : *
14: gb_vt : *
15: em_da : *
16: em_fun : *
17: em_hum : *
18: em_in : *
19: em_mu : *
20: em_om : *
21: em_ov : *
22: em_or : *
23: em_pat : *
24: em_ph : *
25: em_pl : *
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27: em_sts : *
28: em_un : *
29: em_vt : *
30: em_hcg_hum : *
31: em_hcg_inv : *
32: em_hcg_other : *
33: em_hcg_mus : *
34: em_hcg_pin : *
35: em_hcg_rod : *
36: em_hcg_mam : *
37: em_hcg_vrt : *
38: em_sy : *
39: em_hugo_hum : *
40: em_hugo_mus : *
41: em_hugo_other : *

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	776.4	98.8	786	6	187864		187864 Sequence 3
2	776.4	98.8	840	6	AR044779		AR044779 Sequence
3	776.4	98.8	840	6	AR076926		AR076926 Sequence
4	776.4	98.8	840	6	AR078316		AR078316 Sequence
5	776.4	98.8	840	6	AR085419		AR085419 Sequence
6	776.4	98.8	840	6	AR103375		AR103375 Sequence
7	776.4	98.8	840	6	AR106246		AR106246 Sequence
8	776.4	98.8	840	6	AR169232		AR169232 Sequence
9	776.4	98.8	840	6	AR171647		AR171647 Sequence
10	776.4	98.8	840	6	123893		123893 Sequence 1
11	776.4	98.8	840	6	127345		127345 Sequence 1
12	776.4	98.8	840	6	167828		167828 Sequence 1
13	776.4	98.8	879	6	AX090039		AX090039 Sequence
14	776.4	98.8	879	6	HSCGP3MR		215017 H. sapiens m
15	776.4	98.8	1803	9	HSCD40		X67878 H. sapiens m
16	776.4	98.8	1816	9	HUMCD40L		L07414 Human CD40-
17	774.8	98.6	1822	9	HSTRAPA		X69550 H. sapiens T
18	761.2	96.8	839	9	HACD40L		X96710 H. sapiens m
19	760.4	96.7	1058	9	AF344841		AF344841 Cercocodu
20	760.4	96.7	1058	9	AF344859		AF344859 Macaca mu
21	739.6	94.1	974	9	AF344860		AF344860 Aotus tti
22	739.6	94.1	975	9	AF344844		AF344844 Callithri
23	638.8	81.3	864	4	BTCD40LIG		Z48469 B. taurus nr
24	638.2	81.2	1425	6	AR076929		AR076929 Sequence
25	638.2	81.2	1425	6	AR078319		AR078319 Sequence
26	638.2	81.2	1425	6	AR085432		AR085432 Sequence
27	638.2	81.2	1425	6	AR103378		AR103378 Sequence
28	638.2	81.2	1425	6	AR169235		AR169235 Sequence
29	637.2	81.1	929	6	AR076932		AR076932 Sequence
30	637.2	81.1	929	6	AR078322		AR078322 Sequence
31	637.2	81.1	929	6	AR085425		AR085425 Sequence
32	637.2	81.1	929	6	AR103381		AR103381 Sequence
33	637.2	81.1	929	6	AR169238		AR169238 Sequence
34	637.2	81.1	929	6	187867		187867 Sequence 10
35	636	80.9	1566	6	AX455878		AX455878 Sequence
36	622.8	79.2	904	9	AF344853		AF344853 Macaca ne
37	608.4	77.4	788	4	AF079105		AF079105 Felis cat
38	606.8	77.2	786	4	AB040443		AB040443 Sus scrofa
39	589.2	75.0	788	4	AF086711		AF086711 Canis fam
40	573.2	72.9	783	10	AF013985		AF013985 Rattus no
41	571.6	72.7	783	6	AR076918		AR076918 Sequence
42	571.6	72.7	783	6	AR078308		AR078308 Sequence
43	571.6	72.7	783	6	AR085411		AR085411 Sequence
44	571.6	72.7	783	6	AR103367		AR103367 Sequence
45	571.6	72.7	783	6	AR169224		AR169224 Sequence

ALIGNMENTS

RESULT 1
187864
LOCUS 187864
DEFINITION Sequence 3 from patent US 5716805.
ACCESSION 187864
VERSION 187864.1 GI:3407804
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 786)
AUTHORS Strinivasan,S. and Spriggs,M.K.
TITLE Methods of preparing soluble, oligomeric proteins
JOURNAL Patent: US 5716805-A 3 10-FEB-1998;
FEATURES Location/Qualifiers

RESULT 3
 AR076926
 LOCUS AR076926 840 bp DNA linear PAT 31-AUG-2000
 DEFINITION Sequence 11 from patent US 5961974.
 ACCESSION AR076926
 VERSION AR076926.1 GI:10003672
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 840)
 AUTHORS Armitage, R.J., Fanslow, W.C. and Spriggs, M.K.
 TITLE Monoclonal antibodies to CD40 ligand, pharmaceutical composition comprising the same and hybridomas producing the same
 JOURNAL Patent: US 5961974-A 11 05-OCT-1999;
 FEATURES
 source 1..840
 location/Qualifiers
 BASE COUNT 266 a 185 c 175 g 214 t
 ORIGIN

Query Match 98.8%; Score 776.4; DB 6; Length 840;
 Best Local Similarity 99.2%; Pred. No. 7.3e-194;
 Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ATGATGAAACATACACCAACTTCTCCCGATCTGCGGCACTGACCTGCCATCAGC 60
 Db 46 ATGATGAAACATACACCAACTTCTCCCGATCTGCGGCACTGACCTGCCATCAGC 105
 Qy 61 ATGAAATTTTATGATTTACTCTGTTTCTTATCCCAATGATTGATCTGTG 120
 Db 106 ATGAAATTTTATGATTTACTCTGTTTCTTATCCCAATGATTGATCTGTG 165
 Qy 121 CTTTTCGTGTATCTTCTAGAGTTGACAGATGAGATGAGATGAGATCTTCA 180
 Db 166 CTTTTCGTGTATCTTCTAGAGTTGACAGATGAGATGAGATGAGATCTTCA 225
 Qy 181 GAAATTTTATGATTTACTCTGTTTCTTATCCCAATGATTGATCTGTG 240
 Db 226 GAAATTTTATGATTTACTCTGTTTCTTATCCCAATGATTGATCTGTG 285
 Qy 241 TTACTGAACGTGAGAGATTAAAGCGATTGAGCTTTGTAAGATATATGTTA 300
 Db 286 TTACTGAACGTGAGAGATTAAAGCGATTGAGCTTTGTAAGATATATGTTA 345
 Qy 301 AACAAAG 360
 Db 346 AACAAAG 405
 Qy 361 CAAATTTGCGGCACTGATCATAGTGGCGCAGCATGTAACAACTCTGTTCAGTGG 420
 Db 406 CAAATTTGCGGCACTGATCATAGTGGCGCAGCATGTAACAACTCTGTTCAGTGG 465
 Qy 421 GCTGAAAAGAGATCTACACCATGAGCAAACTTGTGTAACCTTGAAAATGAGAAACG 480
 Db 466 GCTGAAAAGAGATCTACACCATGAGCAAACTTGTGTAACCTTGAAAATGAGAAACG 525
 Qy 481 CTGACCGTTTAAAG 540
 Db 526 CTGACCGTTTAAAG 585
 Qy 541 CGGAAAGCTTGAAGTCAAGCTCATTTATTAAGCCAGCTCTGCTTAAAGTCCCGGTAGA 600
 Db 586 CGGAAAGCTTGAAGTCAAGCTCATTTATTAAGCCAGCTCTGCTTAAAGTCCCGGTAGA 645
 Qy 601 TTGAGAGAGATCTTACTCAGAGCTGCAATACCAAGTTCCGCAAACTTGGGGCAA 660
 Db 646 TTGAGAGAGATCTTACTCAGAGCTGCAATACCAAGTTCCGCAAACTTGGGGCAA 705
 Qy 661 CAATCATTTCACTTGGAGAGATTTGAATTGCAACAGTGTCTGTGTTTGTCAAT 720

Db 706 CAATCATTTCACTTGGAGAGATTTGAATTGCAACAGTGTCTGTGTTTGTCAAT 765
 Qy 721 GTGACTGATCCAAAGCAAGTGAAGCAAGTGAAGTGAAGTGAAGTGAAGTGAAG 780
 Db 766 GTGACTGATCCAAAGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 825
 Qy 781 CTCTGA 786
 Db 826 CTCTGA 831

RESULT 4
 AR078316
 LOCUS AR078316 840 bp DNA linear PAT 31-AUG-2000
 DEFINITION Sequence 11 from patent US 5962406.
 ACCESSION AR078316
 VERSION AR078316.1 GI:10005062
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 840)
 AUTHORS Armitage, R.J., Fanslow, W.C., Spriggs, M.K., Srinivasan, S.,
 Gibson, M.G., Morris, A.E. and McGrew, J.T.
 TITLE Recombinant soluble CD40 ligand and polypeptide and pharmaceutical composition containing the same
 JOURNAL Patent: US 5962406-A 11 05-OCT-1999;
 FEATURES
 source 1..840
 location/Qualifiers
 BASE COUNT 266 a 185 c 175 g 214 t
 ORIGIN

Query Match 98.8%; Score 776.4; DB 6; Length 840;
 Best Local Similarity 99.2%; Pred. No. 7.3e-194;
 Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ATGATGAAACATACACCAACTTCTCCCGATCTGCGGCACTGACCTGCCATCAGC 60
 Db 46 ATGATGAAACATACACCAACTTCTCCCGATCTGCGGCACTGACCTGCCATCAGC 105
 Qy 61 ATGAAATTTTATGATTTACTCTGTTTCTTATCCCAATGATTGATCTGTG 120
 Db 106 ATGAAATTTTATGATTTACTCTGTTTCTTATCCCAATGATTGATCTGTG 165
 Qy 121 CTTTTCGTGTATCTTCTAGAGTTGACAGATGAGATGAGATGAGATCTTCA 180
 Db 166 CTTTTCGTGTATCTTCTAGAGTTGACAGATGAGATGAGATGAGATCTTCA 225
 Qy 181 GAAATTTTATGATTTACTCTGTTTCTTATCCCAATGATTGATCTGTG 240
 Db 226 GAAATTTTATGATTTACTCTGTTTCTTATCCCAATGATTGATCTGTG 285
 Qy 241 TTACTGAACGTGAGAGATTAAAGCGATTGAGCTTTGTAAGATATATGTTA 300
 Db 286 TTACTGAACGTGAGAGATTAAAGCGATTGAGCTTTGTAAGATATATGTTA 345
 Qy 301 AACAAAG 360
 Db 346 AACAAAG 405
 Qy 361 CAAATTTGCGGCACTGATCATAGTGGCGCAGCATGTAACAACTCTGTTCAGTGG 420
 Db 406 CAAATTTGCGGCACTGATCATAGTGGCGCAGCATGTAACAACTCTGTTCAGTGG 465
 Qy 421 GCTGAAAAGAGATCTACACCATGAGCAAACTTGTGTAACCTTGAAAATGAGAAACG 480
 Db 466 GCTGAAAAGAGATCTACACCATGAGCAAACTTGTGTAACCTTGAAAATGAGAAACG 525
 Qy 481 CTGACCGTTTAAAG 540
 Db 526 CTGACCGTTTAAAG 585

QY 541 CGGAGAGCTTCGAGCAAGCTCCATTATATGCGAGCTCTGCTAAAGTCCCGGTTGA 600
 DB 586 CGGAGAGCTTCGAGCAAGCTCCATTATATGCGAGCTCTGCTAAAGTCCCGGTTGA 645
 QY 601 TTGAGAGAACTTCTACGAGCTGCAAAATACCAAGTTCGCGCAAACTTGGCGGCA 660
 DB 646 TTGAGAGAACTTCTACGAGCTGCAAAATACCAAGTTCGCGCAAACTTGGCGGCA 705
 QY 661 CAATCCATTCATCTGGAGAGATTTTGAATGCAACAGGCTGCGGTGTGTCAAT 720
 DB 706 CAATCCATTCATCTGGAGAGATTTTGAATGCAACAGGCTGCGGTGTGTCAAT 765
 QY 721 GTGACTGATCCAAAGCCAAAGTGAAGCCATGAGCACTGCTTACGCTTTGGCTTACTCAA 780
 DB 766 GTGACTGATCCAAAGCCAAAGTGAAGCCATGAGCACTGCTTACGCTTTGGCTTACTCAA 825
 QY 781 CTCTGA 786
 DB 826 CTCTGA 831

RESULT 5
 AR085419 840 bp DNA linear PAT 01-SEP-2000
 LOCUS AR085419 Sequence 11 from patent US 5981724.
 DEFINITION
 ACCESSION AR085419
 VERSION AR085419.1 GI:10012188
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 840)
 AUTHORS Armitage,R.J., Fanslow,W.C., Spriggs,M.K., Srinivasan,S.,
 Gibson,M.G., Morris,A.E. and McGrew,J.T.
 TITLE DNA encoding CD40 ligand, a cytokine that binds CD40
 JOURNAL Patent: US 5981724-A 11 09-NOV-1999;
 FEATURES
 source 1..840
 /organism="unknown"

BASE COUNT 266 a 185 c 175 g 214 t
 ORIGIN
 Query Match 98.8%; Score 776.4; DB 6; Length 840;
 Best Local Similarity 99.2%; Pred. No. 7.3e-194;
 Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACCAACCAACTTCTCCCGATCTGGCGGCACTGACCTGCCATCAGC 60
 DB 46 ATGATCGAAACATACCAACCAACTTCTCCCGATCTGGCGGCACTGACCTGCCATCAGC 105
 QY 61 ATGAAATTTTATATGATTTACTTACTGTTTCTTATACCAACCAAGATTTGATCTGTG 120
 DB 106 ATGAAATTTTATATGATTTACTTACTGTTTCTTATACCAACCAAGATTTGATCTGTG 165
 QY 121 CTTTTCCTGTGATCTTATATGAAAGTTGACACAGATGAAAGATTTCTTAT 180
 DB 166 CTTTTCCTGTGATCTTATATGAAAGTTGACACAGATGAAAGATTTCTTAT 225
 QY 181 GAAGATTTGTATTCATGAAACGATACAGATGCAACACAGAGAAAGATCTTATCC 240
 DB 226 GAAGATTTGTATTCATGAAACGATACAGATGCAACACAGAGAAAGATCTTATCC 285
 QY 241 TTACTGAACTGTGAGAGATTTAAAGCCAGTTTGAAGCTTTGTGAAGATTAATGTTA 300
 DB 286 TTACTGAACTGTGAGAGATTTAAAGCCAGTTTGAAGCTTTGTGAAGATTAATGTTA 345
 QY 301 AACAAAGAGAGAGAGAAAGAAAGAAAGCTTTGAATGCAAAAGGTGATCAGATCT 360
 DB 346 AACAAAGAGAGAGAGAAAGAAAGAAAGCTTTGAATGCAAAAGGTGATCAGATCT 405
 QY 361 CAATTTGGCGCACTGTCTAATAGTGGCCAGCAGTAAACAACTCTGTCTTACAGTGG 420
 DB 406 CAATTTGGCGCACTGTCTAATAGTGGCCAGCAGTAAACAACTCTGTCTTACAGTGG 465

QY 421 GCTGAAAGAGATCTACACCATAGAGCAACACTTGTAAACCTGGAAATGAGAAACAG 480
 DB 466 GCTGAAAGAGATCTACACCATAGAGCAACACTTGTAAACCTGGAAATGAGAAACAG 525
 QY 481 CTGACGTTTAAAGCAAGACTCTTATATATCTATGCTCCAGTCACTTCTGTCCAT 540
 DB 526 CTGACGTTTAAAGCAAGACTCTTATATATCTATGCTCCAGTCACTTCTGTCCAT 585
 QY 541 CGGAGAGCTTCGAGCAAGCTCCATTATATGCGAGCTCTGCTAAAGTCCCGGTTGA 600
 DB 586 CGGAGAGCTTCGAGCAAGCTCCATTATATGCGAGCTCTGCTAAAGTCCCGGTTGA 645
 QY 601 TTGAGAGAACTTCTACGAGCTGCAAAATACCAAGTTCGCGCAAACTTGGCGGCA 660
 DB 646 TTGAGAGAACTTCTACGAGCTGCAAAATACCAAGTTCGCGCAAACTTGGCGGCA 705
 QY 661 CAATCCATTCATCTGGAGAGATTTTGAATGCAACAGGCTGCGGTGTGTCAAT 720
 DB 706 CAATCCATTCATCTGGAGAGATTTTGAATGCAACAGGCTGCGGTGTGTCAAT 765
 QY 721 GTGACTGATCCAAAGCCAAAGTGAAGCCATGAGCACTGCTTACGCTTTGGCTTACTCAA 780
 DB 766 GTGACTGATCCAAAGCCAAAGTGAAGCCATGAGCACTGCTTACGCTTTGGCTTACTCAA 825
 QY 781 CTCTGA 786
 DB 826 CTCTGA 831

RESULT 6
 AR103375 840 bp DNA linear PAT 14-FEB-2001
 LOCUS AR103375 Sequence 11 from patent US 6087329.
 DEFINITION
 ACCESSION AR103375
 VERSION AR103375.1 GI:12814963
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 840)
 AUTHORS Armitage,R.J., Fanslow,W.C. and Spriggs,M.K.
 TITLE CD40 ligand polypeptide
 JOURNAL Patent: US 6087329-A 11 11-JUN-2000;
 FEATURES
 source 1..840
 /organism="unknown"

BASE COUNT 266 a 185 c 175 g 214 t
 ORIGIN
 Query Match 98.8%; Score 776.4; DB 6; Length 840;
 Best Local Similarity 99.2%; Pred. No. 7.3e-194;
 Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACCAACCAACTTCTCCCGATCTGGCGGCACTGACCTGCCATCAGC 60
 DB 46 ATGATCGAAACATACCAACCAACTTCTCCCGATCTGGCGGCACTGACCTGCCATCAGC 105
 QY 61 ATGAAATTTTATATGATTTACTTACTGTTTCTTATACCAACCAAGATTTGATCTGTG 120
 DB 106 ATGAAATTTTATATGATTTACTTACTGTTTCTTATACCAACCAAGATTTGATCTGTG 165
 QY 121 CTTTTCCTGTGATCTTATATGAAAGTTGACACAGATGAAAGATTTCTTAT 180
 DB 166 CTTTTCCTGTGATCTTATATGAAAGTTGACACAGATGAAAGATTTCTTAT 225
 QY 181 GAAGATTTGTATTCATGAAACGATACAGATGCAACACAGAGAAAGATCTTATCC 240
 DB 226 GAAGATTTGTATTCATGAAACGATACAGATGCAACACAGAGAAAGATCTTATCC 285
 QY 241 TTACTGAACTGTGAGAGATTTAAAGCCAGTTTGAAGCTTTGTGAAGATTAATGTTA 300
 DB 286 TTACTGAACTGTGAGAGATTTAAAGCCAGTTTGAAGCTTTGTGAAGATTAATGTTA 345

OY	301	AA	CAAAAGAGGAGAGCAAGAGAAAAGAAAACAGCTTTGAAATGCAAAAAGGTATCAGAAATCCT	360
Db	346	AA	CAAAAGAGGAGAGCAAGAGAAAAGAAAACAGCTTTGAAATGCAAAAAGGTATCAGAAATCCT	405
OY	361	CAAA	TTGGGGGCACTGTCATTAAGTGAAGCCAGCAAGTAAAAACAATCTGTTTAAAGATGG	420
Db	406	CAAA	TTGGGGGCACTGTCATTAAGTGAAGCCAGCAAGTAAAAACAATCTGTTTAAAGATGG	465
OY	421	GCT	GAAGAAAGATATCTACACATATGACAAACAACCTTGTAACCTCGAAAATAGGAAACAG	480
Db	466	GCT	GAAGAAAGATATCTACACATATGACAAACAACCTTGTAACCTCGAAAATAGGAAACAG	525
OY	481	CTGA	CCGTTAAAAACAACGAGACTATATATCTATGCCCAGAGTCACTTCGTGTTCCAAAT	540
Db	526	CTGA	CCGTTAAAAACAACGAGACTATATATCTATGCCCAGAGTCACTTCGTGTTCCAAAT	585
OY	541	CGG	GAAGCTTGGAATCAAGCTCACTTTATATAGCAAGCTTCGCTTAAAGTCCCCGGGTAGA	600
Db	586	CGG	GAAGCTTGGAATCAAGCTCACTTTATATAGCAAGCTTCGCTTAAAGTCCCCGGGTAGA	645
OY	601	TTG	GAGAGAAATCTTATCTCAAGACTGCAAAATCCACAAGTTCGCGCAAACTTTGCGGGCAA	660
Db	646	TTG	GAGAGAAATCTTATCTCAAGACTGCAAAATCCACAAGTTCGCGCAAACTTTGCGGGCAA	705
OY	661	CAAT	CAATCACTTCTGGGAGGAGATATTTGAATTCGAACACAGGCTTCGGGTGTTGTCAAT	720
Db	706	CAAT	CAATCACTTCTGGGAGGAGATATTTGAATTCGAACACAGGCTTCGGGTGTTGTCAAT	765
OY	721	GGAG	CGATGATCCAAACCCAAAGTAGACCAAGGACATGGCTTACAGTCTTTGGCTTAACTCAA	780
Db	766	GGAG	CGATGATCCAAACCCAAAGTAGACCAAGGACATGGCTTACAGTCTTTGGCTTAACTCAA	825
OY	781	CTCT	GA 786	
Db	826	CTCT	GA 831	

LOCUS	ARI06246	840 bp	DNA	linear	PAT 14-FEB-2001
DEFINITION	Sequence 7 from patent US 6106832.				
ACCESSION	ARI06246				
VERSION	ARI06246.1	GI:12820776			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 Unpublished.				
AUTHORS	1 (bases 1 to 840)				
TITLE	Spijgers, M.K., Armitage, R.J., Fanslow, W.C. III and Widmer, M.B.				
JOURNAL	Treatment of individual's exhibiting defective CD40L				
FEATURES	Patent: US 6106832-A 7 22-AUG-2000, location/Qualifiers 1..840 /organism="unknown"				
BASE COUNT	266 a 185 c 175 g 214 t				
ORIGIN					
Query Match	98.8%; Score 776.4; DB 6; Length 840;				
Best Local Similarity	99.2%; Pred. No. 7.3e-194;				
Matches 780; Conservative	0; Mismatches 6; Indels 0; Gaps 0;				
Oy	1 ATGATCGAACAATACACCAAACTCTCCCGATCTCGGCGACATGACATGCCCATACG 60				
	46 ATGATCGAACAATACACCAAACTCTCCCGATCTCGGCGACATGACATGCCCATACG 105				
Oy	61 ATGAAATTTTATGATTTACTTACTGTTTCTTCTTACACCAATGATGATGATCTGTG 120				
	106 ATGAAATTTTATGATTTACTTACTGTTTCTTCTTACACCAATGATGATGATGATGCA 165				
Oy	121 CTTTTCGTGTGATCTTCATAGAGGTTTGACAAGATGAAAGATGAAGAAATCTTCAT 180				
	166 CTTTTCGTGTGATCTTCATAGAGGTTTGACAAGATGAAAGATGAAGAAATCTTCAT 225				

Qy	181	GAAGATTTTGTATTCATGAAAGATGACAGAGATGCAACAGGAGAAAGATCCTTATCC	240
Db	226	GAAGATTTGTATTCATGAAAGATGACAGAGATGCAACAGGAGAAATCCTTATCC	285
Qy	241	TTACTGAACCTGAGAGATTAAAGCCAGTTTCAAGCCTTTGTGAAGATATATGTTA	300
Db	286	TTACTGAACCTGAGAGATTAAAGCCAGTTTCAAGCCTTTGTGAAGATATATGTTA	345
Qy	301	AACAAAGAGAGACAAAGAAAGAAACAGCTTTGAATGCAAAAAGGTGATCGAATCCT	360
Db	346	AACAAAGAGAGACAAAGAAAGAAACAGCTTTGAATGCAAAAAGGTGATCGAATCCT	405
Qy	361	CAAAATTCGGCACATGTCATTAAGTGGCCACGCTTAAACAAATCTGTGTTACATGG	420
Db	406	CAAAATTCGGCACATGTCATTAAGTGGCCACGCTTAAACAAACATCTGTGTTACATGG	465
Qy	421	GCTGAAAAAGATACCTACACCAAGACAAACAATGGTAAACCTTGAAAAATGGAAAAAG	480
Db	466	GCTGAAAAAGATACCTACACCAAGACAAACAATGGTAAACCTTGAAAAATGGAAAAAG	525
Qy	481	CTGACCGTTTAAAGACAGAGACCTTATATCTGAAGGCCAAGTACCTTGTTCGAT	540
Db	526	CTGACCGTTTAAAGACAGAGACCTTATATCTGAAGGCCAAGTACCTTGTTCGAT	585
Qy	541	CGGAAAGCTTTCAGATCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCCCGGTAGA	600
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Qy	601	TTGAGAGAGATCTTACTCAGAGCTGAAGTAATCCACAGTTCGGGCAAACTTGGGGGAGA	660
Db	646	TTGAGAGAGATCTTACTCAGAGCTGAAGTAATCCACAGTTCGGGCAAACTTGGGGGAGA	705
Qy	661	CAATTCATTCACCTTGGAGAGATTTGAATTGCAACAGGTGCTTCGATGTTTGTCAAT	720
Db	706	CAATTCATTCACCTTGGAGAGATTTGAATTGCAACAGGTGCTTCGATGTTTGTCAAT	765
Qy	721	GTGACGTATCAAGCAAGTGAACCATGGACCTGGCTTACAGTCCCTTTGGCTTATCTCAA	780
Db	766	GTGACGTATCAAGCAAGTGAACCATGGACCTGGCTTACAGTCCCTTTGGCTTATCTCAA	825
Qy	781	CTCTGA 786	
Db	826	CTCTGA 831	

RESULT	9
LOCUS	ARI69232
DEFINITION	Sequence 11 from patent US 6290972.
ACCESSION	ARI69232
VERSION	ARI69232.1 GI:17907047
KEYWORDS	.
SOURCE ORGANISM	Unknown. Unknown.
REFERENCE AUTHORS	Unclassified. 1 (bases 1 to 840) Amitage,R.J., Fanslow,W.C., Spriggs,M.K., Srinivasan,S. and Gibson,M.G.
TITLE	Method of augmenting a vaccine response by administering CD40 ligand
JOURNAL FEATURES source	Patent: US 6290972-A 11-18-SEP-2001; Location/Qualifiers 1..840 /organism="unknown" 266 a 185 c 175 g 214 t
BASE COUNT ORIGIN	
Best Local Match	98.8%; Score 776.4; DB: 6;
Near Local Similarity	99.2%; Pred. NO. 7.3e-194;
Matches 780; Conservative	0; Mismatches 6; Indels 0; Gaps 0;
ATGATTGAACAATAACCAAACTTCCCGAGTCGGCAGCACGTGACTGCCCATGC	60

Db 46 ATGATCGAAACATACACCAAACTTCTCCCGATCTGGGGCATGAGATCGCCCATGAC 105
 QY 61 ATGAAAATTTTATGATTTACTTACTGTTTCTTTATCACCCTAATGATGATCTGTG 120
 Db 106 ATGAAAATTTTATGATTTACTTACTGTTTCTTTATCACCCTAATGATGATCTGTG 165
 QY 121 CTTTTCCTGCTGATCTTATAGAAAGTTGACAGATAGAAAGATGAAAGATCTTCAT 180
 Db 166 CTTTTCCTGCTGATCTTATAGAAAGTTGACAGATAGAAAGATGAAAGATCTTCAT 225
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 Db 286 TTACTGAATCTGAGAGATTTAAAGCCAGTTTGAAGCTTTGAGAGATTAATGTTA 345
 QY 301 AACAAAGAGAGACGAAAGAAAGAAACAGCTTTGAATGCAAAAAGGTGATCAGATCT 360
 Db 346 AACAAAGAGAGACGAAAGAAAGAAACAGCTTTGAATGCAAAAAGGTGATCAGATCT 405
 QY 361 CAAATGCGGCACATGTCATTAAGTGGCCAGCAGTAAACAGATCTGTGTTACAGTGG 420
 Db 406 CAAATGCGGCACATGTCATTAAGTGGCCAGCAGTAAACAGATCTGTGTTACAGTGG 465
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 QY 481 CTGACCGTTAAAGACAGAGACTTATATATCTATGCCCAAGTCACTTCTGTTCAT 540
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 Db 766 GTGACTGATCCAGCCAGAGTGAAGCCATGCACTGGCTTCACTCTTGGCTTACTCAA 825
 QY 781 CTCTGA 786
 Db 826 CTCTGA 831
 RESULT 9
 AR171647 840 bp DNA linear PAT 17-DEC-2001
 LOCUS AR171647
 DEFINITION Sequence 3 from patent US 6297052.
 ACCESSION AR171647
 VERSION AR171647.1 GI:17910597
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 840)
 AUTHORS Kehry, M. and Castle, B.
 TITLE B cell culture system comprising high density membrane bound CD40
 JOURNAL Patent: US 6297052-A 3 02-OCT-2001;
 FEATURES
 source I. 840

BASE COUNT 263 a 182 c 181 g 214 t
 ORIGIN
 Query Match 98.8%; Score 776.4; DB 6; Length 840;
 Best Local Similarity 99.2%; Pred. No. 7.3e-194;
 Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 ATGATGAAACATACACCAAACTTCTCCCGATCTGGGGCATGAGATCGCCCATGAC 60
 Db 22 ATGATGAAACATACACCAAACTTCTCCCGATCTGGGGCATGAGATCGCCCATGAC 81
 QY 61 ATGAAAATTTTATGATTTACTTACTGTTTCTTTATCACCCTAATGATGATCTGTG 120
 Db 82 ATGAAAATTTTATGATTTACTTACTGTTTCTTTATCACCCTAATGATGATCTGTG 141
 QY 121 CTTTTCCTGCTGATCTTATAGAAAGTTGACAGATAGAAAGATGAAAGATCTTCAT 180
 Db 142 CTTTTCCTGCTGATCTTATAGAAAGTTGACAGATAGAAAGATGAAAGATCTTCAT 201
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 Db 262 TTACTGAATCTGAGAGATTTAAAGCCAGTTTGAAGCTTTGAGAGATTAATGTTA 321
 QY 301 AACAAAGAGAGACGAAAGAAAGAAACAGCTTTGAATGCAAAAAGGTGATCAGATCT 360
 Db 322 AACAAAGAGAGACGAAAGAAAGAAACAGCTTTGAATGCAAAAAGGTGATCAGATCT 381
 QY 361 CAAATGCGGCACATGTCATTAAGTGGCCAGCAGTAAACAGATCTGTGTTACAGTGG 420
 Db 382 CAAATGCGGCACATGTCATTAAGTGGCCAGCAGTAAACAGATCTGTGTTACAGTGG 441
 QY 421 GCTGAAAAAGATATCAACCATGAGCAACATTTGTTAACCCTGAAAAATGGGAAACAG 480
 Db 442 GCTGAAAAAGATATCAACCATGAGCAACATTTGTTAACCCTGAAAAATGGGAAACAG 501
 QY 481 CTGACCGTTAAAGACAGAGACTTATATATCTATGCCCAAGTCACTTCTGTTCAT 540
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 Db 742 GTGACTGATCCAGCCAGAGTGAAGCCATGCACTGGCTTCACTCTTGGCTTACTCAA 801
 QY 781 CTCTGA 786
 Db 802 CTCTGA 807
 RESULT 10
 I23893 840 bp DNA linear PAT 07-OCT-1996
 LOCUS I23893
 DEFINITION Sequence 1 from patent US 5540926.
 ACCESSION I23893
 VERSION I23893.1 GI:1603763
 KEYWORDS
 SOURCE Unknown.

ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 840)
AUTHORS Anuflo, A., Hollenbaugh, D. and Ledbetter, J. A.
TITLE Soluble and its use in B cell stimulation
JOURNAL Patent: US 5540926-A 1 30-JUL-1996;
FEATURES
Source Location/Qualifiers
1. 840
BASE COUNT 263 a 182 c 181 g 214 t
ORIGIN

Query Match 98.8%; Score 776.4; DB 6; Length 840;
Best Local Similarity 99.2%; Pred. No. 7.3e-194;
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGATCGAAGATACACAACTTCTCCCGATCTGCGGCACTGACATGAGCCATCAGC 60
DB 22 ATGATCGAAGATACACAACTTCTCCCGATCTGCGGCACTGAGCTGCCATCAGC 81

QY 61 ATGAAAATTTTATGATTTTACTTACTCTTTTCTTTATCACCCTAAATGATTCATCTG 120
DB 82 ATGAAAATTTTATGATTTTACTTACTCTTTTCTTTATCACCCTAAATGATTCATCTG 141

QY 121 CTTTTCCTGTGATCTTCAATAGAGTTGAGCAAGATAGAGATGAAAGATCTTCAT 180
DB 142 CTTTTCCTGTGATCTTCAATAGAGTTGAGCAAGATAGAGATGAAAGATCTTCAT 201

QY 181 GAAGATTTTGTATTCATGAAAACGATACAGATGCAACACAGGAAAGATCTTCATCT 240
DB 202 GAAGATTTTGTATTCATGAAAACGATACAGATGCAACACAGGAAAGATCTTCATCT 261

QY 241 TTAAGAACTGTGAGAGATTTAAAGCCAGTTGAGGCTTTGTAAAGATATATGTTA 300
DB 262 TTAAGAACTGTGAGAGATTTAAAGCCAGTTGAGGCTTTGTAAAGATATATGTTA 321

QY 301 AACAAAG 360
DB 322 AACAAAG 381

QY 361 CAAATTTGGGCACTGTCAATAGAGAGGCGAGAGTAAACAACTGTGTTCAGTGG 420
DB 382 CAAATTTGGGCACTGTCAATAGAGAGGCGAGAGTAAACAACTGTGTTCAGTGG 441

QY 421 GGTGAAAAGAGATCTACACCATGAGCAACATGTGTAACTGTGAAAATGGGAAACAG 480
DB 442 GGTGAAAAGAGATCTACACCATGAGCAACATGTGTAACTGTGAAAATGGGAAACAG 501

QY 481 CTGACCGTTAAAG 540
DB 502 CTGACCGTTAAAG 561

QY 541 CGGGAAGCTTGAGTCAAGCTCATTTATAGCCAGGCTGTGCTTAAAGTCCCGGTTAA 600
DB 562 CGGGAAGCTTGAGTCAAGCTCATTTATAGCCAGGCTGTGCTTAAAGTCCCGGTTAA 621

QY 601 TTGAGAGAGATCTTACTCAGAGCTGCAAAATACCAAGTTCCGCAAACTTTCGGGCA 660
DB 622 TTGAGAGAGATCTTACTCAGAGCTGCAAAATACCAAGTTCCGCAAACTTTCGGGCA 681

QY 661 CAATCATTTCACTTGGAGAGATTTGAAATGCAACAGGCTGTGCTTAAAGTCCCGGTTAA 720
DB 682 CAATCATTTCACTTGGAGAGATTTGAAATGCAACAGGCTGTGCTTAAAGTCCCGGTTAA 741

QY 721 GTGACTGATCCAAAGCAAGTGAAGCCATGGCACTGGCTTCAAGCTTGTGGCTTAACTCAA 780
DB 742 GTGACTGATCCAAAGCAAGTGAAGCCATGGCACTGGCTTCAAGCTTGTGGCTTAACTCAA 801

QY 781 CTCTGA 786
DB 802 CTCTGA 807

RESULT 11
LOCUS 127345
DEFINITION Sequence 7 from patent US 5565321.
ACCESSION 127345
VERSION 127345.1 GI:1818121
KEYWORDS
SOURCE
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 840)
AUTHORS Spriggs, M. K., Armistage, R. J. and Farnlow, W. C. III.
TITLE Detection of mutations in a CD40 ligand gene
JOURNAL Patent: US 5565321-A 7 15-OCT-1996;
FEATURES
Source Location/Qualifiers
1. 840
BASE COUNT 266 a 185 c 175 g 214 t
ORIGIN

Query Match 98.8%; Score 776.4; DB 6; Length 840;
Best Local Similarity 99.2%; Pred. No. 7.3e-194;
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGATCGAAGATACACAACTTCTCCCGATCTGCGGCACTGAGCTGCCATCAGC 60
DB 46 ATGATCGAAGATACACAACTTCTCCCGATCTGCGGCACTGAGCTGCCATCAGC 105

QY 61 ATGAAAATTTTATGATTTTACTTACTCTTTTCTTTATCACCCTAAATGATTCATCTG 120
DB 106 ATGAAAATTTTATGATTTTACTTACTCTTTTCTTTATCACCCTAAATGATTCATCTG 165

QY 121 CTTTTCCTGTGATCTTCAATAGAGTTGAGCAAGATAGAGATGAAAGATCTTCAT 180
DB 166 CTTTTCCTGTGATCTTCAATAGAGTTGAGCAAGATAGAGATGAAAGATCTTCAT 225

QY 181 GAAGATTTTGTATTCATGAAAACGATACAGATGCAACACAGGAAAGATCTTCATCT 240
DB 226 GAAGATTTTGTATTCATGAAAACGATACAGATGCAACACAGGAAAGATCTTCATCT 285

QY 241 TTAAGAACTGTGAGAGATTTAAAGCCAGTTGAGGCTTTGTAAAGATATATGTTA 300
DB 286 TTAAGAACTGTGAGAGATTTAAAGCCAGTTGAGGCTTTGTAAAGATATATGTTA 345

QY 301 AACAAAG 360
DB 346 AACAAAG 405

QY 361 CAAATTTGGGCACTGTCAATAGAGAGGCGAGAGTAAACAACTGTGTTCAGTGG 420
DB 406 CAAATTTGGGCACTGTCAATAGAGAGGCGAGAGTAAACAACTGTGTTCAGTGG 465

QY 421 GGTGAAAAGAGATCTACACCATGAGCAACATGTGTAACTGTGAAAATGGGAAACAG 480
DB 466 GGTGAAAAGAGATCTACACCATGAGCAACATGTGTAACTGTGAAAATGGGAAACAG 525

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DB 526 CTGACCGTTAAAG 585

QY 541 CGGGAAGCTTGAGTCAAGCTCATTTATAGCCAGGCTGTGCTTAAAGTCCCGGTTAA 600
DB 586 CGGGAAGCTTGAGTCAAGCTCATTTATAGCCAGGCTGTGCTTAAAGTCCCGGTTAA 645

QY 601 TTGAGAGAGATCTTACTCAGAGCTGCAAAATACCAAGTTCCGCAAACTTTCGGGCA 660
DB 646 TTGAGAGAGATCTTACTCAGAGCTGCAAAATACCAAGTTCCGCAAACTTTCGGGCA 705

QY 661 CAATCATTTCACTTGGAGAGATTTGAAATGCAACAGGCTGTGCTTAAAGTCCCGGTTAA 720
DB 706 CAATCATTTCACTTGGAGAGATTTGAAATGCAACAGGCTGTGCTTAAAGTCCCGGTTAA 765

QY 721 GTGACTGATCCAAAGCAAGTGAAGCCATGGCACTGGCTTCAAGCTTGTGGCTTAACTCAA 780

Db 766 GTGACTGATCAAGCCAGAGTACGATGCGCTTCAGCTTCTTGGCTTACTCAAA 825
 Qy 781 CTCTGA 786
 Db 826 CTCTGA 831

RESULT 12

LOCUS 167828 167828 840 bp DNA linear PAT 04-FEB-1998
 DEFINITION Sequence 1 from patent US 5674492.
 ACCESSION 167828
 VERSION 167828.1 GI:2829950
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 840)

Amtlage, R.J., Fenslow, W.C. III, Longo, D.L. and Murphy, W.J.
 TITLE Method of preventing or treating disease characterized by
 neoplastic cells expressing CD40

JOURNAL Patent: US 5674492-A 1 07-OCT-1997;
 FEATURES Location/Qualifiers
 source 1..840

BASE COUNT 266 a 185 c 175 g 214 t
 ORIGIN

Query Match 98.8%; Score 776.4; DB 6; Length 840;
 Best Local Similarity 99.2%; Pred. No. 7.3e-194;
 Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ATGATCGAACAATACCAACCAACTTCTCCCGATCGGCGCCACGTGACCTGCCATCAGC 60
 Db 46 ATGATCGAACAATACCAACCAACTTCTCCCGATCGGCGCCACGTGACCTGCCATCAGC 105
 Qy 61 ATGAAAAATTTTATGTATTTACTTACTGTTTTCTTATCACCAATGATGATCTGTG 120
 Db 106 ATGAAAAATTTTATGTATTTACTTACTGTTTTCTTATCACCAATGATGATCTGTG 165
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 Db 166 CTTTGTGCTGATCTTCTATGAGAGTTGACAAATGAGATGAGATGAGATCTTCAAT 225
 Qy 181 GAAGATTTTGTATTCATGAAAAAGATACAGATGACACACAGAGAAAGATCTTATCC 240
 Db 226 GAAGATTTTGTATTCATGAAAAAGATACAGATGACACACAGAGAAAGATCTTATCC 285
 Qy 241 TTACTGAACGTGAGAGATTTAAAGCAGTTGAGAGCTTTGAGAGATTAATGTTA 300
 Db 286 TTACTGAACGTGAGAGATTTAAAGCAGTTGAGAGCTTTGAGAGATTAATGTTA 345
 Qy 301 AACAAAGAGAGACGAAAGAAAGAAAGCTTTGAAATGCAAAAGGTGATCAATCTT 360
 Db 346 AACAAAGAGAGACGAAAGAAAGAAAGCTTTGAAATGCAAAAGGTGATCAATCTT 405
 Qy 361 CAATTGGCGCACATGTCATTAAGTGGCCAGAGTAACCAATCTGTGTTACAGTGG 420
 Db 406 CAATTGGCGCACATGTCATTAAGTGGCCAGAGTAACCAATCTGTGTTACAGTGG 465
 Qy 421 GCTGAAAAAGATATCAACCATGAGCAACATCTTGTAACCTTGAAAAATGGAAAAAG 480
 Db 466 GCTGAAAAAGATATCAACCATGAGCAACATCTTGTAACCTTGAAAAATGGAAAAAG 525
 Qy 481 CTGACCGTTAAAGACAAAGACTTAATATCTATGACCAGTACCTTCTGTCAAT 540
 Db 526 CTGACCGTTAAAGACAAAGACTTAATATCTATGACCAGTACCTTCTGTCAAT 585
 Qy 541 CGGGAAGCTTGAGTCAAGTCCATTATTAAGCCAGCTTGGCTTAAGTCCCGGTAGA 600
 Db 586 CGGGAAGCTTGAGTCAAGTCCATTATTAAGCCAGCTTGGCTTAAGTCCCGGTAGA 645

Qy 601 TTGAGAGAACTTACTCAGAGCTGCAAAATCCACAGTTCGCGCAAACTTTGGGCGCAA 660
 Db 646 TTGAGAGAACTTACTCAGAGCTGCAAAATCCACAGTTCGCGCGCAAACTTTGGGCGCAA 705
 Qy 661 CAATTCATCTCTGGAGAGATTTGAATTTGCAACAGAGTCTTGGTGTTCAT 720
 Db 706 CAATTCATCTCTGGAGAGATTTGAATTTGCAACAGAGTCTTGGTGTTCAT 765
 Qy 721 GTGACTGATCCAGGCAAGTGAAGCCATGGCACTGGCTTACGCTTGTGGCTTACTCAA 780
 Db 766 GTGACTGATCCAGGCAAGTGAAGCCATGGCACTGGCTTACGCTTGTGGCTTACTCAA 825
 Qy 781 CTCTGA 786
 Db 826 CTCTGA 831

RESULT 13

LOCUS AX090039 879 bp DNA linear PAT 21-MAR-2001
 DEFINITION Sequence 1 from Patent WO0116180.
 ACCESSION AX090039
 VERSION AX090039.1 GI:13444004
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 879)
 AUTHORS Ahuja, S.U. and Bonewald, L.U.
 TITLE Cd40 agonist compositions and methods of use
 JOURNAL Patent: WO 0116180-A 1 08-MAR-2001;
 BOARD OF REGENTS THE UNIVERSITY OF TEXAS SYSTEM (US)

FEATURES Location/Qualifiers
 source 1..879
 /organism="Homo sapiens"
 /db_xref="taxon:9606"

BASE COUNT 274 a 193 c 190 g 222 t
 ORIGIN

Query Match 98.8%; Score 776.4; DB 6; Length 879;
 Best Local Similarity 99.2%; Pred. No. 7.3e-194;
 Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ATGATGAAACATACAAACCACTTCCCGATCTGCGGCGCATGGAAGTCCATCAGC 60
 Db 22 ATGATGAAACATACAAACCACTTCCCGATCTGCGGCGCATGGAAGTCCATCAGC 81
 Qy 61 ATGAAAAATTTTATGTATTTACTTACTGTTTTCTTATCACCAATGATGATCTGTG 120
 Db 82 ATGAAAAATTTTATGTATTTACTTACTGTTTTCTTATCACCAATGATGATCTGTG 141
 Qy 121 CTTTGTGCTGATCTTCTATGAGAGTTGACAAATGAGATGAGATGAGATCTTCAAT 180
 Db 142 CTTTGTGCTGATCTTCTATGAGAGTTGACAAATGAGATGAGATGAGATCTTCAAT 201
 Qy 181 GAAGATTTTGTATTCATGAAAAAGATACAGATGACACACAGAGAAAAATCTTATCC 240
 Db 222 GAAGATTTTGTATTCATGAAAAAGATACAGATGACACACAGAGAAAAATCTTATCC 261
 Qy 241 TTACTGAACGTGAGAGATTTAAAGCAGTTGAGAGCTTTGAGAGATTAATGTTA 300
 Db 262 TTACTGAACGTGAGAGATTTAAAGCAGTTGAGAGCTTTGAGAGATTAATGTTA 321
 Qy 301 AACAAAGAGAGACGAAAGAAAGAAAGCTTTGAAATGCAAAAGGTGATCAATCTT 360
 Db 322 AACAAAGAGAGACGAAAGAAAGAAAGCTTTGAAATGCAAAAGGTGATCAATCTT 381
 Qy 361 CAATTGGCGCACATGTCATTAAGTGGCCAGAGTAACCAATCTGTGTTACAGTGG 420
 Db 382 CAATTGGCGCACATGTCATTAAGTGGCCAGAGTAACCAATCTGTGTTACAGTGG 441
 Qy 421 GCTGAAAAAGATATCAACCATGAGCAACATCTTGTAACCTTGAAAAATGGAAAAAG 480

KEYWORDS

glycoprotein.
Homo sapiens.

SOURCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 1803)

AUTHORS

Spriggs, M.

TITLE

Submitted

JOURNAL

Submitted (28-JUL-1992)

REFERENCE

2 (bases 1 to 1803)

AUTHORS

Spriggs, M., Armitage, R. J., Strockbine, L., Clifford, K. N., Macduff, B. W., Sato, T. A., Maliszewski, C. R. and Famblow, W. C.

TITLE

Recombinant human CD40 ligand stimulates B cell proliferation and immunoglobulin E secretion

JOURNAL

J. Exp. Med. 176 (6), 1543-1550 (1992)

MEDLINE

93094757

PIRME

1281209

FEATURES

Location/Qualifiers

CDS

1..1803

ORIGIN

/organism="Homo sapiens"

BASE COUNT

510 a 456 c 344 g 493 t

sig_peptide

/product="CD40 ligand"

Query Match

Best Local Similarity 98.8%; Score 776.4; DB 9; Length 1803;

Matches

780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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DB 46 ATGATCGAAACATACAAACCACTTCCCGATCGGCGGCACTGAGCCCAACAGC 105
QY 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCCTGATGATGATGATG 120
DB 106 ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCCTGATGATGATGATG 165
QY 121 CTTTGTGCTGATCTTCTGATGAGTGGACAAAGATGAAAGATGAAATCTTCAT 180
DB 166 CTTTGTGCTGATCTTCTGATGAGTGGACAAAGATGAAAGATGAAATCTTCAT 225
QY 181 GAAGATTTTGTATCATGAAACGATACAGATGCAACAGAGAAAGATCTTATCC 240
DB 226 GAAGATTTTGTATCATGAAACGATACAGATGCAACAGAGAAAGATCTTATCC 285
QY 241 TTACTGAGCTGAGGAGATTAAGCCAGTTGAGGCTTTGTGAGGATATATGTTA 300
DB 286 TTACTGAGCTGAGGAGATTAAGCCAGTTGAGGCTTTGTGAGGATATATGTTA 345
QY 301 AACAAAGAGAGACGAAAGAAAGAGCTTTGAAATGCAAAAGGATGATCAATCTC 360
DB 346 AACAAAGAGAGACGAAAGAAAGAGCTTTGAAATGCAAAAGGATGATCAATCTC 405
QY 361 CAAATTTGGGACATGCTAAGTGAAGGCGAGCTGTAAGCAATCTGTTTACAGTGG 420
DB 406 CAAATTTGGGACATGCTAAGTGAAGGCGAGCTGTAAGCAATCTGTTTACAGTGG 465
QY 421 GCTGAAAAAGATCTACCATGAGCAACCTTGTTAACCCTGAAAAATGGAAAAAG 480

DB 466 GCTGAAAAAGATCTACCATGAGCAACCTTGTTAACCCTGAAAAATGGAAAAAG 525
QY 481 CTGACCGTTAAAGAGAGAGCTTATATATCTATGAGCCCAAGTCACTTCTGTTCAAT 540
DB 526 CTGACCGTTAAAGAGAGAGCTTATATATCTATGAGCCCAAGTCACTTCTGTTCAAT 585
QY 541 CGGAAAGCTTGAAGTCAAGCTCCATTATATGACGAGCTTGGCTTAAAGTCCCGGATGA 600
DB 586 CGGAAAGCTTGAAGTCAAGCTCCATTATATGACGAGCTTGGCTTAAAGTCCCGGATGA 645
QY 601 TTGAGAGATTTTATCTAGAGCTGCAATATCCAGAGTTCGCAAACTTGGCGGCA 660
DB 646 TTGAGAGATTTTATCTAGAGCTGCAATATCCAGAGTTCGCAAACTTGGCGGCA 705
QY 661 CAATCATTCCTTGGAGAGATTTGAAATTCGAACAGAGTCTTGGCTTGTTCAT 720
DB 706 CAATCATTCCTTGGAGAGATTTGAAATTCGAACAGAGTCTTGGCTTGTTCAT 765
QY 721 GTGACTGATCCAAAGGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 780
DB 766 GTGACTGATCCAAAGGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 825
QY 781 CTCTGA 786
DB 826 CTCTGA 831

Search completed: March 9, 2003, 02:11:29
Job time : 2051.61 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: March 8, 2003, 21:32:03 ; Search time 1291.53 Seconds
(without alignments)
9856.249 Million cell updates/sec

Title: US-08-982-272-4
Perfect score: 786
Sequence: 1 ATGATCGAAACATACACCA.....TTGGCTTACTCAACACTCTGA 786

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 segs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
EST:
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2: em_ests:
3: em_ests:
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6: em_ests:
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16: em_ests:
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27: em_ests:

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Match	Length	ID	Description
1	355.8	45.3	492	12	BF599437 263218 MA
2	280.4	35.7	398	10	AM488605 75217 MAR
3	69.6	8.9	638	9	A1982044 pat. PK007
4	50.2	6.4	1027	17	A2166561 SP_0088_B
5	48.8	6.2	412	14	BM854912 K-EST0137
6	48.8	6.2	997	17	CNS005TE AL060767 Drosophi1

7	48.8	6.2	999	14	BO935454	BO935454 AGNCOURT
8	48.4	6.0	1043	17	CNS0145P	AL103735 Drosophi1
9	47.2	6.0	396	12	BF820152	BF820152 MRI-RT002
10	47.2	6.0	486	10	AV714252	AV714252 AV714252
11	47.2	6.0	578	10	AV724813	AV724813 AV724813
12	47.2	6.0	583	13	BI713130	BI713130 1602E03.Y
13	47.2	6.0	586	12	BF791160	BF791160 602251255
14	47.2	6.0	797	9	AL534423	AL534423 AL534423
15	47.2	6.0	845	12	BF715238	BF715238 602676117
16	47.2	6.0	845	13	BI601432	BI601432 603249012
17	47.2	6.0	861	12	BF573761	BF573761 602077072
18	47.2	6.0	873	12	BF616023	BF616023 602643456
19	47.2	6.0	874	12	BF715241	BF715241 602676120
20	47.2	6.0	823	17	A2438784	A2438784 1M0229106
21	46.8	6.0	553	9	AA312300	AA312300 EST182997
22	46.6	5.9	458	9	AL514085	AL514085 AL514085
23	46.4	5.9	562	9	AL564525	AL564525 AL564525
24	46.2	5.9	433	9	AA115682	AA115682 21664120
25	46.2	5.9	772	12	BF763229	BF763229 602735348
26	46.2	5.9	777	13	BI598192	BI598192 603251552
27	46.2	5.9	877	13	BO643814	BO643814 AGNCOURT
28	46.2	5.9	432	12	BE888601	BE888601 601512987
29	46.2	5.9	636	12	BF718854	BF718854 602720545
30	46.2	5.9	1101	17	CNS0039G	AL063921 Drosophi1
31	45.8	5.8	382	9	AA352023	AA352023 EST59947
32	45.6	5.8	302	9	AA852210	AA852210 NHTBCae11
33	45.6	5.8	385	14	TO8874	TO8874 EST06165 in
34	45.6	5.8	389	10	AV704993	AV704993 AV704993
35	45.6	5.8	434	9	AA081760	AA081760 znt2E08.r
36	45.6	5.8	437	10	AV729112	AV729112 AV729112
37	45.6	5.8	460	13	BI598293	BI598293 603245475
38	45.6	5.8	479	14	BO130442	BO130442 1186C01.x
39	45.6	5.8	494	14	BG983924	BG983924 115-CN006
40	45.6	5.8	508	10	AM408255	AM408255 UI-HF-BKO
41	45.6	5.8	512	10	AM729297	AM729297 QV4-BT038
42	45.6	5.8	515	12	BE895474	BE895474 601437955
43	45.6	5.8	523	10	BE397864	BE397864 601290502
44	45.6	5.8	560	12	BG539029	BG539029 603568390
45	45.6	5.8	565	9	A1929671	A1929671 au53C07.Y

ALIGNMENTS

RESULT 1
LOCUS BF599437 492 bp mRNA linear EST 25-APR-2001
DEFINITION 263218 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BF599437
VERSION BF599437.1 GI:11695919
KEYWORDS EST.

ORGANISM

Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.

REFERENCE

Smith T.P.L., Grose, W.M., Preking, B.A., Roberts, A.J., Stone, R.T.,
Caes, E., Wray, J.E., White, J., Cho, J., Fahnenkrug, S.C., Bennett,
G.U., Heaton, M.P., Laegreid, W.M., Rohrer, G.A., Chitko-Mckon, C.G.,
Petea, G., Holt, I., Karaymcheva, S., Liang, F., Quackenbush, J. and
Keeler, J.W.

TITLE

Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle

JOURNAL

Medline
21180013
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@ma1.marc.usda.gov

Single pass sequencing. Bases called and alt_trimmed with phred

v0.980904.e. Vector identified by cross_match with the -minscore 18 and -mismatch 12 options.

PCR Primers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCCTCAGTCACGACG
Plate: 33 row: N column: 5
Seq primer: ATTGAGTGCACCTATG.

FEATURES

Location/Qualifiers

1..492
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 3BOV"
/issue_type="pooled"
/lab_host="DH10B"

/note="Vector: PCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendinosus muscle, and fetal
longissimus muscle."

BASE COUNT 163 a 103 c 104 g 122 t

ORIGIN

Query Match

Best Local Similarity 45.3%; Score 355.8; DB 12; Length 492;
Matches 390; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATCAACAACTTCTCCGATCTCGGCACTGACCTCCATCAGC 60
Db 46 ATGATCGAAACATCACTCACTTCTCCGATCTCGGCACTGACCTCCATCAGT 105
QY 61 ATGAAATTTTATGATTTTACTTACTGTTTCTTATCAACCAATGATGATCTGTG 120
Db 106 ATGAAATTTTATGATTTTACTTACTGTTTCTTATCAACCAATGATGATGATGAGG 165
QY 121 CTTTTCCTGTATCTTCAATGAGTTGAGCAAGATGAGATGAGATCTTCAT 180
Db 166 CTTTTCCTGTATCTTCAATGAGTTGAGCAAGATGAGATGAGATGAGATCTTCAT 225
QY 181 GAAGATTTTATGATTTTACTTACTGTTTCTTATCAACCAATGATGATCTTCAT 240
Db 226 GAAGATTTTATGATTTTACTTACTGTTTCTTATCAACCAATGATGATCTTCAT 285
QY 241 TTAAGAACTGTGAGAGATTTAAAGCAAGTTGAGCAAGATGATGATCTTCAT 300
Db 286 TTAAGAACTGTGAGAGATTTAAAGCAAGTTGAGCAAGATGATGATCTTCAT 345
QY 301 AACAAAG 360
Db 346 AACAAAG 405
QY 361 CAAATTCGCGCACTGTCAATTAAGAGGCGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Db 406 CAGATTCGCGCACTGTCAATTAAGAGGCGAGAGAGAGAGAGAGAGAGAGAGAGAG 465
QY 421 GCTGAAAGAGATCTTACACCATGAGC 447
Db 466 GCTGAAAGAGATCTTACACCATGAGC 492

RESULT 2

LOCUS AM486605 398 bp mRNA linear EST 25-APR-2001
DEFINITION 75217 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION AM486605
VERSION AM486605.1 GI:7056711
KEYWORDS EST.

SOURCE

ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.

REFERENCE

1 (bases 1 to 398)
Smith, T.P.L., Grose, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Cass, E., Wray, J.E., White, D., Cho, J., Fanzenkug, S.C., Bennett

G.L., Heaton, M.P., Laegreid, W.M., Rohrer, G.A., Chitko-McKown, C.G.,
Pette, G., Holt, I., Karamecheva, S., Liang, F., Quackenbush, J. and
Keele, J.W.

Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)

JOURNAL

MEDLINE

COMMENT

USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 20
and -mismatch 12 options.

PCR Primers

FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCCTCAGTCACGACG
Plate: 34 row: F column: 23
Seq primer: ATTGAGTGCACCTATG.

FEATURES

Location/Qualifiers

1..398
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 1BOV"
/issue_type="pooled"
/lab_host="DH10B"

/note="Vector: PCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from lymph node, ovary,
fat, hypothalamus, and pituitary."

BASE COUNT

ORIGIN

134 a 77 c 82 g 105 t

Query Match

Best Local Similarity 35.7%; Score 280.4; DB 10; Length 398;
Matches 303; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATCAACAACTTCTCCGATCTCGGCACTGACCTCCATCAGC 60
Db 53 ATGATCGAAACATCACTCACTTCTCCGATCTCGGCACTGACCTCCATCAGT 112
QY 61 ATGAAATTTTATGATTTTACTTACTGTTTCTTATCAACCAATGATGATCTGTG 120
Db 113 ATGAAATTTTATGATTTTACTTACTGTTTCTTATCAACCAATGATGATCTGTG 172
QY 121 CTTTTCCTGTATCTTCAATGAGTTGAGCAAGATGAGATGAGATCTTCAT 180
Db 173 CTTTTCCTGTATCTTCAATGAGTTGAGCAAGATGAGATGAGATCTTCAT 232
QY 181 GAAGATTTTATGATTTTACTTACTGTTTCTTATCAACCAATGATGATCTTCAT 240
Db 233 GAAGATTTTATGATTTTACTTACTGTTTCTTATCAACCAATGATGATCTTCAT 292
QY 241 TTAAGAACTGTGAGAGATTTAAAGCAAGTTGAGCAAGATGAGATCTTCAT 300
Db 293 TTAAGAACTGTGAGAGATTTAAAGCAAGTTGAGCAAGATGAGATCTTCAT 352
QY 301 AACAAAG 346
Db 353 AACAAAG 398

RESULT 3

LOCUS A1982044 638 bp mRNA linear EST 07-MAY-2001
DEFINITION pat.pK0072.c9.f chicken activated T cell cDNA Gallus gallus cDNA
ACCESSION A1982044
VERSION A1982044.1 GI:5885072
KEYWORDS EST.
SOURCE chicken.
ORGANISM Gallus gallus

Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409

Email: yongsung@mail.kr.ibm.re.kr
Plate: 58 row: D column: 01
High quality sequence stop: 412.
Location/Qualifiers

FEATURES

source

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S21SNUS20-58-D01"
/clone_11b="S21SNUS20"
/sex="F"
/tissue_type="Stomach"
/cell_type="Floating aggregates"
/cell_line="SNU-520"
/lab_host="Top10F"
/note="Organ: Stomach; Vector: pTZ189P1; Site: 1; EcoRI; Site 2; NotI. The poly (A) RNA was dephosphorylated with bacterial alkaline phosphatase (BAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

BASE COUNT

147 a 72 c 119 g 74 t

Query Match

Best Local Similarity 50.4%; Score 48.8; DB 14; Length 412;
Matches 119; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

Oy 238 TCCTTACTGACCTGAGAGATTAAACCCGTTTGAAGCTTTGTGAAGATATATAG 297
Db 171 TTCATCATTTACAGTGGTGAATTAATTTGGATATAGTTCGAGACAGACTA 230
Oy 298 TTAACAAAGAGAGACGAAAGAAACAGCTTTGAAATGCAAAAGTGATCAGAT 357
Db 231 CTCAAATAGTGACACCAATTTGCAAGAACGAGAACCTTCAAAAGCCAAATCAGAG 290
Oy 358 CCTCAATTTGGGACATGTCATAGTAGGCGCAGCTTAAACAACATCTGTGTACAG 417
Db 291 CAGTATGATAGGGAAGATGAGAGGGCTGCCCAAGAAAGAAACATCTGTGTCCAA 350
Oy 418 TGGGCTGAAAGAGATCTACACCTAGCAACAACCTTGTATACCTTGAAATGG 473
Db 351 CAGAAAAATGTGAGATGAAACCAAAACAAACAGAAACACCTGGAATGG 406

RESULT 6

CNS005TE/c

LOCUS

DEFINITION

BACR1K22 of RPI-98 library from Drosophila melanogaster (fruit

fly), genomic survey sequence.

ACCESSION

AL060767

VERSION

AL060767.1

GI:4943573

KEYWORDS

GSS.

SOURCE

Drosophila melanogaster.

ORGANISM

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 997)

AUTHORS

Genoscope.
Direct Submission
TITLE
JOURNAL
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE [E-mail : seqret@genoscope.cns.fr
- Web : www.genoscope.cns.fr]
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org> The BDGP Drosophila
melanogaster BAC library was prepared by Kazuo Ogoe, Genoscope and
Aaron Mammeter in Pletier de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
P1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

source

/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="BACR1K22"
/clone_11b="RPI-98"
/note="end : TET3"

BASE COUNT

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Matches 59; Conservative 143; Mismatches 160; Indels 0; Gaps 0;

Oy 140 ATAGAAGTTGCAACAAGATGAGAGATTAATTCATGAGATTTGTATCATGA 199
Db 850 AGRRRARGAGGRRGRRGRRRARRRARRRARRRARRRARRRARRRARRR 791
Oy 200 AAGCATGACGAGATGCAACACAGAGAAAGATCTTATCTTCTGATGAGAGCA 259
Db 790 RAKGRRGRRGRRGRRGRRRARRRARRRARRRARRRARRRARRRARRR 731
Oy 260 TTAAGGCGCTTGAAGCTTTGTGAAGATTAATGTTAAACAAAGAGAGCAAGA 319
Db 730 RRRRRRRRAGARRRARRRARRRARRRARRRARRRARRRARRRARRR 671
Oy 320 AAGAAACAGCTTGAATGCAAAAGATGATGAAATCTTCAATTTGGCGCATGCA 379
Db 670 GARRRRGRRRRRRRRRRRRRARRRARRRARRRARRRARRRARRRARRR 611
Oy 380 TAAAGGCGCAGCAATAAACAATCTGTGTTACAGTGGCTGAAAAAGATCTACA 439
Db 610 RRRRRRRRARRRARRRARRRARRRARRRARRRARRRARRRARRRARRR 551
Oy 440 CCATGACCAACCTTGGTAACTGGAAGAAAGGAAACAGCTGACCTTTAAACAG 499
Db 550 RRRRRRRRARRRARRRARRRARRRARRRARRRARRRARRRARRRARRR 491
Oy 500 GA 501
Db 490 RR 489

RESULT 7

BO935454

LOCUS

DEFINITION

AGENCOUNT 8733337 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:6372460

5', mRNA sequence.

ACCESSION

BO935454

VERSION

BO935454.1

GI:22350937

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE 1 (bases 1 to 999)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: csapds-remail.nih.gov
 Tissue Procurement: DCTD/DRP/Gazdar
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: L10CM2548 row: e column: 05
 High quality sequence start: 309
 High quality sequence stop: 663.

FEATURES

source

1..999
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:6372460"
 /clone_1ib="NIH MGC 18"
 /tissue_type="large cell carcinoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: lung; Vector: pOT7; Site 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dr priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCGCAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC library."

BASE COUNT 328 a 190 c 254 g 227 t
 ORIGIN

Query Match 6.2%; Score 48.8; DB 14; Length 999;
 Best Local Similarity 50.4%; Pred. No. 0.14;
 Matches 119; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

Qy 238 TCCTTCTGACCTGAGAGATTAATTAACGAGCTTGTGAGAGATTAATG 297
 Db 223 TTCTATCATTTACAGTGTGATTAATTAATTTGGATGAATGGTCCGAGACGAGTA 282
 Qy 298 TTAAACAAAGAGAGACGAGAAAGAAACAGCTTTGAATGCAAAAGGTGATGAAT 357
 Db 283 CTCATAATAGGTGACCAATTTGCAAGAAATTTAGAACTTCAAAAACCAATCAGAG 342
 Qy 358 CCTCAATTTGCGGACATGATTAAGAGGCGACAGTAACAATCTGTGTTACAG 417
 Db 343 CAGTATGCAAGAGGAGATGAGGGGCTGCCAGAGAAAGAGACATCTGTCTGCA 402
 Qy 418 TGGGCTGAAAAAGATCTACACATGACCAACCTTGTAACTCTGAAAAATGG 473
 Db 403 CAGAAAAATGTTGAAGTAAAAAGAAAGAAACAAACAGAAACACCTGAAATGG 458

RESULT 8
 CDS0145P/c 1043 bp DNA linear GSS 26-JUL-1999
 LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC
 DEFINITION BACN11G11 of DrosBAC library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.
 ACCESSION AL103735 GI:5615346
 VERSION AL103735.1 GI:5615346
 KEYWORDS GSS.
 SOURCE Drosophila melanogaster.
 ORGANISM Drosophila melanogaster.
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 REFERENCE 1 (bases 1 to 1043)

AUTHORS Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage;
 BP 191 91006 Evry cedex - FRANCE (E-mail: seqref@genoscope.cns.fr)
 Web: www.genoscope.cns.fr/

COMMENT

Determination of this BAC-end sequence was carried out as part of a
 collaboration with the European Drosophila Genome Project (EDGP) -
<http://www.edgp.ebi.ac.uk>. This Drosophila melanogaster BAC
 library (Dros BAC) was made by Alain Billard at CEPH (Centre
 d'Etude du Polymorphisme Humain) with funding provided by a MGC
 project grant. The DNA was prepared from embryos by Alain Bucheton
 and Genevieve Payan. It has been constructed in the vector
 pBelobAC11.

FEATURES

source

1..1043
 /organism="Drosophila melanogaster"
 /db_xref="taxon:7227"
 /clone="BACN11G11"
 /clone_1ib="DrosBAC"
 /plasmid="pBelobAC11"
 /note="end: T7"

BASE COUNT 277 a 96 c 121 g 382 t 167 others
 ORIGIN

Query Match 6.2%; Score 48.4; DB 17; Length 1043;
 Best Local Similarity 35.1%; Pred. No. 0.18;
 Matches 113; Conservative 51; Mismatches 158; Indels 0; Gaps 0;

Qy 61 ATGAAATTTTATGATTTACTTCTGTTTCTTATACCCAAATGATGATCTG 120
 Db 916 WTDATTTTCTTTGATTTGATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 857
 Qy 121 CTTTTCCTGATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 180
 Db 856 TTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 797
 Qy 181 GAAGTTTGTATTCATGAAACGATACAGAGTACACAGAGAAATCTTATCC 240
 Db 796 TTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 737
 Qy 241 TTATGAACTGAGAGATTAATTAACGAGTTTGAAGCTTTGAGAGATTAATGTTA 300
 Db 736 TATATTAATTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 677
 Qy 301 AACAAAG 360
 Db 676 TAAWAAAAAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAA 617
 Qy 361 CAATTTGCGGACATGTCATTA 382
 Db 616 WATATTTTWTAT 595

RESULT 9
 BF820152 396 bp mRNA linear EST 13-JAN-2001
 LOCUS MRL-RT0025-171100-003-c06 RT0025 Homo sapiens CDNA, mRNA sequence.
 DEFINITION BF820152
 ACCESSION BF820152
 VERSION BF820152.1 GI:12158440
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 396)
 AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
 Nagel,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.P.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.H.,
 Brunstein,A., deOliveira,P.S., Buber,P., Jongeneel,C.V., O'Hare,
 M.J., Soares,F., Brentani,R.K., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags

/tissue-type="Hypothalamus"
/dev-stage="adult"
/lab-host="SOLR"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 206 a 98 c 148 g 126 t
ORIGIN
Query Match 6.0%; Score 47.2; DB 10; Length 578;
Best Local Similarity 50.0%; Pred. No. 0.35;
Matches 118; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

QY 238 TCCTTCTGAACTGTGAGAGATTAAAGCCAGTTTGAAGCTTTGTGAAGATATATATG 297
DB 28 TTCTATCATTCAGTGTGTGAAATTAATTTGGATGATATGCGTCCGAGACAGAGTA 87
QY 298 TTAACAAAGAGAGACGAGAAAGAAACAGCTTTGAATGTGAAGATGATACAAAT 357
DB 88 CTCGAATAGTGTGACACCAATTTGCAGAAACGAGAACTTGAAGAAACCAATCAGAG 147
QY 358 CCTCAATTTGGCGCACTGTCAATGAGCGCAGCAAGTAAACAACTGTGTACAG 417
DB 148 CAGTATGACAGAGGAGAGATGATGAGGCTGCCAGAAAGAAATCACTGTGTCTGCA 207
QY 418 TGGGCTGAAAAAGATCTACCATGACCAACTTGTGTAACCTGGAAATGG 473
DB 208 CAGAAAAATGTTGAAGTGAACGAAAAAGAAACGAAACCACTGTGAAATGG 263

RESULT 12
LOCUS B1713130 583 bp mRNA linear EST 11-MAR-2002
DEFINITION ie02f03.y1 HR85 islet Homo sapiens cDNA clone IMAGE:5085845 5'
ACCESSION B1713130
VERSION B1713130.1 GI:15688825
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 583)

REFERENCE
AUTHORS Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
Lemishka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hillier, L., Marra, M., Page, D., Wylie, J., Martin, J., Blais, A.,
Schmitt, A., Theising, B., Ritzer, E., Ronko, I., Bennett, J., Cardenas,
M., Gibbons, M., McCann, R., Cole, R., Tsagarashvili, R., Williams, T.,
Jackson, Y., and Bowers, Y.
TITLE Endocrine Pancreas Consortium
JOURNAL Unpublished (2000)
COMMENT Other ESTs: ie02f03.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biochem.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center for information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Seq primer: -40RP from Glibco
High quality sequence stop: 471.
Location/Qualifiers
1. 583

FEATURES
source
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5085845"
/clone_lib="HR85 islet"
/tissue-type="Purified pancreatic islet"
/lab_host="DH10B"

/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
Site-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@im.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."

BASE COUNT 206 a 101 c 149 g 127 t
ORIGIN
Query Match 6.0%; Score 47.2; DB 13; Length 583;
Best Local Similarity 50.0%; Pred. No. 0.35;
Matches 118; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

QY 238 TCCTTCTGAACTGTGAGAGATTAAAGCCAGTTTGAAGCTTTGTGAAGATATATATG 297
DB 104 TTCTATCATTCAGTGTGTGAAATTAATTTGGATGATATGCGTCCGAGACAGAGTA 163
QY 298 TTAACAAAGAGAGACGAGAAAGAAACAGCTTTGAATGTGAAGATGATACAAAT 357
DB 164 CTCGAATAGTGTGACACCAATTTGCAGAAACGAGAACTTGAAGAAACCAATCAGAG 223
QY 358 CCTCAATTTGGCGCACTGTCAATGAGCGCAGCAAGTAAACAACTGTGTACAG 417
DB 224 CAGTATGACAGAGGAGAGATGATGAGGCTGCCAGAAAGAAATCACTGTGTCTGCA 283
QY 418 TGGGCTGAAAAAGATCTACCATGACCAACTTGTGTAACCTGGAAATGG 473
DB 284 CAGAAAAATGTTGAAGTGAACGAAAAAGAAACGAAACCACTGTGAAATGG 339

RESULT 13
LOCUS BF791160 586 bp mRNA linear EST 12-JAN-2001
DEFINITION 602251255F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4338636 5',
ACCESSION BF791160
VERSION BF791160.1 GI:12096214
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 586)

REFERENCE
AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMNL at:
http://image.llnl.gov
Plate: LNCM1214 row: n column: 13
High quality sequence stop: 582.
Location/Qualifiers
1. 586

FEATURES
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4338636"
/clone_lib="NIH MGC 81"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: muscle (skeletal); Vector: pDNR-LIB
(Clontech); Site_1: SfiI (ggccgctggcc); Site_2: SfiI
(ggccatcggcc); 5' and 3' adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CACGCCATATGACC-3'
and 3' adaptor sequence:
5'-ATCTAGAGCCGAGGCGCGCCAGACAG-3' (where B = A,

; Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3',
size-selected for average insert size 2.3 kb and
normalized to ROT 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIMH/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."

BASE COUNT

284 a 151 c 228 g 182 t

ORIGIN

Query Match

Best Local Similarity 50.0%; Score 47.2; DB 12; Length 845;

Matches 118; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

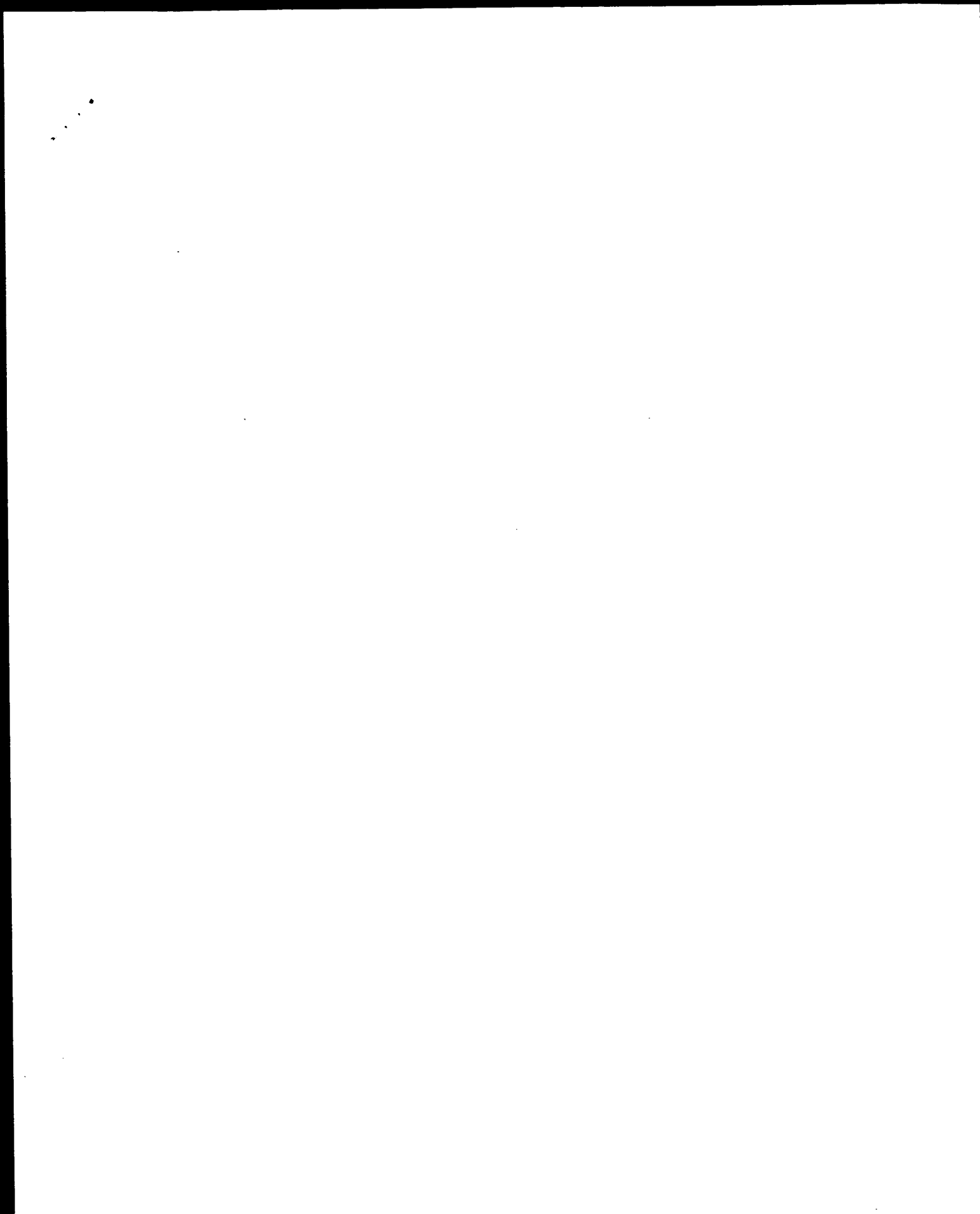
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QY 238 TCCTTACTGAACTGTGAGAGATTAAAGCCAGTTTGAAGCTTTGTGAAGATATATG 297
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Db 177 TTCATACATTACAGTGTGATTAATAATCGGATGAATGGGTTCCGGAGAGCAGAGTA 236

QY 298 TTAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 357
      |||||
Db 237 CTCGAATAGTGGACACCAATTTGGCAAGAACAGGAGAACTTCAAAAAGCCAAATCAGAG 296

QY 358 CCTCAATTCGCGCACATGTCAATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTACAG 417
      |||||
Db 297 CAGTATGCAAGAGGGAAGATGAGAGGGGCTGCCCGAGAAAGAGACATCGGTCTGCA 356

QY 418 TGGGCTGAAAAAGATCTACACCATGAGCAACAATTGTAACTCTGGAATGG 473
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Db 357 CAGAAAAATGTTGAAGTGAAGAAAAAGAAAAAGAAAAAGAAAAAGCACTGGAAATGG 412
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Search completed: March 9, 2003, 04:42:14
Job time : 1297.53 secs



GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 8, 2003, 18:30:53 ; Search time 164.215 Seconds
(without alignments)
10778.963 Million cell updates/sec

Title: US-08-982-272-4

Perfect score: 786

Sequence: 1 ATGATCGAAACATCAACCA.....TTGGCTTACTCAACCTCTGA 786

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2185239 segs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	786	100.0	786	19	AAV39000
2	776.4	98.8	786	15	AAO63959
3	776.4	98.8	786	19	AAV38997
4	776.4	98.8	786	19	AAV12852
5	776.4	98.8	840	14	AAO41506
6	776.4	98.8	840	15	AAO67123
7	776.4	98.8	840	16	AAO57563
8	776.4	98.8	840	18	AAV3782
9	776.4	98.8	840	19	AAV61063

10	776.4	98.8	840	20	AA227525	Human CD40-L codin
11	776.4	98.8	879	22	AA55539	Nucleotide sequenc
12	776.4	98.8	1816	21	AAA51745	Human CD40 ligand
13	776.4	98.8	1816	23	AA586571	DNA encoding novel
14	773.4	98.4	840	18	AA758122	Human CD40L mutain
15	773.2	98.4	840	15	AA057984	Genomic sequence o
16	771.6	98.2	840	16	AA094091	Human CD40-L CDNA.
17	763.6	97.2	786	19	AAV39003	Exemplary CD40 lig
18	754	95.9	786	19	AAV39002	Exemplary CD40 lig
19	717.2	91.2	783	19	AAV42184	Exemplary nucleoti
20	648.2	82.5	1552	22	AA425525	Nucleotide sequenc
21	642.8	81.8	865	22	AA582933	HIV-1 gp120 V3 100
22	642.8	81.8	906	22	AA582932	HIV-1 gp120 V3 100
23	642.8	81.8	2209	22	AA582929	HIV-1 gp120-human
24	642.8	81.8	2252	22	AA582928	HIV-1 gp120-human
25	638.8	81.3	864	19	AAV39004	CD40 ligand gene u
26	638.2	81.2	1425	14	AAO41516	Human CD40-L/Fc fu
27	638.2	81.2	1425	20	AA227534	Human CD40-L/Fc fu
28	637.2	81.1	929	18	AA58123	CDNA encoding yeas
29	637.2	81.1	929	18	AA227537	Human trimeric CD4
30	636	80.9	1566	24	ABK12874	Chimeric SA-CD40L
31	606.8	77.2	885	21	AA255540	Feline CD154 CDNA.
32	603.8	76.8	780	21	AA255542	Feline CD154 CDNA
33	603.8	76.8	780	21	AA255543	Feline CD154 CDNA
34	592.4	75.4	783	19	AAV39001	Exemplary CD40 lig
35	587.6	74.8	1878	21	AA255534	Canine CD154 CDNA.
36	587.6	74.8	1878	21	AA255535	Canine CD154 CDNA.
37	584.6	74.4	780	21	AA255536	Canine CD154 CDNA
38	584.6	74.4	780	21	AA255537	Canine CD154 CDNA
39	581.8	74.1	783	19	AAV38999	Exemplary CD40 lig
40	581.8	74.1	783	15	AAO63960	Mouse CD40-L type
41	571.6	72.7	783	19	AAV12853	CD40 ligand coding
42	571.6	72.7	783	19	AA227824	Mouse CD40-L codin
43	571.6	72.5	783	20	AAV38998	CD40 ligand gene u
44	570	72.5	783	19	AAV61062	Mouse CD40 ligand
45	570	72.5	818	19	AAV61062	Mouse CD40 ligand

ALIGNMENTS

AAV39000	standard; DNA; 786 BP.
AAV39000;	
23-SEP-1998 (first entry)	
Exemplary CD40 ligand gene used in the course of the invention.	
CD40 ligand; alteration; immunoreactivity; human cell;	
accessory molecule ligand; AMU; gene therapy; treatment; neoplasia;	
autoimmune disorder; rheumatoid arthritis; vaccine; chimera; ss.	
Chimeric - Mus sp.	
Chimeric - Homo sapiens.	
MO9826061-A2.	
18-JUN-1998.	
08-DEC-1997; 97WO-US22740.	
01-DEC-1997; 97US-0982272.	
09-DEC-1997; 96US-0032145.	
(REGC) UNIV CALIFORNIA.	
Cantwell M, Kipps TJ, Shatma S;	
WPI; 1998-348521/30.	

PT Vectors containing accessory molecule ligand genes - used for
 PT altering immunoreactivity of cells, particularly for treatment of
 PT neoplasia or autoimmune disorders, e.g. rheumatoid arthritis
 XX
 PS Disclosure; Page 105; 167pp; English.

XX The present sequence represents an exemplary CD40 ligand gene,
 CC comprising nucleotides encoding the extracellular domain (Domains III
 CC and IV) of human CD40 ligand gene (AAV38999) are operatively linked to
 CC nucleotides encoding the murine Cd40 ligand transmembrane domain (Domain
 CC I) (AAV38997) which is operatively linked to the human CD40 ligand gene
 CC cytoplasmic domain (Domain II). The sequence is used to exemplify the
 CC method of the invention. The specification describes a method for
 CC altering the immunoreactivity of human cells which comprises introducing
 CC a gene encoding an accessory molecule ligand (AML) into the cells so that
 CC the AML is expressed on the surface of the cells. Vectors containing the
 CC AML genes can be used in gene therapy for treating neoplasia or
 CC autoimmune disorders such as rheumatoid arthritis. They can also be used
 CC for vaccination to produce immunity against a virus cell, bacteria,
 CC protein, fungus or neoplasia.

SQ Sequence 786 BP; 250 A; 168 C; 167 G; 201 T; 0 other;

Query Match 100.0%; Score 786; DB 19; Length 786;

Best Local Similarity 100.0%; Pred. No. 1.4e-214;
 Matches 786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATCGAAGACATACCAACCTTCTCCCGACCTGGGCGCATCGATCCCATCAGC 60
 DB 1 ATGATCGAAGACATACCAACCTTCTCCCGACCTGGGCGCATCGATCCCATCAGC 60
 QY 61 ATGAAAATTTTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 120
 DB 61 ATGAAAATTTTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 120
 QY 121 CTTTGTGCTGTATCTTTATGAAAGGTTGGAAGATGAAAGATGAAAGATGAAAG 180
 DB 121 CTTTGTGCTGTATCTTTATGAAAGGTTGGAAGATGAAAGATGAAAGATGAAAG 180
 QY 181 GAAATTTTGTATTCATGAAACGATACAGAGATGCAACAGAGAAAGATCTTATCC 240
 DB 181 GAAATTTTGTATTCATGAAACGATACAGAGATGCAACAGAGAAAGATCTTATCC 240
 QY 241 TTAATGAACTGTAGAGATTAAGGCAAGTTGAAAGGCTTTGGAAGATTAATGTTA 300
 DB 241 TTAATGAACTGTAGAGATTAAGGCAAGTTGAAAGGCTTTGGAAGATTAATGTTA 300
 QY 301 AACAAAGAGAGACGAAGAAAGAAACAGCTTTGAATGCAAAAAGGTGATCGAATCT 360
 DB 301 AACAAAGAGAGACGAAGAAAGAAACAGCTTTGAATGCAAAAAGGTGATCGAATCT 360
 QY 361 CAAATGGGCGACATGCTCATAGAGGCGAGAGTAAGCAACATCTGTGTACAGTGG 420
 DB 361 CAAATGGGCGACATGCTCATAGAGGCGAGAGTAAGCAACATCTGTGTACAGTGG 420
 QY 421 GCTGAAAAGGATATACACCATGAGCAACACTTGTGAAACCTTGGAAAATGGAACG 480
 DB 421 GCTGAAAAGGATATACACCATGAGCAACACTTGTGAAACCTTGGAAAATGGAACG 480
 QY 481 CTGACCGTTAAAGACAAAGACTCATATATCATGAGCCCAAGTACCTTCTTCAT 540
 DB 481 CTGACCGTTAAAGACAAAGACTCATATATCATGAGCCCAAGTACCTTCTTCAT 540
 QY 541 CGGAAAGCTTGAGTCAGCTCATTTATAGCCAGCTTGTCTTAAAGTCCCGGTAGA 600
 DB 541 CGGAAAGCTTGAGTCAGCTCATTTATAGCCAGCTTGTCTTAAAGTCCCGGTAGA 600
 QY 601 TTGAGAGAACTTACTCAGAGTCGAATACCAAGTTCCGCAAACTTGGCGCA 660
 DB 601 TTGAGAGAACTTACTCAGAGTCGAATACCAAGTTCCGCAAACTTGGCGCA 660
 QY 661 CAATCATTTACTTGGAGAGATTTGAATGCAACGAGTCTTGGGTGTTGCAAT 720
 DB 661 CAATCATTTACTTGGAGAGATTTGAATGCAACGAGTCTTGGGTGTTGCAAT 720

DB 661 CAATCATTTACTTGGAGAGATTTGAATGCAACGAGTCTTGGGTGTTGCAAT 720
 QY 721 GTACATGATCCCAAGCAGAGAGCCATGAGCACTGGCTTACGCTTTGGCTTACCA 780
 DB 721 GTACATGATCCCAAGCAGAGAGCCATGAGCACTGGCTTACGCTTTGGCTTACCA 780
 QY 781 CTCTGA 786
 DB 781 CTCTGA 786
 RESULT 2
 AA063959 standard; cDNA to mRNA; 786 BP.
 ID AA063959;
 AC AA063959;
 XX 11-JAN-1995 (first entry)
 DT Human CD40-L type II transmembrane protein coding sequence.
 DE Leucine zipper; trimerisation; trimeric CD40-L; fusion protein;
 KW hetero-oligomer; homo-oligomer; type II transmembrane protein;
 XX soluble CD40-L; tumour necrosis factor family; ss.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT 1..786
 FT CDS /tag= a
 FT /product= human CD40-L
 FT /note= "nucleotides 148-783 code for the
 FT extracellular region (amino acids 50-261)"
 XX
 XX MO9410308-A.
 XX PD 11-MAY-1994.
 XX PF 20-OCT-1993; 93MO-US10034.
 XX PR 23-OCT-1992; 92US-0969703.
 XX PR 13-AUG-1993; 93US-0107353.
 XX PA (IMMUNEX CORP.
 XX PI Spriggs MK, Srinivasan S;
 XX WP1: 1994-167465/20.
 XX P-PSDB: AAR33969.
 PT Prepn. of soluble oligomeric mammalian proteins - using host
 PT cells to express a fusion protein comprising a leucine zipper
 PT domain and a heterologous mammalian protein
 XX
 PS Example 1; Page 22-23; 35pp; English.
 CC A DNA fragment encoding the extracellular (soluble) region of human
 CC CD40-L was ligated to a synthetic oligonucleotide sequence coding
 CC for a leader peptide, a 33 amino acid leucine zipper sequence
 CC (AAR53968) and the Flag (RTM) linker sequence. Cells expressing the
 CC fusion construct are grown to accumulate oligomeric, soluble CD40-L
 CC in the supernatant. The leucine zipper sequence spontaneously
 CC trimerises in solution and fusion proteins comprising
 CC the sequence fused to a heterologous mammalian protein also form
 CC oligomers.
 CC
 SQ Sequence 786 BP; 250 A; 168 C; 168 G; 200 T; 0 other;
 Query Match 98.8%; Score 776.4; DB 15; Length 786;
 Best Local Similarity 99.2%; Pred. No. 8.1e-214;
 Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 ATGATCGAAGACATACCAACCTTCTCCCGACCTGGGCGCATCGATCCCATCAGC 60


```

Db 541 CGGAGAGCTTCGAGTCAAGCTTCCTTATTCGAGCTTCCTTAAAGTCCCGGTAGA 600
Qy 601 TTGAGAGAAATCTTACTAGAGCTGCAAAATCCAGTTCGCGCAAACTTGGCGGCAA 660
Db 601 TTGAGAGAAATCTTACTAGAGCTGCAAAATCCAGTTCGCGCAAACTTGGCGGCAA 660
Qy 661 CAATCCATTCAGTGGAGAGATTTTGAATTCGCAACAGGCTTGGGTGTGTCAAT 720
Db 661 CAATCCATTCAGTGGAGAGATTTTGAATTCGCAACAGGCTTGGGTGTGTCAAT 720
Qy 721 GTGACTGATCCAAAGCCAGTAGCCATGCGCTTCACTGCTTGTGCTTCAAA 780
Db 721 GTGACTGATCCAAAGCCAGTAGCCATGCGCTTCACTGCTTGTGCTTCAAA 780
Qy 781 CTCTGA 786
Db 781 CTCTGA 786

```

RESULT 4

AAV12852 standard; cDNA to mRNA; 786 BP.

```

ID AAV12852
XX AAV12852;
AC AAV12852;
XX
DT 13-MAY-1998 (first entry)
XX
DE CD40 ligand coding sequence.
XX
KM Leucine zipper; fusion protein production; soluble oligomeric protein;
KM heterologous mammalian type II transmembrane protein; activated T cell;
KM heterologous mammalian type I transmembrane protein; antibody production;
KM CD40-L; B-cell proliferation; CD27-L; lymphocyte antigen; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..786
FT /*tag= a
XX
PN US716805-A.
XX
PD 10-FEB-1998.
XX
PF 18-MAY-1995; 95US-0446922.
XX
PR 18-MAY-1995; 95US-0446922.
PR 25-OCT-1991; 91US-0783707.
PR 05-DEC-1991; 91US-0805723.
PR 23-OCT-1992; 92US-0969703.
PR 13-AUG-1993; 93US-0107353.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Sprigge MK, Srinivasan S;
XX
DR WPI; 1998-144739/13.
XX
DR P-PSDB; AAM41178.
XX
PT Soluble oligomeric fusion proteins - comprising leucine zipper fused
XX to extracellular region of transmembrane protein
XX
PS Example 1; column 19-20; 21pp; English.
XX

```

This sequence is the coding sequence for the human CD40 ligand (CD40-L). The encoded protein can be used in a fusion protein produced using the CC method of the invention. The method is for preparing soluble oligomeric CC protein by culturing a host cell transfected with a vector for the CC fusion protein. The soluble oligomeric proteins comprise a leucine zipper fused to the N terminus of the extracellular region of a heterologous CC mammalian type II transmembrane protein or to the C terminus of the extracellular region of a heterologous mammalian type I transmembrane

protein, where the leucine zipper is a peptide comprising at least part of AAM41171 or AAM41172, optionally with conservative amino acid substitutions, provided that the peptide trimerizes in solution. A soluble fusion protein comprising the leucine zipper of AAM41171 linked CC to the extracellular region of CD40-L (a type II transmembrane protein CC that is found on activated T cells and acts as a ligand for the B-cell CC antigen CD40) stimulates B-cell proliferation and antibody production in CC a similar manner to membrane-bound CD40-L. A soluble fusion protein CC comprising the leucine zipper of AAM41172 linked to the extracellular CC region of CD27-L (a type II transmembrane protein that binds to the CC lymphocyte antigen CD27) inhibits binding of CD27c (a fusion protein CC comprising the extracellular region of CD27 and a human IgG1 Fc region) CC to EBV-transformed B cells expressing CD27-L.

Sequence 786 BP; 250 A; 168 C; 168 G; 200 T; 0 other;

Query Match 98.8%; Score 776.4; DB 19; Length 786;

Best Local Similarity 99.2%; Pred. No. 8.1e-214; Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy 1 ATGATGAAACATACAAACAAATTTCCCGGATCTGGGCACTGACCTCCATACG 60
Db 1 ATGATGAAACATACAAACAAATTTCCCGGATCTGGGCACTGACCTCCATACG 60
Qy 61 ATGAAATTTTAAATATTACTTACTGTTTCCCTTATCCACCAATGATTGATCTG 120
Db 61 ATGAAATTTTAAATATTACTTACTGTTTCCCTTATCCACCAATGATTGATCTG 120
Qy 121 CTTTGGCTGTGATCTTATCATAGAGTTGGACAAAGTATGAAAGAAATCTTCAT 180
Db 121 CTTTGGCTGTGATCTTATCATAGAGTTGGACAAAGTATGAAAGAAATCTTCAT 180
Qy 181 GAAGATTTTGTATCATGAAACGATACAGATGCAACACAGAGAAAGATCTTATCC 240
Db 181 GAAGATTTTGTATCATGAAACGATACAGATGCAACACAGAGAAAGATCTTATCC 240
Qy 241 TTACTGAATCTGGAGAGATTTAAAGCCGTTGAAGCTTGTGAAGATATATATTA 300
Db 241 TTACTGAATCTGGAGAGATTTAAAGCCGTTGAAGCTTGTGAAGATATATATTA 300
Qy 301 AACAAAGAGAGACCAAGAAAGAAACAGCTTGAATGCAAAAGATGATCAGATCT 360
Db 301 AACAAAGAGAGACCAAGAAAGAAACAGCTTGAATGCAAAAGATGATCAGATCT 360
Qy 361 CAATTTGCGGACATGTCATATAGTAGGCGACAGCTTAAACCAATCTGTATCACTGG 420
Db 361 CAATTTGCGGACATGTCATATAGTAGGCGACAGCTTAAACCAATCTGTATCACTGG 420
Qy 421 GCTGAAAAGATACATACACATAGCAACAACTTGTAAACCTTGAAATGGAACAG 480
Db 421 GCTGAAAAGATACATACACATAGCAACAACTTGTAAACCTTGAAATGGAACAG 480
Qy 481 CTGACGCTTAAAGCAAGGACCTATATATCTATGCGCAAGCTTCACTTGTTCAT 540
Db 481 CTGACGCTTAAAGCAAGGACCTATATATCTATGCGCAAGCTTCACTTGTTCAT 540
Qy 541 CGGAGAGCTTCAGTCAAGCTCAATTAATAGCCAGCTTCTGCTTAAAGTCCCGGTAGA 600
Db 541 CGGAGAGCTTCAGTCAAGCTCAATTAATAGCCAGCTTCTGCTTAAAGTCCCGGTAGA 600
Qy 601 TTGAGAGAAATCTTACTAGAGCTGCAAAATCCAGTTCGCGCAAACTTGGCGGCAA 660
Db 601 TTGAGAGAAATCTTACTAGAGCTGCAAAATCCAGTTCGCGCAAACTTGGCGGCAA 660
Qy 661 CAATCCATTCAGTGGAGAGATTTTGAATTCGCAACAGGCTTGGGTGTGTCAAT 720
Db 661 CAATCCATTCAGTGGAGAGATTTTGAATTCGCAACAGGCTTGGGTGTGTCAAT 720
Qy 721 GTGACTGATCCAAAGCCAGTAGCCATGCGCTTCACTGCTTGTGCTTCAAA 780
Db 721 GTGACTGATCCAAAGCCAGTAGCCATGCGCTTCACTGCTTGTGCTTCAAA 780
Qy 781 CTCTGA 786

```

Db 781 CTCGA 786

RESULT 5
AAQ41506
ID AAQ41506 standard; DNA; 840 BP.

XX AAQ41506;

XX 12-AUG-1993 (first entry)

XX CD40-L DNA.

XX Human; CD40-L; CD40; type II; membrane; polypeptide; extracellular;
XX transmembrane; region; intracellular; soluble; activity; B cell;
XX proliferation; induction; antibody; secretion; Igr; agonist;
XX antagonist; binding assay; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 46..831

XX /*tag= a

XX MO9308207-A.

XX 29-APR-1993.

XX 23-OCT-1992; 92MO-US08990.

XX 25-OCT-1991; 91US-0783707.

XX 05-DEC-1991; 91US-0805723.

XX (IMMEX) IMMEX CORP.

XX Armitage RJ, Fanslow WC, Springs MK;

XX WPI; 1993-152417/18.

XX P-PSDB; AAR36701.

XX New cytokine CD40-L as CD40 agonist and antagonist - is used for

XX treating allergies, lupus, rheumatoid arthritis,

XX graft-versus-host disease and insulin-dependent diabetes mellitus

XX Claim 1; Fig 2; 80pp; English.

XX

XX This sequence encodes a human CD40-L polypeptide which binds to CD40.

XX CD40-L is a type II membrane polypeptide which has an extracellular

XX region at its C-terminus, a transmembrane region and an

XX intracellular region at its N-terminus. A soluble form of CD40-L

XX lacks the transmembrane domain. CD40-L activity is mediated by

XX binding with CD40 and induces B cell proliferation and induction of

XX antibody secretion, including Igr. Membrane bound CD40-L acts as a

XX CD40 agonist and soluble CD40-L acts as a CD40 antagonist. CD40-L

XX can be used in a binding assay to detect cells expressing CD40.

Sequence 840 BP; 266 A; 185 C; 175 G; 214 T; 0 other;

Query Match 98.8%; Score 776.4; DB 14; Length 840;

Best Local Similarity 99.2%; Pred. No. 8,4e-214;

Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ATGATCGAAGACATACCAAACTTCTCCCGATCTGCGCGCATGACCTGCCATCAGC 60

Db 46 ATGATCGAAGACATACCAAACTTCTCCCGATCTGCGCGCATGACCTGCCATCAGC 105

Qy 61 ATGAAATTTTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 120

Db 106 ATGAAATTTTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 165

Qy 121 CTTTGTCTGTATCTTCAATGAAGGTGACAGATGAAGATGAAGATGAAGATCTTCAT 180

Db 166 CTTTGTCTGTATCTTCAATGAAGGTGACAGATGAAGATGAAGATGAAGATCTTCAT 225

Qy 181 GAAGATTTTGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 240

Db 226 GAAGATTTTGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 285

Qy 241 TTACTGAATCTGTAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 300

Db 286 TTACTGAATCTGTAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 345

Qy 301 AACAAAGAGAGACGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 360

Db 346 AACAAAGAGAGACGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 405

Qy 361 CAAATTTGGGCAATGCTCAATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420

Db 406 CAAATTTGGGCAATGCTCAATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 465

Qy 421 GCTGAAAAGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 480

Db 466 GCTGAAAAGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 525

Qy 481 CTGACCGTTAAAGACAG 540

Db 526 CTGACCGTTAAAGACAG 585

Qy 541 CGGAAAGCTTGAAGTCAAGCTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 600

Db 586 CGGAAAGCTTGAAGTCAAGCTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 645

Qy 601 TTGAGAGAGATTTTAACTGAG 660

Db 646 TTGAGAGAGATTTTAACTGAG 705

Qy 661 CAATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 720

Db 706 CAATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 765

Qy 721 GTGACTGATCAAG 780

Db 766 GTGACTGATCAAG 825

Qy 781 CTCGA 786

Db 826 CTCGA 831

RESULT 6

ID AAQ67123 standard; DNA; 840 BP.

XX AAQ67123;

XX 23-MAR-1995 (first entry)

XX CD40 ligand gene.

XX Probe; primer; PCR; amplify; polymerase chain reaction; detection;

XX mutation; CD40 ligand gene; Igr; ss.

XX Synthetic.

XX Key Location/Qualifiers

XX CDS 46..831

XX /*tag= a

XX /product= CD40 ligand

XX MO9417196-A.

XX 04-AUG-1994.

XX 21-JAN-1994; 94MO-US00786.

PR 22-JAN-1993; 93US-0009258.
 PR 20-JAN-1994; 94US-0184422.
 XX (IMMV) IMMUNEX CORP.
 XX Armitage RJ, Davison BL, Fanslow WC, Renshaw BR;
 PI Spriggs MK, Wildmer MB;
 XX WPI; 1994-264109/32.
 DR P-PSDB; AAR57469.
 PT Method for detecting mutation in CD 40 ligand gene - comprises
 XX amplification of nucleic acid, and mutational analysis
 XX
 PS Disclosure; Page 22-24; 38pp; English.
 CC This sequence represents the CD40 ligand gene. Mutations within
 CC this gene were identified by the method of the invention. The
 CC method comprises isolating DNA from an individual and selectively
 CC amplifying the isolated DNA derived from the CD40 ligand gene. The
 CC amplification product is then analysed to determine if there is a
 CC mutation present and determining if a protein expressed from the
 CC ligand gene will bind CD40. The detection of mutations in the CD40
 CC ligand gene allows subsequent treatment of a syndrome resulting in
 CC elevated levels of serum IgM and diminished levels of other Ig
 CC isotypes, due to mutation in the CD40 ligand gene. ie. X-linked
 CC hyperIgM syndrome.
 XX
 SQ Sequence 840 BP; 266 A; 185 C; 175 G; 214 T; 0 other;
 Query Match 98.8%; Score 776.4; DB 15; Length 840;
 Best Local Similarity 99.2%; Pred. No. 8.4e-214;
 Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACACCAACCTTCCCGATCGCGGACATGAGCCCATCAGC 60
 DB 46 ATGATCGAAACATACACCAACCTTCCCGATCGCGGACATGAGCCCATCAGC 105
 QY 61 ATGAAATTTTATGATTTTACTTACTGTTTCTTATCACCCTTGAATGATCTGTG 120
 DB 106 ATGAAATTTTATGATTTTACTTACTGTTTCTTATCACCCTTGAATGATCTGTG 165
 QY 121 CTTTGGCTGATCTTATGATGAGTGGACAAATGAAAGATGAAATCTTCTAT 180
 DB 166 CTTTGGCTGATCTTATGATGAGTGGACAAATGAAAGATGAAATCTTCTAT 225
 QY 181 GAAGTTTGTATTCATGAAACGATACAGATGCAACACAGGAAATCTTATCC 240
 DB 226 GAAGTTTGTATTCATGAAACGATACAGATGCAACACAGGAAATCTTATCC 285
 QY 241 TTAAGTAACTGTAGAGATTTAAAGCCAGTTTGAAGGCTTTGTAAGATATATGTTA 300
 DB 286 TTAAGTAACTGTAGAGATTTAAAGCCAGTTTGAAGGCTTTGTAAGATATATGTTA 345
 QY 301 AACCAAGAGAGACGAAAGAAACAGCTTGAATTCACAAAAGGTGATCAATCTT 360
 DB 346 AACCAAGAGAGACGAAAGAAACAGCTTGAATTCACAAAAGGTGATCAATCTT 405
 QY 361 CAATTCGCGCACATGTCATTAAGTGGCCAGACGTAACCAATCTGTGTTACAGTGG 420
 DB 406 CAATTCGCGCACATGTCATTAAGTGGCCAGACGTAACCAATCTGTGTTACAGTGG 465
 QY 421 GGTGAAAAAGATATCTACACATGAGCAACATCTTGTAACCTTGAAATGGGAAACG 480
 DB 466 GGTGAAAAAGATATCTACACATGAGCAACATCTTGTAACCTTGAAATGGGAAACG 525
 QY 481 CTGACCGTTAAAGACAGAGACTTATATATATATATATATATATATATATATAT 540
 DB 526 CTGACCGTTAAAGACAGAGACTTATATATATATATATATATATATATATATAT 585
 QY 541 CGGAAAGCTTGAGATCAAGTCCATTTATAGCAGGCTTGTCTTAAAGTCCCGGTTAA 600
 DB 586 CGGAAAGCTTGAGATCAAGTCCATTTATAGCAGGCTTGTCTTAAAGTCCCGGTTAA 645

QY 601 TTGAGAGAACTTACTCAGAGCTGCAATAACCAAGTTCGCCCAAACTTTGGGCA 660
 DB 646 TTGAGAGAACTTACTCAGAGCTGCAATAACCAAGTTCGCCCAAACTTTGGGCA 705
 QY 661 CAATTCATCTTCTGGAGAGATTTGAATTTGAACCGAGTGTCTGCTTGTCAAT 720
 DB 706 CAATTCATCTTCTGGAGAGATTTGAATTTGAACCGAGTGTCTGCTTGTCAAT 765
 QY 721 GTGACTGATCCAGCAGTGAAGCCATGACATGACATGCTTCCCTTTGGCTTAA 780
 DB 766 GTGACTGATCCAGCAGTGAAGCCATGACATGACATGCTTCCCTTTGGCTTAA 825
 QY 781 CTCTGA 786
 DB 826 CTCTGA 831

RESULT 7
 AAT05763
 ID AAT05763 standard; DNA; 840 BP.
 XX
 AC AAT05763;
 XX
 DT 18-MAR-1996 (first entry)
 XX
 DE Human CD40 ligand DNA.
 XX
 KW High density membrane-bound CD40 ligand; B-lymphocyte; B-cell;
 KW differentiation; proliferation; baculovirus; Spodoptera frugiperda;
 KW Sf9; insect cell culture; tumour necrosis factor receptor; ss.
 OS Homo sapiens.
 XX
 PN MO952935-A1.
 XX
 PD 09-NOV-1995.
 XX
 PF 28-APR-1995; 95WO-US05448.
 XX
 PR 28-APR-1994; 94US-0234580.
 XX
 PA (BOEH) BOEHRINGER INGELHEIM PHARM INC.
 XX
 PI Caesle BE, Kehry M;
 XX
 DR WPI; 1995-393038/50.
 XX
 PT P-PSDB; AAR85486.
 PT High density membrane bound CD40 ligand - for stimulating the
 PT proliferation of B cells in vitro or in vivo, partic. for producing
 PT differentiated cells
 PS Disclosure; Fig 1; 74pp; English.
 CC The nucleotide sequence given in AAT05763 encodes a human high-density,
 CC membrane-bound (hmb) CD40 ligand (AAR85486) that induces long-term
 CC proliferation of B-cells in culture. These proliferating B-cells
 CC can be induced to differentiate into antibody-prod. cells. The
 CC nucleotide sequence is incorporated into a baculovirus vector that
 CC is used to transfect Sf9 insect cells for prodn. of recombinant
 CC hmbCD40.
 XX
 SQ Sequence 840 BP; 263 A; 182 C; 181 G; 214 T; 0 other;
 Query Match 98.8%; Score 776.4; DB 16; Length 840;
 Best Local Similarity 99.2%; Pred. No. 8.4e-214;
 Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGATGAAACATACCAACAACTTCTCCCGATCTGCGGCACTGAGCTGCCATCAGC 60
 Db 22 ATGATGAAACATACCAACAACTTCTCCCGATCTGCGGCACTGAGCTGCCATCAGC 81
 QY 61 ATGAAATTTTATGATTTTACTTACTGTTTCTTATCAACCAATGATGATCTGTG 120
 Db 82 ATGAAATTTTATGATTTTACTTACTGTTTCTTATCAACCAATGATGATGATGATCA 141
 QY 121 CTTTTCGTGTATCTTCAATAGAGTTGAGCAAGATGATGATGATGATGATGATGAT 180
 Db 142 CTTTTCGTGTATCTTCAATAGAGTTGAGCAAGATGATGATGATGATGATGATGAT 201
 QY 181 GAAGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATGAT 240
 Db 202 GAAGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATGAT 261
 QY 241 TTACTGAATCTGAGAGATTTAAAGCCAGTTTGAAGCTTTGTAAGATGATGATGAT 300
 Db 262 TTACTGAATCTGAGAGATTTAAAGCCAGTTTGAAGCTTTGTAAGATGATGATGAT 321
 QY 301 AACAAAG 360
 Db 322 AACAAAG 381
 QY 361 CAATTTGCGGACATGTCATTAAGTGGGCGAGAGTAAACAAATCTGTGTACAGTGG 420
 Db 382 CAATTTGCGGACATGTCATTAAGTGGGCGAGAGTAAACAAATCTGTGTACAGTGG 441
 QY 421 GCTGAAAGAGATCTTACATGAGCAACATTTGTTAACTTGGAAATGAGAAACAG 480
 Db 442 GCTGAAAGAGATCTTACATGAGCAACATTTGTTAACTTGGAAATGAGAAACAG 501
 QY 481 CTGACCGTTTAAAGACAGAGACTTATTTATCTATGATGATGATGATGATGATGAT 540
 Db 502 CTGACCGTTTAAAGACAGAGACTTATTTATCTATGATGATGATGATGATGATGAT 561
 QY 541 CGGAAAGCTTGTGATCACTGATTTTATGAGCAAGCTTGTGTTAACTTGGAAATGAG 600
 Db 562 CGGAAAGCTTGTGATCACTGATTTTATGAGCAAGCTTGTGTTAACTTGGAAATGAG 621
 QY 601 TTGAGAGAACTTACTCAGAGCTGCAATTAACCAAGTTTCCGCAACCTTCCGAGCA 660
 Db 622 TTGAGAGAACTTACTCAGAGCTGCAATTAACCAAGTTTCCGCAACCTTCCGAGCA 681
 QY 661 CAATCATTCTTGTGAGAGATTTTGAATGCAACAGGCTTGTGTTAACTTGGAAATGAG 720
 Db 682 CAATCATTCTTGTGAGAGATTTTGAATGCAACAGGCTTGTGTTAACTTGGAAATGAG 741
 QY 721 GTGACTGATCAAGCAAGTGAAGCACTGAGCTTCACTGCTTGTGTTAACTTGGAAAT 780
 Db 742 GTGACTGATCAAGCAAGTGAAGCACTGAGCTTCACTGCTTGTGTTAACTTGGAAAT 801
 QY 781 CTCTGA 786
 Db 802 CTCTGA 807

RESULT 8
 AAT93782
 ID AAT93782 standard; cDNA; 840 BP.
 XX
 AC AAT93782;
 XX
 DT 16-FEB-1998 (first entry)
 XX
 DE cDNA of CD40L, a novel cytokine ligand for CD40.
 XX
 KW Cytokine; activated CD4+ T cell; CD40; CD40L; monoclonal antibody;
 KM neoplastic cell proliferation; B-cell lymphoma; immune deficiency; AIDS;
 XX melanoma; carcinoma; ss.
 OS Homo sapiens.
 XX

PH Key Location/Qualifiers
 FT CDS 46..831
 FT /*tag= a
 XX US5674492-A.
 XX
 XX 07-OCT-1997.
 XX
 XX 21-DEC-1994; 94US-0360923.
 XX
 XX 23-DEC-1993; 93US-0172664.
 XX
 XX (IMV) IMMUNEX CORP.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Armlage RJ, Fanelow WC, Longo DL, Murphy WJ;
 DR WPI, 1997-502273/46.
 XX F-PSDB; AAW34669.
 XX
 XX Treating or preventing neoplastic disease associated with
 PT CD40-expressing cells - particularly B-cell lymphoma, by
 PT administration of CD40-binding protein, preferably antibody or
 PT soluble CD40-ligand
 XX
 PS Claim 3; Columns 19-22; 21pp; English.
 XX
 XX The present sequence represents the cDNA sequence of a novel cytokine
 CC ligand for CD40 called CD40L. CD40L is a type II membrane polypeptide,
 CC which is expressed by activated CD4+ T cells, and causes B cell
 CC proliferation and induction of antibody secretion. The protein can be
 CC used to produce monoclonal antibodies, which in turn bind to
 CC CD40-expressing cells. This inhibits binding of soluble CD40 to its
 CC ligand CD40. The monoclonal antibody against CD40L is used to inhibit
 CC proliferation of neoplastic cells, and is particularly useful in treating
 CC B-cell lymphoma (e.g. where induced after transplants or in other cases
 CC of immune deficiency such as AIDS), and also melanoma or carcinoma. Since
 CC the monoclonal antibodies inhibit neoplastic cells directly, they may not
 CC need to be coupled to a toxin or radioisotope, avoiding toxic effects on
 CC normal B cells.
 XX
 SQ Sequence 840 BP; 266 A; 185 C; 175 G; 214 T; 0 other;
 Query Match 98.8%; Score 776.4; DB 18; Length 840;
 Best Local Similarity 99.2%; Pred. No. 8.4e-214;
 Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGATGAAACATACCAACAACTTCTCCCGATCTGCGGCACTGAGCTGCCATCAGC 60
 Db 46 ATGATGAAACATACCAACAACTTCTCCCGATCTGCGGCACTGAGCTGCCATCAGC 105
 QY 61 ATGAAATTTTATGATTTTACTTACTGTTTCTTATCAACCAATGATGATCTGTG 120
 Db 106 ATGAAATTTTATGATTTTACTTACTGTTTCTTATCAACCAATGATGATGATGATCA 165
 QY 121 CTTTTCGTGTATCTTCAATAGAGTTGAGCAAGATGATGATGATGATGATGATGAT 180
 Db 166 CTTTTCGTGTATCTTCAATAGAGTTGAGCAAGATGATGATGATGATGATGATGAT 225
 QY 181 GAAGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATGAT 240
 Db 226 GAAGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATGAT 285
 QY 241 TTACTGAATCTGAGAGATTTAAAGCCAGTTTGAAGCTTTGTAAGATGATGATGAT 300
 Db 286 TTACTGAATCTGAGAGATTTAAAGCCAGTTTGAAGCTTTGTAAGATGATGATGAT 345
 QY 301 AACAAAG 360
 Db 346 AACAAAG 405
 QY 361 CAATTTGCGGACATGTCATTAAGTGGGCGAGAGTAAACAAATCTGTGTACAGTGG 420

Db 406 CAAATTGCGGCACATGTCATTAAGTGAAGCCAGTAAACACATCTGTGTAACTG 465
 Qy 421 GCTGAAAAAGATCTACACCATGAGCAACACTTGTAACTCTGAAAAATGGAAACAG 480
 Db 466 GCTGAAAAAGATCTACACCATGAGCAACACTTGTAACTCTGAAAAATGGAAACAG 525
 Qy 481 CTGACCGTTAAAGACAGACTCTATTTATCTATGCGCCAGTCACTTCTGTTCAT 540
 Db 526 CTGACCGTTAAAGACAGACTCTATTTATCTATGCGCCAGTCACTTCTGTTCAT 585
 Qy 541 CGGAGAGCTTCAAGTCAAGCTCTTATTAAGCCAGCTTCTGCTTAAAGTCCCGGTTAGA 600
 Db 586 CGGAGAGCTTCAAGTCAAGCTCTTATTAAGCCAGCTTCTGCTTAAAGTCCCGGTTAGA 645
 Qy 601 TTGAGAGAGATCTTACTCAGAGCTGCAAAATACCCAGATTCCGCAAACTTGGCGGCA 660
 Db 646 TTGAGAGAGATCTTACTCAGAGCTGCAAAATACCCAGATTCCGCAAACTTGGCGGCA 705
 Qy 661 CAATCCATTCACCTTGGAGAGAGTATTTGAATTGCAACAGAGTCTCGGTGTTGTCAAT 720
 Db 706 CAATCCATTCACCTTGGAGAGAGTATTTGAATTGCAACAGAGTCTCGGTGTTGTCAAT 765
 Qy 721 GTGACTGATCAAGCAAGTGAAGCCATGAGCAGTGGCTTCAAGTCTTGGCTTACTCAA 780
 Db 766 GTGACTGATCAAGCAAGTGAAGCCATGAGCAGTGGCTTCAAGTCTTGGCTTACTCAA 825
 Qy 781 CTCTGA 786
 Db 826 CTCTGA 831
 RESULT 9
 AA61063
 ID AA61063 standard; DNA; 840 BP.
 AC AA61063;
 DT 08-DEC-1998 (first entry)
 XX Human CD40 ligand encoding DNA sequence.
 DE Human CD40 ligand encoding DNA sequence.
 XX Human; CD40 ligand; TNF receptor family; activated T cell;
 KM type 2 membrane glycoprotein; cell proliferation; differentiation;
 KM B cell; de.
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT CDS 22..807
 FT /tag= a
 FT /product= "CD40 ligand"
 XX
 PN US817516-A.
 XX
 PD 06-OCT-1998.
 XX
 PF 28-APR-1995; 95US-0431055.
 XX
 PR 28-APR-1995; 95US-0431055.
 PR 28-APR-1994; 94US-0234580.
 XX
 PA (BOEH) BOEHRINGER INGELHEIM PHARM INC.
 XX
 PI Castle B, Kehry M;
 XX
 DR WPI; 1998-556393/47.
 DR P-PSDB; AAW71751.
 XX
 PT Increased proliferation of B cells in culture - by incubating them
 PT in the presence of membrane-bound CD40 ligand
 XX
 PS Example 1; Fig 1; 37pp; English.
 XX

CC The present sequence encodes human CD40 ligand which is used in the
 CC method of the invention. The method has been developed for proliferating
 CC B cells to increase their number at least 100-fold. The method
 CC comprises: (a) providing high density, membrane bound CD40 ligand; and
 CC (b) culturing one or more B cells in the presence of this ligand. The
 CC culture results in a proliferation in the number of B cells of at least
 CC 100 fold. Also described is a method as above where the B cells are
 CC induced to differentiate into antibody-producing cells in the presence
 CC of one or more cytokines. The method can be used for stimulating B-cell
 CC proliferation in vitro or in vivo, e.g. for treating conditions in which
 CC B-cell proliferation and activation is suppressed. Eight rounds of
 CC division over six days can be achieved, corresponding to a 256-fold
 CC increase in cell numbers, which is a vast increase compared to previous
 CC culturing methods.
 CC
 CC
 CC Sequence 840 BP; 263 A; 182 C; 181 G; 214 T; 0 other;
 CC
 CC
 CC Query Match 98.8%; Score 776.4; DB 19; Length 840;
 CC Best Local Similarity 99.2%; Pred. No. 8-4e-214;
 CC Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 Qy 1 ATGATGAAACATCAACCAACTTCTCCGATCTGCGGCACTGACCTGCCATCAGC 60
 Db 22 ATGATGAAACATCAACCAACTTCTCCGATCTGCGGCACTGACCTGCCATCAGC 81
 Qy 61 ATGAAATTTTATGATTTTACTTCTGTTTCTTATCAACCAATGATTCGATCTG 120
 Db 82 ATGAAATTTTATGATTTTACTTCTGTTTCTTATCAACCAATGATTCGATCAGA 141
 Qy 121 CTTTGGCTGATGATCTTCAAGAGTTGGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 180
 Db 142 CTTTGGCTGATGATCTTCAAGAGTTGGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 201
 Qy 181 GAAGATTTTATGATTTTATGAAACGATCAAGATGCAACAGAGAAAGATCTTATCC 240
 Db 202 GAAGATTTTATGATTTTATGAAACGATCAAGATGCAACAGAGAAAGATCTTATCC 261
 Qy 241 TTAATCAAGTGAAGAGATTAAGAGCCGTTGAAGCTTGTGAAGATATATGTTA 300
 Db 262 TTAATCAAGTGAAGAGATTAAGAGCCGTTGAAGCTTGTGAAGATATATGTTA 321
 Qy 301 AACAAAGAGAGACGAGAAAGAAACAGCTTGAATGCAAAAGGTGATCAAAATCCT 360
 Db 322 AACAAAGAGAGACGAGAAAGAAACAGCTTGAATGCAAAAGGTGATCAAAATCCT 381
 Qy 361 CAAATTCGCGCAGATGATCAATGAGGCGAGAGTAAACACATCTGTGTCACTGG 420
 Db 382 CAAATTCGCGCAGATGATCAATGAGGCGAGAGTAAACACATCTGTGTCACTGG 441
 Qy 421 GCTGAAAAAGATCTACACCATGAGCAACACTTGTAACTCTGAAAAATGGAAACAG 480
 Db 442 GCTGAAAAAGATCTACACCATGAGCAACACTTGTAACTCTGAAAAATGGAAACAG 501
 Qy 481 CTGACCGTTAAAGACAGACTCTATTTATCTATGCGCCAGTCACTTCTGTTCAT 540
 Db 502 CTGACCGTTAAAGACAGACTCTATTTATCTATGCGCCAGTCACTTCTGTTCAT 561
 Qy 541 CGGAGAGCTTCAAGTCAAGCTCTTATTAAGCCAGCTTCTGCTTAAAGTCCCGGTTAGA 600
 Db 562 CGGAGAGCTTCAAGTCAAGCTCTTATTAAGCCAGCTTCTGCTTAAAGTCCCGGTTAGA 621
 Qy 601 TTGAGAGAGATCTTACTCAGAGCTGCAAAATACCCAGATTCCGCAAACTTGGCGGCA 660
 Db 622 TTGAGAGAGATCTTACTCAGAGCTGCAAAATACCCAGATTCCGCAAACTTGGCGGCA 681
 Qy 661 CAATCCATTCACCTTGGAGAGAGTATTTGAATTGCAACAGAGTCTCGGTGTTGTCAAT 720
 Db 682 CAATCCATTCACCTTGGAGAGAGTATTTGAATTGCAACAGAGTCTCGGTGTTGTCAAT 741
 Qy 721 GTGACTGATCAAGCAAGTGAAGCCATGAGCAGTGGCTTCAAGTCTTGGCTTACTCAA 780
 Db 742 GTGACTGATCAAGCAAGTGAAGCCATGAGCAGTGGCTTCAAGTCTTGGCTTACTCAA 801

Qy 781 CTCTGA 786
Db 802 CTCTGA 807

RESULT 10

AAZ27525
ID AAZ27525 standard; cDNA; 840 BP.

AAZ27525;

13-DEC-1999 (first entry)

Human CD40-L coding sequence.

CD40-L; CD40 receptor ligand; anti-human CD40-L monoclonal antibody;
binding inhibitor; trimeric CD40-L; anti-immunoglobulin M;
peripheral blood B cell; proliferation inhibitor; ss.

Homo sapiens.

US5961974-A.

05-OCT-1999.

24-MAY-1994; 94US-0249189.

25-OCT-1991; 91US-0783707.

05-DEC-1991; 91US-0805723.

23-OCT-1992; 92US-0969703.

(IMV) IMMUNEX CORP.

Spriggs MK, Fanslow WC, Armitage RJ;

WPI; 1999-579604/49.

P-PSDB; AAY39398.

Anti-human CD40-L ligand monoclonal antibodies -

Disclosure; Fig 2; 59pd; English.

This sequence encodes the human CD40 receptor ligand (CD40-L). The
invention relates to anti-human CD40-L monoclonal antibodies M90 secreted
by hybridoma hCD40L-M90 (ATCC HB-12055) and M91 secreted by hybridoma
hCD40L-M91 (ATCC HB-12056). M90 and M91 inhibit CD40-L binding to CD40
and the ability of trimeric CD40-L and anti-immunoglobulin M to induce
proliferation of peripheral blood B cells.

Sequence 840 BP; 266 A; 185 C; 175 G; 214 T; 0 other;

Query Match 98.8%; Score 776.4; DB 20; Length 840;

Best local similarity 99.2%; Pred. No. 8.4e-214; Indels 0; Gaps 0;

Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ATGATCGAAACATACCAAACTTCTCCGATCTGCGGCACTGACCTGCCATCAGC 60

Db 46 ATGATCGAAACATACCAAACTTCTCCGATCTGCGGCACTGACCTGCCATCAGC 105

Qy 61 ATGAAATTTTATGATTTTATCTACTGTTTCTTATCACCAGAAATGATTTGATCTG 120

Db 106 ATGAAATTTTATGATTTTATCTACTGTTTCTTATCACCAGAAATGATTTGATCTG 165

Qy 121 CTTTTCGCTGATCTTCTCATAGAAAGTTGACAAAGATGAAGATGAAGATCTTCAT 180

Db 166 CTTTTCGCTGATCTTCTCATAGAAAGTTGACAAAGATGAAGATGAAGATCTTCAT 225

Qy 181 GAAGATTTTATTCATGAAGAAAGATACAGATGCAACAGAGAAAGATCTTCATCC 240

Db 226 GAAGATTTTATTCATGAAGAAAGATACAGATGCAACAGAGAAAGATCTTCATCC 285

Qy 241 TTACTGAACCTGTGAGAGATTAAGCAAGTTGAAGCTTTGTGAAGATATATGTTA 300

Db 286 TTACTGAACCTGTGAGAGATTAAGCAAGTTGAAGCTTTGTGAAGATATATGTTA 345

Qy 301 AACAAAG 360

Db 346 AACAAAG 405

Qy 361 CAATTTGGGACATGTCATTAAGTGGCCAGAGATGAAGAAACATCTGTGTTACAGTGG 420

Db 406 CAATTTGGGACATGTCATTAAGTGGCCAGAGATGAAGAAACATCTGTGTTACAGTGG 465

Qy 421 GCTGAAAAGGATATCTACACATGAGCAACAACCTTGATACCTTGGAAAAATGGAAACAG 480

Db 466 GCTGAAAAGGATATCTACACATGAGCAACAACCTTGATACCTTGGAAAAATGGAAACAG 525

Qy 481 CTGACCGTTAAAGACAAAGATCTATATATATGATGACCAAGTACCTTGGTCCAT 540

Db 526 CTGACCGTTAAAGACAAAGATCTATATATATGATGACCAAGTACCTTGGTCCAT 585

Qy 541 CGGAAAGCTTGAGTCAAGCTTCATTTATAGCCAGCTTCTGCTTAAAGTCCCGGTAGA 600

Db 586 CGGAAAGCTTGAGTCAAGCTTCATTTATAGCCAGCTTCTGCTTAAAGTCCCGGTAGA 645

Qy 601 TTGAGAGAAATCTTATCTGAGAGCTGCAAAATACCAAGTCCGAGCAACCTTGCGGGCA 660

Db 646 TTGAGAGAAATCTTATCTGAGAGCTGCAAAATACCAAGTCCGAGCAACCTTGCGGGCA 705

Qy 661 CAATCATTTCACTTGGAGAGATTTGAATTGCAACAGGTGCTTGCTGTTGTCAT 720

Db 706 CAATCATTTCACTTGGAGAGATTTGAATTGCAACAGGTGCTTGCTGTTGTCAT 765

Qy 721 GTGACTGATCAAGCAAGTGGAGCATGAGCATGAGCTTCAAGTCTTGGCTTACCA 780

Db 766 GTGACTGATCAAGCAAGTGGAGCATGAGCATGAGCTTCAAGTCTTGGCTTACCA 825

Qy 781 CTCTGA 786

Db 826 CTCTGA 831

RESULT 11

AAFS5539
ID AAFS5539 standard; DNA; 879 BP.

AAFS5539;

29-MAY-2001 (first entry)

Nucleotide sequence of human gp39 protein, a CD40 ligand.

gp39; CD40 ligand; osteoblast cell death; apoptosis; bone loss;

osteoporosis; osteonecrosis; inflammatory arthritis; estrogen loss;

ovariectomy; hysterectomy; lupus nephritis; Takayasu's arteritis;

Wegener's granulomatosis; nephritis; myositis; scleroderma;

thrombocytopenia; asthma; lung disease; cancer; ss.

Homo sapiens.

Key Location/Qualifiers

CD5 22..807

W0200116180-A2.

08-MAR-2001.

24-AUG-2000; 2000WO-US23276.

27-AUG-1999; 99US-0151250.

(TEXA) UNIV TEXAS SYSTEM.

Ahuja SS, Bonewald LF;

XX Sequence 1816 BP; 520 A; 461 C; 343 G; 492 T; 0 other;

Query Match 98.8%; Score 776.4; DB 21; Length 1816;

Best Local Similarity 99.2%; Pred. No. 1.2e-213;

Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACAAACCAACTCTCCCGATCTGCGGCACTGAGTCCCATCAGC 60
 DB 40 ATGATCGAAACATACAAACCAACTCTCCCGATCTGCGGCACTGAGTCCCATCAGC 99
 QY 61 ATGAAATTTTATGATTTACTTACTCTTTTCTTTATCCCAATATGATGATCTG 120
 DB 100 ATGAAATTTTATGATTTACTTACTCTTTTCTTTATCCCAATATGATGATCTG 159
 QY 121 CTTTTCCTGCTGATCTTCAATAGAGTTGCAAGATAGATAGATAGATCTTCAT 180
 DB 160 CTTTTCCTGCTGATCTTCAATAGAGTTGCAAGATAGATAGATAGATCTTCAT 219
 QY 181 GAAGATTTTATTCATGAAAGATGATGATGATGATGATGATGATGATGATGATGAT 240
 DB 220 GAAGATTTTATTCATGAAAGATGATGATGATGATGATGATGATGATGATGATGAT 279
 QY 241 TTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
 DB 280 TTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 339
 QY 301 AACAAAG 360
 DB 340 AACAAAG 399
 QY 361 CAATATGCGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 DB 400 CAATATGCGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 459
 QY 421 GCTGAAAGAGATCTACCATGAGCAACTTGTGTAACCTGGAATATGGAATACAG 480
 DB 460 GCTGAAAGAGATCTACCATGAGCAACTTGTGTAACCTGGAATATGGAATACAG 519
 QY 481 CTGACCGTTAAAGACAGAGCTTATATATCTATGCTCCCAAGTCACTTGTTCAT 540
 DB 520 CTGACCGTTAAAGACAGAGCTTATATATCTATGCTCCCAAGTCACTTGTTCAT 579
 QY 541 CGGAAAGCTTGAAGTCAAGTCCATTATACCAAGCTGCTTAAATCCCCCGGTAGA 600
 DB 580 CGGAAAGCTTGAAGTCAAGTCCATTATACCAAGCTGCTTAAATCCCCCGGTAGA 639
 QY 601 TTGAGAGAAATCTTACTCAGAGCTGCAATACCAAGTTCGCGCAAACTTTCGCGCA 660
 DB 640 TTGAGAGAAATCTTACTCAGAGCTGCAATACCAAGTTCGCGCAAACTTTCGCGCA 699
 QY 661 CAATCATTCCTTGGAGAGATTTGAATTTGAACAGAGTCTTGGTTCAT 720
 DB 700 CAATCATTCCTTGGAGAGATTTGAATTTGAACAGAGTCTTGGTTCAT 759
 QY 721 GTGACTGATCCAGCCAGTGAACCATGCACTGCTTCAAGCTTTGGCTTACTCAAA 780
 DB 760 GTGACTGATCCAGCCAGTGAACCATGCACTGCTTCAAGCTTTGGCTTACTCAAA 819
 QY 781 CTCTGA 786
 DB 820 CTCTGA 825

RESULT 13

AAS86571 ID AAS86571 standard; cDNA; 1816 BP.

XX AC AAS86571;

XX DT 13-FEB-2002 (first entry)

DE DNA encoding novel human diagnostic protein #23375.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KM food supplement; medical imaging; diagnostic; genetic disorder; ss.
 XX Homo sapiens.

XX MO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001MO-US08631.

XX 31-MAR-2000; 2000US-0540217.

XX 23-AUG-2000; 2000US-0649167.

XX (HYSSE-) HYSSE INC.

XX Dtmnac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

XX P-PSDB; ABG2384.

PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity

XX Claim 1; SEQ ID No 22375; 103bp; English.

XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (II) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human
 CC diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 1816 BP; 520 A; 461 C; 343 G; 492 T; 0 other;

Query Match 98.8%; Score 776.4; DB 23; Length 1816;

Best Local Similarity 99.2%; Pred. No. 1.2e-213;

Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACAAACCAACTCTCCCGATCTGCGGCACTGAGTCCCATCAGC 60
 DB 40 ATGATCGAAACATACAAACCAACTCTCCCGATCTGCGGCACTGAGTCCCATCAGC 99
 QY 61 ATGAAATTTTATGATTTACTTACTCTTTTCTTTATCCCAATATGATGATCTG 120
 DB 100 ATGAAATTTTATGATTTACTTACTCTTTTCTTTATCCCAATATGATGATCTG 159
 QY 121 CTTTTCCTGCTGATCTTCAATAGAGTTGCAAGATAGATAGATAGATCTTCAT 180
 DB 160 CTTTTCCTGCTGATCTTCAATAGAGTTGCAAGATAGATAGATAGATCTTCAT 219
 QY 181 GAAGATTTTATTCATGAAAGATGATGATGATGATGATGATGATGATGATGATGAT 240
 DB 220 GAAGATTTTATTCATGAAAGATGATGATGATGATGATGATGATGATGATGATGAT 279

QY 241 TTACTGAACCTGTGAGAGATTAAAGCAGTTTGAAGCTTTGTGAGAGATTAATGTTA 300
 DB 280 TTACTGAACCTGTGAGAGATTAAAGCAGTTTGAAGCTTTGTGAGAGATTAATGTTA 339
 QY 301 AACAAAGAGAGACGAG 360
 DB 340 AACAAAGAGAGACGAG 399
 QY 361 CAAATTCGCGCAGATCTCTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
 DB 400 CAAATTCGCGCAGATCTCTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 459
 QY 421 GCTGAAAAGAGATCTACACCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
 DB 460 GCTGAAAAGAGATCTACACCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 519
 QY 481 CTGACCGTTAAAGACAG 540
 DB 520 CTGACCGTTAAAGACAG 579
 QY 541 CGGAGAGCTTCGAGTCAAGCTTCATTTATGCGAGCTTCCTGCTAAAGTCCCGGTGA 600
 DB 580 CGGAGAGCTTCGAGTCAAGCTTCATTTATGCGAGCTTCCTGCTAAAGTCCCGGTGA 639
 QY 601 TTCGAGAGATCTTACTCAGAGCTGCAAAATACCAAGTCCCGCAAACTTGGCGGCA 660
 DB 640 TTCGAGAGATCTTACTCAGAGCTGCAAAATACCAAGTCCCGCAAACTTGGCGGCA 699
 QY 661 CAATTCATTCACCTTGGAGAGAGATTTGATTTGCAACCAAGTCTTCGGTGTTCAT 720
 DB 700 CAATTCATTCACCTTGGAGAGAGATTTGATTTGCAACCAAGTCTTCGGTGTTCAT 759
 QY 721 GTGACTGATCCAGCCAGTGCATGAGCAGTGCCTTACGCTTGGCTTACTCAAA 780
 DB 760 GTGACTGATCCAGCCAGTGCATGAGCAGTGCCTTACGCTTGGCTTACTCAAA 819
 QY 781 CTCTGA 786
 DB 820 CTCTGA 825
 RESULT 14
 AAT58122
 ID AAT58122 standard; cDNA; 840 BP.
 AC AAT58122;
 XX 19-SEP-1997 (first entry)
 DE Human CD40L mutein coding sequence, with substitution at codon 194.
 XX CD40 ligand; membrane bound glycoprotein; B cell proliferation;
 KM antibody secretion; immunoglobulin E; cytokine; mutein; ss.
 OS Homo sapiens.
 XX Synthetic.
 XX Key Location/Qualifiers
 FT CDS 46..831
 FT /product= a
 FT /note= "Encodes CD40L mutein
 FT position 194 is replaced by Trp, Ser, Asp
 FT or Lys"
 FT mutation 625..627
 FT /tag= b
 FT /note= "Wild-type TGC (Cys) codon is mutated to
 FT a codon for Trp, Ser, Asp or Lys"
 XX MO640918-A2.
 XX 19-DEC-1996.
 XX

PF 06-JUN-1996; 96MO-US09632.
 XX
 PR 07-JUN-1995; 95US-0484624.
 PR 07-JUN-1995; 95US-0477733.
 XX
 PA (IMMUNEX CORP.
 PI Armitage RJ, Fanslow WC, Gibson MG, Spriggs MK,
 PI Striavaan S;
 XX
 DR WPI: 1997-052320/05.
 DR P-PSDB; AAM09113, AAM09114, AAM09115, AAM09116.
 XX
 PT New CD40 ligand mutein with higher CD40 affinity than native ligand
 PT - useful in binding assays, and for therapy of disorders and
 PT diseases involving low levels of B cells and antibody secretion
 XX
 PS Claim 1, Page -; 31pp; English.
 CC This sequence covers cDNA coding for human CD40L mutein polypeptides
 CC in which the wild-type Cys residue at position 194 has been
 CC replaced by a Trp, Ser, Asp or Lys residue. The muteins, designated
 CC C194W, C194S, C194D and C194K, are functional analogues of CD40L
 CC and as such are useful to induce B cell proliferation and antibody
 CC secretion. This property may be used to treat disorders associated
 CC with low levels of B cells or antibody secretion. The new CD40L
 CC muteins have a higher binding affinity for human CD40 than native
 CC CD40L and can be used in binding assays.
 CC (Note: The present sequence does not appear in the specification;
 CC it has been produced by modifying the wild-type coding sequence,
 CC which is given on pages 19-20, at codon 194).
 XX
 SQ Sequence 840 BP; 266 A; 184 C; 174 G; 213 T; 3 other;
 Query Match 98.4%; Score 773.4; DB 18; Length 840;
 Best Local Similarity 98.9%; Pred. No. 6.1e-213;
 Matches 777; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 QY 1 ATGATGAAACATACACCAAACTTCTCCGAGCTGCGGCACTGGACATGCGATAGC 60
 DB 46 ATGATGAAACATACACCAAACTTCTCCGAGCTGCGGCACTGGACATGCGATAGC 105
 QY 61 ATGAAATTTTATGATTTTACTTACTCTGTTTCTTATCAACCAAAATGATGATCTGTG 120
 DB 106 ATGAAATTTTATGATTTTACTTACTCTGTTTCTTATCAACCAAAATGATGATCTGTG 165
 QY 121 CTTTTCCTGCTATCTTCAATAGAGTTGCAAGATTAAGATTAAGATTAAGATCTTCAAT 180
 DB 166 CTTTTCCTGCTATCTTCAATAGAGTTGCAAGATTAAGATTAAGATTAAGATCTTCAAT 225
 QY 181 GAAATTTTGTATTCATGAAAGATACAGATGCAACAGAGAGAAATCTTATCC 240
 DB 226 GAAATTTTGTATTCATGAAAGATACAGATGCAACAGAGAGAAATCTTATCC 285
 QY 241 TTACTGACCTGTGAGAGATTAAAGCAGTTTGAAGCTTTGTGAGAGATTAATGTTA 300
 DB 286 TTACTGACCTGTGAGAGATTAAAGCAGTTTGAAGCTTTGTGAGAGATTAATGTTA 345
 QY 301 AACAAAGAGAGACGAG 360
 DB 346 AACAAAGAGAGACGAG 405
 QY 361 CAAATTCGCGCAGATCTCTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
 DB 406 CAAATTCGCGCAGATCTCTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 465
 QY 421 GCTGAAAAGAGATCTACACCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
 DB 466 GCTGAAAAGAGATCTACACCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 525
 QY 481 CTGACCGTTAAAGACAG 540
 DB 526 CTGACCGTTAAAGACAG 585

Qy 541 CCGGAAGCTTCGAGTCAAGCTTCATTATAGCCAGCCCTGCTTAAGATCCCGGTTAG 600
 Db 586 CCGGAAGCTTCGAGTCAAGCTTCATTATAGCCAGCCCTGCTTAAGATCCCGGTTAG 645
 Qy 601 TTGGAGAGATCTTACTGAGAGCTGCAATATCCAGTTCCGCAACCTTGGGGGCA 660
 Db 646 TTGGAGAGATCTTACTGAGAGCTGCAATATCCAGTTCCGCAACCTTGGGGGCA 705
 Qy 661 CAATCCATTCCTGGGAGAGATTTGAAATTTGCAACAGAGTCTCGGTGTGTTGCAAT 720
 Db 706 CAATCCATTCCTGGGAGAGATTTGAAATTTGCAACAGAGTCTCGGTGTGTTGCAAT 765
 Qy 721 GNGACTGATCCAGCCAGTGAAGCCATGAGCACTGGCTTCACTGCTTGGCTTACTCAA 780
 Db 766 GNGACTGATCCAGCCAGTGAAGCCATGAGCACTGGCTTCACTGCTTGGCTTACTCAA 825
 Qy 781 CTCTGA 786
 Db 826 CTCTGA 831

RESULT 15

ID AA057984 standard; DNA; 840 BP.

AC AA057984;

DT 20-AUG-1994 (first entry)

DE Genomic sequence of human gp39.

KM gp39; T-cell antigen; CD40 ligand; B-cell proliferation;

KW B-cell differentiation; ss.

OS Homo sapiens.

FT Key Location/Qualifiers

FT CDS 22..807

FN EF585943-A.

PD 09-MAR-1994.

PF 03-SEP-1993; 93EP-0114153.

PR 04-SEP-1992; 92US-0940605.

PA (BRIM) BRISTOL-MYERS SQUIBB CO.

PI Aruffo AA, Hollenbaugh D, Ledbetter JA, Aruffo A;

DR WPI: 1994-076264/10.

DR P-PSDB; AAR59548.

PT New nucleic acid encoding human gp39 T cell antigen - which is a
 PT ligand for the CD40 receptor, causing proliferation and
 PT differentiation of B cells and some cancer cells

PS Claim 1; Fig 1; 39pp; English.

CC The complete nucleic acid sequence of human gp39 (hgp39) protein
 CC (corresp. to cDNA) and the complete AA sequence of hgp39 are
 CC presented in AA057984 and AAR59548 respectively and contd. in plasmid
 CC CDW8-hgp39, deposited with the ATCC as E. coli, CDW8 MC1061/p3-hgp39
 CC and assigned accession No. 69050. The human T cell antigen gp39 is a
 CC ligand for the CD40 receptor. Soluble gp39 may be produced using the
 CC expression vector CD8-gp39.

SQ Sequence 840 BP; 263 A; 180 C; 183 G; 214 T; 0 other;

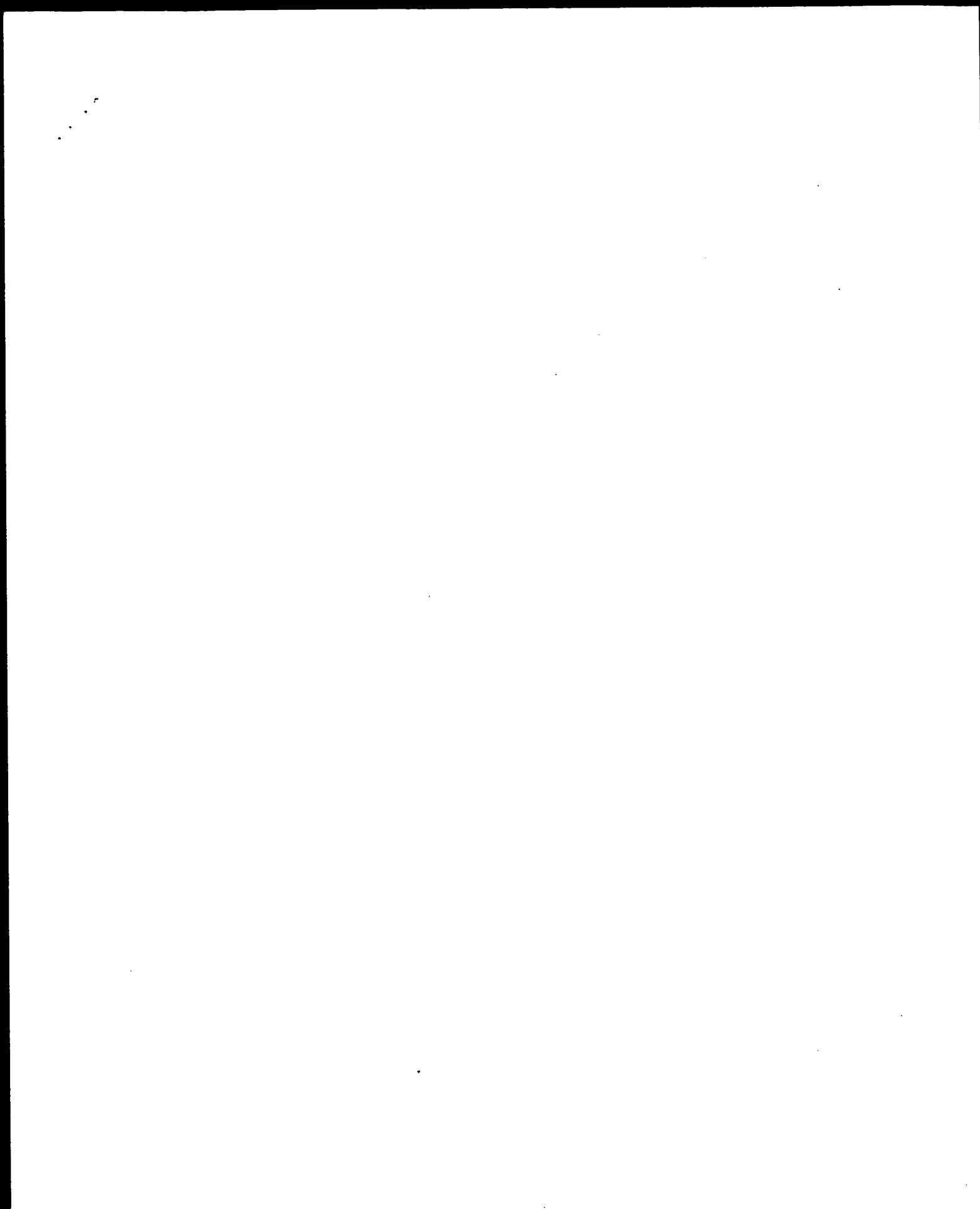
Query Match

98.4%; Score 773.2; DB 15; Length 840;

Best Local Similarity 99.0%; Pred. No. 7e-213;
 Matches 778; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 ATGATCGAAGATACCAACCAACCTTCTCCCGATCTGCGGCGCACTGACATGAC 60
 Db 22 ATGATCGAAGATACCAACCAACCTTCTCCCGATCTGCGGCGCACTGACATGAC 81
 Qy 61 ATGAAATTTTATGATTTTATTTATTTCTTTCTTTCTTTATATCCCAATGATGAT 120
 Db 82 ATGAAATTTTATGATTTTATTTATTTCTTTCTTTCTTTATATCCCAATGATGAT 141
 Qy 121 CTTTTTGTGTATCTTCAATGAGGTGAGACAGATGAGATGAGATGAGATGAGAT 180
 Db 142 CTTTTTGTGTATCTTCAATGAGGTGAGACAGATGAGATGAGATGAGATGAGAT 201
 Qy 181 GAAAGTTTGTATTTATGAAACGATACAGATGAGATGAGATGAGATGAGATGAGAT 240
 Db 202 GAAAGTTTGTATTTATGAAACGATACAGATGAGATGAGATGAGATGAGATGAGAT 261
 Qy 241 TTACTGAACTGTGAGAGATTTAAAGCCAGTTTGAAGCTTGTGAGATATATGTTA 300
 Db 262 TTACTGAACTGTGAGAGATTTAAAGCCAGTTTGAAGCTTGTGAGATATATGTTA 321
 Qy 301 AACCAAG 360
 Db 322 AACCAAG 381
 Qy 361 CAATTTGGGCAATGCTATTAAGTGAAGCCAGCAATTAACATCTGTGTATGAGTGG 420
 Db 382 CAATTTGGGCAATGCTATTAAGTGAAGCCAGCAATTAACATCTGTGTATGAGTGG 441
 Qy 421 GCTGAAAAAGATATATCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
 Db 442 GCTGAAAAAGATATATCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 501
 Qy 481 CTGACCGTTAAAGACAG 540
 Db 502 CTGACCGTTAAAGACAG 561
 Qy 541 CCGGAAGCTTCGAGTCAAGCTTCATTATAGCCAGCCCTGCTTAAGATCCCGGTTAG 600
 Db 562 CCGGAAGCTTCGAGTCAAGCTTCATTATAGCCAGCCCTGCTTAAGATCCCGGTTAG 621
 Qy 601 TTGGAGAGATCTTACTGAGAGCTGCAATATCCAGTTCCGCAACCTTGGGGGCA 660
 Db 622 TTGGAGAGATCTTACTGAGAGCTGCAATATCCAGTTCCGCAACCTTGGGGGCA 681
 Qy 661 CAATCCATTCCTGGGAGAGATTTGAAATTTGCAACAGAGTCTCGGTGTGTTGCAAT 720
 Db 682 CAATCCATTCCTGGGAGAGATTTGAAATTTGCAACAGAGTCTCGGTGTGTTGCAAT 741
 Qy 721 GNGACTGATCCAGCCAGTGAAGCCATGAGCACTGGCTTCACTGCTTGGCTTACTCAA 780
 Db 742 GNGACTGATCCAGCCAGTGAAGCCATGAGCACTGGCTTCACTGCTTGGCTTACTCAA 801
 Qy 781 CTCTGA 786
 Db 802 CTCTGA 807

Search completed: March 8, 2003, 22:12:46
 Job time: 166.215 secs



Qy	181	GAAGATTTTGATTCATGAAAACGATCAAGATGCACAACAGAGAAAGATCTTATTC	240
Db	193	GAAGATTTTGATTCATTAATAAAGCTAAAGATGCACAAAGAGAAAGATCTTATTC	252
Qy	241	TTATCGAATCTGTGAGAGATTTAAAGCATTTGAAAGCTTTGTGAAGATTTATGTGA	300
Db	253	TTGTGAAATCTGTGAGAGATGAAAGCATTTGAAAGCTTTGTGAAGATTTATGTGA	312
Qy	301	AACAAAGAGAGACGAAGAAAGAAACAGCTTTGAATGCAAAAAGGTGATCGAATCT	360
Db	313	AACAAAGAGAGAGAAAGAAAGAAACAGCTTTGAATGCAAAAAGGTGATGAGATCT	369
Qy	361	CAAAATGGGGACATGTCATTAAGTAGGCCGCGAGTAAACCATCTGTGTACAGTGG	420
Db	370	CAAAATGGGGACACGTTGTAAAGCAACCATGATAGCAGATCTGTTCTACAGTGG	429
Qy	421	GCTGAAAAGGATCTACACCATGAGCAACACTTGTGTAACCTGGAAAATGGAAACAG	480
Db	430	GCCAGAAAAGGATTTATACATGAAAAGCACTTGTGTAACCTGGAAAATGGAAACAG	489
Qy	481	CTGACCGTTAAACACACAGGACATATTATCTGATGCCCAAGTCACTTGTGTCAT	540
Db	490	CTACCGTTAAACACAGGAGACTATTATGTCTACACCAAGTCACTTGTGTCAT	549
Qy	541	CGGAAAGCTTGAAGTCAAGCTCATTTATAGCAAGCTCTTGCGTAAATGCTCCCGGTGA	600
Db	550	CGGAAAGCTTGAAGTCAAGCCCATTTACGTGGGCTCTGCGTGAAGCCACAGCATTTGA	609
Qy	601	TTGAGAGATCTTACTACAGAGCTGCAATATCCACAGTTCGGCAAACTTGGCGGCA	660
Db	610	TCGAGAGATCTTACTCAAGGGGCAAAATCCACAGTTCCTCCAGCTTTGGCGGAG	669
Qy	661	CAATCATTTCACTTGGGAGAGATTTGAATGCAACAGAGTGTCTCGGTGTTGTCAAT	720
Db	670	CAATCTGTTCACCTTGGGCGGAGGTTGAATTAACAAGCTGGGTCTCTGTGTGTCAAC	729
Qy	721	GTCAGATCAACACCAAGTAGAGCATGACATGCGCTTACGCTCTTTGGCTTACTCAA	780
Db	730	GTCAGAGAGCAACCAAGTAGATCCACAGAGTGGCTTCTACTTTTGGCTTACTCAA	789
Qy	781	CTCTGA 786	
Db	790	CTCTGA 795	

```

RESULT 2
US-09-875-453-9
Sequence 9, Application US/09875453
Publication No. US20030027320A1
GENERAL INFORMATION:
APPLICANT: Kim, Jungshuh P.
APPLICANT: Starr, Douglas B.
APPLICANT: Tam, Albert W.
APPLICANT: Laurance, Megan E.
APPLICANT: Michelotti, Emil F.
APPLICANT: Velligan, Mark D.
APPLICANT: Laitour, Derek R.
APPLICANT: Thomas, Rita L.
APPLICANT: Kongsachith, Ana
APPLICANT: Sheppard, Liana T.
APPLICANT: Lim, Moon Young
APPLICANT: Bruce, Thomas W.
TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
FILE REFERENCE: 4600-0135.30
CURRENT APPLICATION NUMBER: US/09/875,453
CURRENT FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 60/209,549
PRIOR FILING DATE: 2000-06-06
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 1
LENGTH: 2395

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-875-453-9

Query Match      18.84; Score 147.8; DB 9; Length 2395;
Best Local Similarity 88.04; Pred. No. 9.8e-31;
Matches 161; Conservative 0; Mismatches 22; Indels 0; Gaps

QY      1  ATGATCGAAACATACACCAAACTTCTCCCGATCTCGGCGCATGGACTCCCATACG  60
Db      1939  ATGATCGAAACATACACCAAACTTCTCCCGATCTCGGCGCATGGACTCCCATACG  1998

QY      61  ATGAAAATTTTATGATATTTACTACGTTTTCCCTATACACCAATATTTGATCTGTG  120
Db      1999  ATGAAAATTTTATGATATTTACTACTGTTTTTCTATACACCAAGATATTTGGGTGCGA  2058

QY      121  CTTTTCGTGTGATCTTCATAGAGGTGGACAGATAGAGATGAAAAGGATCTTCAT  180
Db      2059  CTTTTCGTGTGATCTTCATAGAGGCTGGACAGAGTAAGATGAACCAAGCTTTTAT  2118

QY      181  GAA 183
Db      2119  TAA 2121

```

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RESULT 3
US-09-960-352-11218
; Sequence 11218, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FTE REFERENCE: 16511.006/37-21(1028)C
; CURRENT APPLICATION NUMBER: US/09/960.352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 11218
; LENGTH: 424
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 48-LIB3058-026-Q1-K1-D12
US-09-960-352-11218

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QY      68 TTTTANGTATTACTTACTGCTTTTCTTACACCCAAATGATTGATCTGCGCTTTG 127
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Db      30 TTTTATTTTTTTTTTTTTTTTTTTTTTTTTTTTGGTTTTTTTTTTTTTTTTTTTT 89
      |||
QY      128 CTGTGATCTTCATGAAAGTTGACAGATGAAAGATGAAAGATCTTCAGAGATT 187
      |||
Db      90 TTTTTTTTTTTAAATTTAAAAATAAAAATAAAAATAAAAATAAAAATAAAAAT 149
      |||
QY      188 TTGTATTCATGAAACGATACAGATGCACACAGAGAAAGATCCTTCTCTTACGA 247
      |||
Db      150 TAAAAAAATTTAAAAATTTAAAAATTTAAAAATTTAAAAATTTTGTTTAAA 209
      |||
QY      248 ACTGT---GAGAGATTAAAGCCAGTGAAGCTTTGTGAGAGATATATGTTAAAC 303
      |||
Db      210 AATATAAAAAAATTTATTTATAGAAATTTTAAAAAAATAAAAAAGAGATTTTAA 269
      |||
QY      304 AAAGGAGACGAAAGAAAGAAAACAGCTTGAAATGCAAAAGGTGATCGAATCTCTAA 363
      |||
Db      270 AAAAAAAATGAAATTTTAAAAAGAAATTAAGTTATTTAAAAAAGATATAAAA 329
      |||
QY      364 ATT 366
      |||

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Db 330 ATT 332

RESULT 4
US-09-960-352-2222

Sequence 2222, Application US/09960352
Patent No. US2002013139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Byatt, John C.
APPLICANT: Machialagan, Naappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 2222
LENGTH: 418
TYPE: DNA
ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 10-LIB3058-040-Q1-K1-C5
US-09-960-352-2222

Query Match 4.8%; Score 37.6; DB 10; Length 418;
Best Local Similarity 47.5%; Pred. No. 0.84;
Matches 112; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

Qy 238 TCCTTAAGTGAAGGAGATTAAACCGCTTTGAAGCTTTGTGAAGATATATATG 297
Db 6 TCTATCTTTACAGCTGTGTAATTAATTTGGATGATGCGTCCAGAAAGCAGATA 65
Qy 298 TTAACAAAGAGAGACGAGAAAGAAACAGCTTTGAATGCAAAAGATATCAGAT 357
Db 66 CTCAAGTATGTGATACCACTACAGAAACAGAGAACTTCAAGAGCAATCAGAG 125
Qy 358 CCTCAATTCGGCAGATCTCATATAGTGAAGCCAGAGTAACACATCTGTATCAG 417
Db 126 CAGTATGCAAGGAGGAGATGCGAGGGCTGCCCTGAAAGAAACTGCTGGGCTCAG 185
Qy 418 TGGGCTGAAAAGATACATACATGACATGAGCAACATCTGTACCCGAAATG 473
Db 186 CAGAAATCTTACGTAAGACAAAGAAACAAACAGAAACACTGCGAAATG 241

RESULT 5
US-09-938-842A-3756

Sequence 3756, Application US/09938842A
Patent No. US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCLIP300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 3756
LENGTH: 2000
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-3756

Query Match 4.8%; Score 37.6; DB 9; Length 2000;
Best Local Similarity 49.5%; Pred. No. 1.7; 99; Indels 0; Gaps 0;
Matches 97; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

Qy 67 ATTTTATGATTTACTACTGTTTCCCTTATCCCAATGATGATGCTGCTTT 126
Db 818 ATGTGTAGTGTGCTTTTCTTTTCCCAAGTATTTATCTGTAACTATA 877
Qy 127 GCTGTATCTTCAATAGAGTTGAGCAAGATAGAAAGATCTTCAAGAT 186
Db 878 CTTCATATGATATATATGATGATGATGATGATGATGATGATGAT 937
Qy 187 TTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 246
Db 938 TAAGTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 997
Qy 247 AACTGAGAGATTA 262
Db 998 AAATTTAGTTTATA 1013

RESULT 6

US-09-790-988-1/C
Sequence 1, Application US/09790988
Patent No. US20020127687A1
GENERAL INFORMATION:
APPLICANT: SHIGENOBU SHUJI
APPLICANT: WATANABE, HIDEMI
APPLICANT: SATOKI, YOSHIYUKI
TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
FILE REFERENCE: 081356/0159
CURRENT APPLICATION NUMBER: US/09/790,988
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: JP2000-107160
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 1
LENGTH: 640681
TYPE: DNA
ORGANISM: Buchnera sp.
US-09-790-988-1

Query Match 4.8%; Score 37.4; DB 10; Length 640681;
Best Local Similarity 52.2%; Pred. No. 27;
Matches 83; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

Qy 64 AAAATTTTATGATTTACTACTGTTTCCCTTATCCCAATGATGATGCTGCTT 123
Db 574504 AATATTTTATGATTTTAAATGATTTTATTTTAAATTAATTAATTTTCTTA 574445
Qy 124 TTTGCTGTATCTTCAATGAGTTGAGCAAGATGAAAGATCTTCAAGAA 183
Db 574444 TTTTCAAGCTGTGATCTCTGCGCAAGAGATGCTGAGCATGTGATTAACGA 574385
Qy 184 GATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 222
Db 574384 ATTATCTTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 574346

RESULT 7

US-09-938-842A-3149/C
Sequence 3149, Application US/09938842A
Patent No. US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCLIP300-3
US-09-938-842A-3756

;; CURRENT APPLICATION NUMBER: US/09/938,842A
;; PRIOR FILING DATE: 2001-08-24
;; PRIOR APPLICATION NUMBER: US 60/227,866
;; PRIOR FILING DATE: 2000-08-24
;; PRIOR APPLICATION NUMBER: US 60/264,647
;; PRIOR FILING DATE: 2001-01-16
;; PRIOR APPLICATION NUMBER: US 60/300,111
;; PRIOR FILING DATE: 2001-06-22
;; NUMBER OF SEQ ID NOS: 5379
;; SEQ ID NO 3149
;; LENGTH: 1352
;; TYPE: DNA
;; ORGANISM: Arabidopsis thaliana
US-09-938-842A-3149

Query Match
Best Local Similarity 4.7%; Score 37; DB 9; Length 1352;
Matches 91; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 71 TTAGTATTTACTTACTGTTTCTTATCCCAATGATGATGCTGCTTTTGGCTG 130
DB 372 TTAGTGTGATTTCTTGTGTAATGACCAATTTGTTGATCACAACACTTATG 313
QY 131 TGTATCTTATAGAGCTTGACAGATGAGATGAAAGATCTTCATGAAGTTTG 190
DB 312 CTAATTAAGAAACAGGTTTCTACACTGACAAATAAATTAACGCAAAAGATATTA 253
QY 191 TATTCATGAAAACATACAGATGACACAGAGAAAGATCTTCATGAACT 250
DB 252 GCAAGTAAGCATTAATTTGATCATATATMACAAAGAAAGCTTATGATCTTATTAAGCA 193
QY 251 G 251
DB 192 G 192

RESULT 8
US-09-938-842A-5264
;; Sequence 5264 Application US/09938842A
;; Patent No. US20020160378A1
;; GENERAL INFORMATION:
;; APPLICANT: Harper, Jeff
;; APPLICANT: Krepes, Joel
;; APPLICANT: Wang, Xun
;; APPLICANT: Zhu, Tong
;; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
;; FILE REFERENCE: SAME, AND METHODS OF USE
;; CURRENT APPLICATION NUMBER: US/09/938,842A
;; PRIOR FILING DATE: 2001-08-24
;; PRIOR APPLICATION NUMBER: US 60/227,866
;; PRIOR FILING DATE: 2000-08-24
;; PRIOR APPLICATION NUMBER: US 60/264,647
;; PRIOR FILING DATE: 2001-01-16
;; PRIOR APPLICATION NUMBER: US 60/300,111
;; NUMBER OF SEQ ID NOS: 5379
;; SEQ ID NO 5264
;; LENGTH: 1352
;; TYPE: DNA
;; ORGANISM: Arabidopsis thaliana
US-09-938-842A-5264

Query Match
Best Local Similarity 4.7%; Score 37; DB 9; Length 1352;
Matches 91; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 71 TTAGTATTTACTTACTGTTTCTTATCCCAATGATGATGCTGCTTTTGGCTG 130
DB 981 TTAGTGTGATTTCTTGTGTAATGACCAATTTGTTGATCACAACACTTATG 1040
QY 131 TGTATCTTATAGAGCTTGACAGATGAGATGAAAGATCTTCATGAAGTTTG 190

DB 1041 CTAATTAAGAAACAGGTTTCTACACTGAGAACAAAAAATTAACGCAAAAGATATTA 1100
QY 191 TATTCATGAAAACATACAGAGATGCAACACAGAGAAAGATCTTCATGAACT 250
DB 1101 GCAAGTAAGCATTAATTTGATCATATTAACAAAGAAAGCTTATGATCTTATTAAGCA 1160
QY 251 G 251
DB 1161 G 1161

RESULT 9
US-09-874-470-5/c
;; Sequence 5 Application US/09874470
;; Patent No. US20020071842A1
;; GENERAL INFORMATION:
;; APPLICANT: Gumperz, Jenny E
;; APPLICANT: Brenner, Michael B
;; APPLICANT: Behar, Samuel M
;; TITLE OF INVENTION: Soluble CD1 Compositions and Uses Thereof
;; FILE REFERENCE: B00801/70212
;; CURRENT APPLICATION NUMBER: US/09/874,470
;; PRIOR FILING DATE: 2001-06-05
;; PRIOR APPLICATION NUMBER: US 60/209,416
;; PRIOR FILING DATE: 2000-06-05
;; NUMBER OF SEQ ID NOS: 12
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 5
;; LENGTH: 10351
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-874-470-5

Query Match
Best Local Similarity 4.6%; Score 35.8; DB 10; Length 10351;
Matches 106; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

QY 164 ATGAAGAAATCTTCATGAGATTTGTATTCATGAAACATACAGATGCAACACAG 223
DB 6762 ATGAAGAAATGACAAAGAGAAAGAAACAAATTTAAGCATTAAGATTTCAAGGGA 6703
QY 224 GAGAAATCTTATCTTACTGAACTGAGAGATTAAGCCAGTTGAAGGCTTGG 283
DB 6702 GAAATTTGCTGGAAATCATATGAGACTAGAGCTTACTGCGCAAGGGAAGAAATTT 6643
QY 284 TGAAGATATATGTTAAACAAAGAGACGAGAAAGAAACAGCTTGAATGCAAA 343
DB 6642 TGGGGAAGAAATTTGAAGATATTAAGATCTTGAATTAATGAAGAAAGTGTGA 6583
QY 344 AAGGTATCAGATCTCAAAATTTGCGGCACTGTCATTAAGTGA 386
DB 6582 GATGGGAAGGCTATCAGAGAGATGAGAAATTTGCTCATTAATTA 6540

RESULT 10
US-09-960-352-10262/c
;; Sequence 10262 Application US/09960352
;; Patent No. US20020137139A1
;; GENERAL INFORMATION:
;; APPLICANT: Warren, Wesley C.
;; APPLICANT: Tao, Nengbing
;; APPLICANT: Byatt, John C.
;; APPLICANT: Mathialagan, Nagappan
;; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
;; FILE REFERENCE: 16511, 006/37-21(10298)C
;; CURRENT APPLICATION NUMBER: US/09/960,352
;; PRIOR FILING DATE: 2001-09-24
;; NUMBER OF SEQ ID NOS: 15112
;; SEQ ID NO 10262
;; LENGTH: 451
;; TYPE: DNA
;; ORGANISM: Bos taurus

OTHER INFORMATION: Clone ID: 44-LIB3058-031-Q1-K1-C8
US-09-960-352-10262

Query Match 4.3%; Score 34; DB 10; Length 451;
Best Local Similarity 47.6%; Pred. No. 8.5;
Matches 100; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

Qy 155 AGATGAGATGAAAGAACTTCATGAAATTTGTTTCATGAAACGATACGAGAT 214
Db 419 AAAAAAAAAAAAAAAAAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAT 360
Qy 215 GCAACACAGAAAGATCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 274
Db 359 AAAGA 300
Qy 275 AAGCTTTGAGAGATATATGTTAAACAAGAGAGAGAGAGAGAGAGAGAGAG 334
Db 299 AAAG 240
Qy 335 AATGCAAAAGCTGATCAGATCTCTCAA 364
Db 239 AAAAAAAAAAAAAAAAAAGAAAAAAAAA 210

RESULT 11
US-10-063-547-95
Sequence 95, Application US/10063547
Publication No. US20020182638A1

GENERAL INFORMATION:

APPLICANT: Eaton, Dan L.
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Matanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/063,547
CURRENT FILING DATE: 2002-05-02
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 95
LENGTH: 1073
TYPE: DNA
ORGANISM: Homo Sapien
US-10-063-547-95

Query Match 4.3%; Score 34; DB 9; Length 1073;
Best Local Similarity 54.9%; Pred. No. 13;
Matches 67; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

Qy 224 GAGAAAGATCCTTATCTTACTGAACTGTGAGAGATTAAAGCCAGTTTGAAGCTTTG 283
Db 939 GAAATATACATTAATGCTGCTGATGATGATGATGATGATGATGATGATGATG 998
Qy 284 TGAAGATATATGTTAAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 343
Db 999 AAAGA 1058
Qy 344 AA 345
Db 1059 AA 1060

RESULT 12
US-10-174-590-305
Sequence 305, Application US/10174590
Publication No. US20030008352A1
GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Ulan
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C42
CURRENT APPLICATION NUMBER: US/10/174,590
CURRENT FILING DATE: 2002-06-18
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 305
LENGTH: 1073
TYPE: DNA
ORGANISM: Homo Sapien
US-10-174-590-305

Query Match 4.3%; Score 34; DB 9; Length 1073;
Best Local Similarity 54.9%; Pred. No. 13;
Matches 67; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

Qy 224 GAGAAAGATCCTTATCTTACTGAACTGTGAGAGATTAAAGCCAGTTTGAAGCTTTG 283
Db 939 GAAATATACATTAATGCTGCTGATGATGATGATGATGATGATGATGATGATG 998
Qy 284 TGAAGATATATGTTAAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 343
Db 999 AAAGA 1058
Qy 344 AA 345
Db 1059 AA 1060

RESULT 13
US-10-176-758-305
Sequence 305, Application US/10176758
Publication No. US20030008353A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Ulan
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C104
CURRENT APPLICATION NUMBER: US/10/176,758
CURRENT FILING DATE: 2002-06-21
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 305
LENGTH: 1073
TYPE: DNA
ORGANISM: Homo Sapien
US-10-176-758-305

Query Match 4.3%; Score 34; DB 9; Length 1073;
Best Local Similarity 54.9%; Pred. No. 13;
Matches 67; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

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OM nucleic - nucleic search, using sw model

Run on: March 8, 2003, 21:49:58 ; Search time 33.6448 Seconds
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7164.491 Million cell updates/sec

Title: US-08-982-272-4

Perfect score: 786

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Total number of hits satisfying chosen parameters: 882724

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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4: /cgn2_6/prodata/2/ina/6B COMB, seq: *
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SUMMARIES

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1	776.4	98.8	786	1	US-08-446-922-3
2	776.4	98.8	786	5	PCT-US93-10034-3
3	776.4	98.8	840	1	US-07-940-605A-1
4	776.4	98.8	840	1	US-08-184-422-7
5	776.4	98.8	840	1	US-08-360-923A-1
6	776.4	98.8	840	1	US-08-431-055-3
7	776.4	98.8	840	2	US-08-630-096-1
8	776.4	98.8	840	2	US-08-249-189-11
9	776.4	98.8	840	2	US-08-484-624A-11
10	776.4	98.8	840	2	US-08-477-733B-11
11	776.4	98.8	840	3	US-08-763-995-1
12	776.4	98.8	840	3	US-09-088-913A-11
13	776.4	98.8	840	3	US-08-589-771B-7
14	776.4	98.8	840	4	US-08-769-819-11
15	776.4	98.8	840	4	US-08-770-974-11
16	776.4	98.8	840	4	US-08-858-197-3
17	776.4	98.8	840	4	US-08-770-981-11
18	776.4	98.8	840	4	US-09-399-106-11
19	638.2	81.2	1425	2	US-08-249-189-15
20	638.2	81.2	1425	2	US-08-484-624A-15
21	638.2	81.2	1425	2	US-08-477-733B-15
22	638.2	81.2	1425	2	US-09-088-913A-15
23	638.2	81.2	1425	4	US-08-769-819-15
24	638.2	81.2	1425	4	US-08-770-974-15
25	638.2	81.2	1425	4	US-08-770-981-15
26	638.2	81.2	1425	4	US-09-399-106-15
27	637.2	81.1	929	1	US-08-446-922-10

28	637.2	81.1	929	2	US-08-249-189-20	Sequence 20, Appl
29	637.2	81.1	929	2	US-08-484-624A-20	Sequence 20, Appl
30	637.2	81.1	929	3	US-08-477-733B-20	Sequence 20, Appl
31	637.2	81.1	929	3	US-09-088-913A-20	Sequence 20, Appl
32	637.2	81.1	929	4	US-08-769-819-20	Sequence 20, Appl
33	637.2	81.1	929	4	US-08-770-974-20	Sequence 20, Appl
34	637.2	81.1	929	4	US-08-770-981-20	Sequence 20, Appl
35	637.2	81.1	929	4	US-09-399-106-20	Sequence 20, Appl
36	571.6	72.7	783	1	US-08-446-922-5	Sequence 5, Appl
37	571.6	72.7	783	2	US-08-249-189-1	Sequence 1, Appl
38	571.6	72.7	783	2	US-08-484-624A-1	Sequence 1, Appl
39	571.6	72.7	783	2	US-08-477-733B-1	Sequence 1, Appl
40	571.6	72.7	783	3	US-09-088-913A-1	Sequence 1, Appl
41	571.6	72.7	783	3	US-08-769-819-1	Sequence 1, Appl
42	571.6	72.7	783	4	US-08-770-974-1	Sequence 1, Appl
43	571.6	72.7	783	4	US-08-770-981-1	Sequence 1, Appl
44	571.6	72.7	783	4	US-09-399-106-1	Sequence 1, Appl
45	571.6	72.7	783	5	PCT-US93-10034-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-08-446-922-3
Sequence 3, Application US/08446922
Patent No. 5716805
GENERAL INFORMATION:
APPLICANT: Spriggs, Melanie
TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSER: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: Apple Macintosh
SOFTWARE: Microsoft Word for Apple, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,922
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/107,353
FILING DATE: 08-13-93
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 1003-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 786 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHECAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Human
STRAIN: CD40-L
FEATURE:

NAME/KEY: CDS
LOCATION: 1..783
US-08-446-922-3

Query Match 98.8%; Score 776.4; DB 1; Length 786;
Best Local Similarity 99.2%; Pred. No. 2.6e-219;
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACCAACCACTTCTCCCGATCGGCGGCACTGGACCTGCACG 60
DB 1 ATGATCGAAACATACCAACCACTTCTCCCGATCGGCGGCACTGGACCTGCACG 60
QY 61 ATGAAATTTTATGATTTACTTACTGTTTTCTTATCACCCTAATGATGATCTGTG 120
DB 61 ATGAAATTTTATGATTTACTTACTGTTTTCTTATCACCCTAATGATGATGATCTGTG 120
QY 121 CTTTTCGCTGATCTCATGAAAGTTGGAAGATGAAAGATGAAATCTTCTAT 180
DB 121 CTTTTCGCTGATCTCATGAAAGTTGGAAGATGAAAGATGAAAGATGAAATCTTCTAT 180
QY 181 GAAGATTTTGTATTCATGAAACGATACAGATGCAACAGAGAAAGATCTTATCC 240
DB 181 GAAGATTTTGTATTCATGAAACGATACAGATGCAACAGAGAAAGATCTTATCC 240
QY 241 TTAAGTAACTGTGAGAGATTTAAAGCAAGTTGAAGCTTTGTGAAGATATATGTTA 300
DB 241 TTAAGTAACTGTGAGAGATTTAAAGCAAGTTGAAGCTTTGTGAAGATATATGTTA 300
QY 301 AACAAAGAGAGACGAAAGAAAGAAACGCTTTGAAATGCAAAAGGATGATCAATCT 360
DB 301 AACAAAGAGAGACGAAAGAAAGAAACGCTTTGAAATGCAAAAGGATGATCAATCT 360
QY 361 CAATTCGCGACATGTCATTAAGTGGCGAGCAAGTAAACAATCTGTGTACAGTGG 420
DB 361 CAATTCGCGACATGTCATTAAGTGGCGAGCAAGTAAACAATCTGTGTACAGTGG 420
QY 421 GCTGAAAAAGATCTACACCACTGAGCAACATCTTGTAACCTTGAAAAATGGAAAAAG 480
DB 421 GCTGAAAAAGATCTACACCACTGAGCAACATCTTGTAACCTTGAAAAATGGAAAAAG 480
QY 481 CTGACCGTTAAAGACAGAAAGTCTATATATCTATGCCCAAGTACCTTCTGTCCAT 540
DB 481 CTGACCGTTAAAGACAGAAAGTCTATATATCTATGCCCAAGTACCTTCTGTCCAT 540
QY 541 CGGGAAGCTTGAGTCAAGCTCTATTAAGCAAGCTCTGCTAAAGTCCCGGGTAA 600
DB 541 CGGGAAGCTTGAGTCAAGCTCTATTAAGCAAGCTCTGCTAAAGTCCCGGGTAA 600
QY 601 TTGAGAGATCTTACTCAAGCTGCAAAATACCAAGTTCCGCAAACTTTCGCGGCA 660
DB 601 TTGAGAGATCTTACTCAAGCTGCAAAATACCAAGTTCCGCAAACTTTCGCGGCA 660
QY 661 CAATCATTCTCTGAGAGAGATTTGAAATGCAACAGAGCTGCGGTGTTGTCAT 720
DB 661 CAATCATTCTCTGAGAGAGATTTGAAATGCAACAGAGCTGCGGTGTTGTCAT 720
QY 721 GTGACTGATCCAAAGCCAAAGTGAAGCCATGCACTGGCTTCACTCTTGTACTCAAA 780
DB 721 GTGACTGATCCAAAGCCAAAGTGAAGCCATGCACTGGCTTCACTCTTGTACTCAAA 780
QY 781 CTCTGA 786
DB 781 CTCTGA 786

RESULT 2
PCT-US93-10034-3
Sequence 3, Application PC/TUS9310034
GENERAL INFORMATION:
APPLICANT: Spriggs, Melanie
APPLICANT: Srinivasan, Subhashini
TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric
TITLE OF INVENTION: Proteins

NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10034
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 1003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 786 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Human
STRAIN: CDA0-L
FEATURE:
NAME/KEY: CDS
LOCATION: 1..783
PCT-US93-10034-3
Query Match 98.8%; Score 776.4; DB 5; Length 786;
Best Local Similarity 99.2%; Pred. No. 2.6e-219;
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACCAACCACTTCTCCCGATCGGCGGCACTGGACCTGCACG 60
DB 1 ATGATCGAAACATACCAACCACTTCTCCCGATCGGCGGCACTGGACCTGCACG 60
QY 61 ATGAAATTTTATGATTTACTTACTGTTTTCTTATCACCCTAATGATGATCTGTG 120
DB 61 ATGAAATTTTATGATTTACTTACTGTTTTCTTATCACCCTAATGATGATGATCTGTG 120
QY 121 CTTTTCGCTGATCTCATGAAAGTTGGAAGATGAAAGATGAAATCTTCTAT 180
DB 121 CTTTTCGCTGATCTCATGAAAGTTGGAAGATGAAAGATGAAAGATGAAATCTTCTAT 180
QY 181 GAAGATTTTGTATTCATGAAACGATACAGATGCAACAGAGAAAGATCTTATCC 240
DB 181 GAAGATTTTGTATTCATGAAACGATACAGATGCAACAGAGAAAGATCTTATCC 240
QY 241 TTAAGTAACTGTGAGAGATTTAAAGCAAGTTGAAGCTTTGTGAAGATATATGTTA 300
DB 241 TTAAGTAACTGTGAGAGATTTAAAGCAAGTTGAAGCTTTGTGAAGATATATGTTA 300
QY 301 AACAAAGAGAGACGAAAGAAAGAAACGCTTTGAAATGCAAAAGGATGATCAATCT 360
DB 301 AACAAAGAGAGACGAAAGAAAGAAACGCTTTGAAATGCAAAAGGATGATCAATCT 360
QY 361 CAATTCGCGACATGTCATTAAGTGGCGAGCAAGTAAACAATCTGTGTACAGTGG 420
DB 361 CAATTCGCGACATGTCATTAAGTGGCGAGCAAGTAAACAATCTGTGTACAGTGG 420

APPLICANT: MIDMER, MICHAEL
TITLE OF INVENTION: DETECTION AND TREATMENT OF MUTATIONS
TITLE OF INVENTION: IN A CD40 LIGAND GENE
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.1
SOFTWARE: MS Word for Apple 5.1, Version a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/184,422
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/009,258
FILING DATE: 01/22/93
ATTORNEY/AGENT INFORMATION:
NAME: PERKINS, PATRICIA ANNE
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2810-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46..831
US-08-184-422-7
Query Match 98.8%; Score 776.4; DB 1; Length 840;
Best Local Similarity 99.2%; Pred. No. 2,6e-219;
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACCAACCACTCTCCCGGATCGGGCGCACTGCACTGCCCATCAGC 60
DB 46 ATGATCGAAACATACCAACCACTCTCCCGGATCGGGCGCACTGCACTGCCCATCAGC 105
QY 61 ATGAAATTTTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 120
DB 106 ATGAAATTTTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 165
QY 121 CTTTGGCTGTATCTTCATAGAGGTGAGCAAGTGAAGATGAAGATCTTCAT 180
DB 166 CTTTGGCTGTATCTTCATAGAGGTGAGCAAGTGAAGATGAAGATCTTCAT 225
QY 181 GAAGATTTTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 240
DB 226 GAAGATTTTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 285
QY 241 TTAAGCACTGTGAGGATTAAGGCTTTGAGAGGATTAATTAATTAATTAATTAAT 300
DB 286 TTAAGCACTGTGAGGATTAAGGCTTTGAGAGGATTAATTAATTAATTAATTAAT 345
QY 301 AACAAAGAGAGCAAGAAAGAAAGCACTTTGAATGCAAAAAGGTGATCAGAACTCT 360

DB 346 AACAAAGAGAGCAAGAAAGAAAGCACTTTGAATGCAAAAAGGTGATCAGAACTCT 405
QY 361 CAATTTGGCGCATGTCATTAAGTGGCGAGCAAGTAAACAACTGTGTACAGTGG 420
DB 406 CAATTTGGCGCATGTCATTAAGTGGCGAGCAAGTAAACAACTGTGTACAGTGG 465
QY 421 GCTGAAAAGATPACTACCATTAAGCAACCTTGTAACTGTGAAAATGGAACAG 480
DB 466 GCTGAAAAGATPACTACCATTAAGCAACCTTGTAACTGTGAAAATGGAACAG 525
QY 481 CTAGCGTTTAAAGCAAGGACTCTATTATATATGATCCCAAGTACCTTCTGTTCAAT 540
DB 526 CTAGCGTTTAAAGCAAGGACTCTATTATATATGATCCCAAGTACCTTCTGTTCAAT 585
QY 541 CGGAGAGCTTGAGTCAAGCTCATTATTAAGCAAGCTTGTCTTAAAGTCCCGGTAGA 600
DB 586 CGGAGAGCTTGAGTCAAGCTCATTATTAAGCAAGCTTGTCTTAAAGTCCCGGTAGA 645
QY 601 TTGAGAGGAATCTTACTAGAGCTGCAAAATACCAAGTTCGCGCAACCTTGCGGCA 660
DB 646 TTGAGAGGAATCTTACTAGAGCTGCAAAATACCAAGTTCGCGCAACCTTGCGGCA 705
QY 661 CAATCACTTCACTTGGAGAGATTTGATTTGATTCACCAAGTCTTGGTGTTCAT 720
DB 706 CAATCACTTCACTTGGAGAGATTTGATTTGATTCACCAAGTCTTGGTGTTCAT 765
QY 721 GTGACGATTCAGGCAAGGAGTGAAGTGAATGCAACAGGTCCTTGGTGTTCAT 780
DB 766 GTGACGATTCAGGCAAGGAGTGAAGTGAATGCAACAGGTCCTTGGTGTTCAT 825
QY 781 CTCTGA 786
DB 826 CTCTGA 831
RESULT 5
US-08-360-923A-1
Sequence 1, Application US/08360923A
Patent No. 567492
GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: FANSLAW, WILLIAM
APPLICANT: LONGO, DAN L.
APPLICANT: MURPHY, WILLIAM
TITLE OF INVENTION: METHOD OF PREVENTING OR TREATING
TITLE OF INVENTION: DISEASE CHARACTERIZED BY NEOPLASTIC CELLS
TITLE OF INVENTION: EXPRESSING CD40
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: Apple Macintosh System 7.1
SOFTWARE: Microsoft Word for Macintosh, Version #5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,923A
FILING DATE: December 21, 1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USN 08/172,664
FILING DATE: December 23, 1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2818-A

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 587-0430
 TELEFAX: (206) 233-0644
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 840 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 IMMEDIATE SOURCE:
 CLONE: CD40-L
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 46..831
 US-08-360-923A-1

Query Match 98.8%; Score 776.4; DB 1; Length 840;
 Best Local Similarity 99.2%; Pred. No. 2.6e-219;
 Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGATGAAACATACACCAACTCTCCCGATCTGCGGCACTGGAATGCCATCAGC 60
 DB 46 ATGATGAAACATACACCAACTCTCCCGATCTGCGGCACTGGAATGCCATCAGC 105
 QY 61 ATGAAATTTTATGATTTATTTACTTCTTTTCTTATCACCCAAATGATGATCTGTG 120
 DB 106 ATGAAATTTTATGATTTATTTACTTCTTTTCTTATCACCCAAATGATGATGATCTGTG 165
 QY 121 CTTTGTCTGTATCTTATAGAGGTGACAAATAGATGAAGATCTTCAT 180
 DB 166 CTTTGTCTGTATCTTATAGAGGTGACAAATAGATGAAGATCTTCAT 225
 QY 181 GAAGATTTTATGATTTATTTACTTCTTTTCTTATCACCCAAATGATGATCTGTG 240
 DB 226 GAAGATTTTATGATTTATTTACTTCTTTTCTTATCACCCAAATGATGATGATCTGTG 285
 QY 241 TTAAGTATGATGATTTAAAGCCAGTTTGAAGCTTTGTGAAGATATATGTTA 300
 DB 286 TTAAGTATGATGATTTAAAGCCAGTTTGAAGCTTTGTGAAGATATATGTTA 345
 QY 301 AACAAAG 360
 DB 346 AACAAAG 405
 QY 361 CAATTTGCGGACATGTCATAGTGAAGCCAGTAAACAAATCTGTGTTACAGTGG 420
 DB 406 CAATTTGCGGACATGTCATAGTGAAGCCAGTAAACAAATCTGTGTTACAGTGG 465
 QY 421 GGTGAAAGAGATCTACCAATGAGCAACATTTGTTAAGCTTTGTTAAGAGAGAG 480
 DB 466 GGTGAAAGAGATCTACCAATGAGCAACATTTGTTAAGCTTTGTTAAGAGAGAG 525
 QY 481 CTGACCGTTAAAGACAGAGATCTATTATATCTATCCCAAGTCACTTGTTCAT 540
 DB 526 CTGACCGTTAAAGACAGAGATCTATTATATCTATCCCAAGTCACTTGTTCAT 585
 QY 541 CGGGAAGCTTGAGTCAAGCTCAATTTATAGCAAGCTTGTCTTAAATGCTTGTGTA 600
 DB 586 CGGGAAGCTTGAGTCAAGCTCAATTTATAGCAAGCTTGTCTTAAATGCTTGTGTA 645
 QY 601 TTGAGAGATCTTACTCAGAGCTGCAATACCAAGTTCCGCAAACTTGGGAGCA 660
 DB 646 TTGAGAGATCTTACTCAGAGCTGCAATACCAAGTTCCGCAAACTTGGGAGCA 705
 QY 661 CAATTCATCTTGGAGAGATTTGAAATTTGCAACCAAGTCTTGGTGTTCAT 720
 DB 706 CAATTCATCTTGGAGAGATTTGAAATTTGCAACCAAGTCTTGGTGTTCAT 765

QY 721 GTGACGATCCAAAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
 DB 766 GTGACGATCCAAAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 825
 QY 781 CTCTGA 786
 DB 826 CTCTGA 831

RESULT 6

US-08-431-055-3
 Sequence 3, Application US/08431055
 Patent No. 5817516

GENERAL INFORMATION:
 APPLICANT: KEHRY, MERILYN R
 APPLICANT: CASTLE, BRIAN E
 TITLE OF INVENTION: METHODS FOR PROLIFERATING AND
 TITLE OF INVENTION: DIFFERENTIATING B CELLS, AND USES THEREOF
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
 STREET: 100 NEW YORK AVE. N.W. SUITE 600
 CITY: WASHINGTON
 STATE: D.C.
 ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/431,055
 FILING DATE: 28-APR-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/234,580
 FILING DATE: 28-APR-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: MILLMAN, ROBERT A
 REGISTRATION NUMBER: 36,217

REFERENCE/DOCKET NUMBER: 1011.1030000/RAM
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 371-2600
 TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
 LENGTH: 840 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 22..807
 US-08-431-055-3

Query Match 98.8%; Score 776.4; DB 1; Length 840;
 Best Local Similarity 99.2%; Pred. No. 2.6e-219;
 Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACCAACTCTCCCGATCTGCGGCACTGGAATGCCATCAGC 60
 DB 22 ATGATCGAAACATACCAACTCTCCCGATCTGCGGCACTGGAATGCCATCAGC 81
 QY 61 ATGAAATTTTATGATTTATTTACTTCTTTTCTTATCACCCAAATGATGATCTGTG 120
 DB 82 ATGAAATTTTATGATTTATTTACTTCTTTTCTTATCACCCAAATGATGATCTGTG 141
 QY 121 CTTTGTCTGTATCTTATAGAGGTGACAAATAGATGAAGATCTTCAT 180
 DB 142 CTTTGTCTGTATCTTATAGAGGTGACAAATAGATGAAGATCTTCAT 201
 QY 181 GAAGATTTTATGATTTATTTACTTCTTTTCTTATCACCCAAATGATGATCTGTG 240

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Db 202 GAGATTTTGTATTCATGAAACGATACAGATGACACAGAGAAATCTTATCC 261
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Qy 241 TTAAGAACTGTGAGAGATTTAAAGCCAGTTTGAAGCTTTGAGATATATGTTA 300
|||
Db 262 TTAAGAACTGTGAGAGATTTAAAGCCAGTTTGAAGCTTTGAGATATATGTTA 321
|||
Qy 301 AACAAAGAGAGACGAGAAAGAAACAGCTTTGAATGCAAAAAGGATGATGAAATCCT 360
|||
Db 322 AACAAAGAGAGACGAGAAAGAAACAGCTTTGAATGCAAAAAGGATGATGAAATCCT 381
|||
Qy 361 CAAATTGGCGCACTGTCTAATGAGAGCCGACGATGAAACAACTCTGTGTTCAGTGG 420
|||
Db 382 CAAATTGGCGCACTGTCTAATGAGAGCCGACGATGAAACAACTCTGTGTTCAGTGG 441
|||
Qy 421 GCTGAAAAGGATCTACACCATGAGCAACAGTTGTAACCTGGAATAATGGAAACAG 480
|||
Db 442 GCTGAAAAGGATCTACACCATGAGCAACAGTTGTAACCTGGAATAATGGAAACAG 501
|||
Qy 481 CTGACCGTTAAAGACAGAGACTTATATATCTATGCCAAAGTCACTTCTGTTCAT 540
|||
Db 502 CTGACCGTTAAAGACAGAGACTTATATATCTATGCCAAAGTCACTTCTGTTCAT 561
|||
Qy 541 CGGAGAGCTTGAGTCAAGCTCTATTTAGCAGAGCTCTGCTTAAAGTCCCGGTAGA 600
|||
Db 562 CGGAGAGCTTGAGTCAAGCTCTATTTAGCAGAGCTCTGCTTAAAGTCCCGGTAGA 621
|||
Qy 601 TTGAGAGAACTTCTACAGAGCTGCAATATCCACAGATCCGCAAACTTCCGGGCA 660
|||
Db 622 TTGAGAGAACTTCTACAGAGCTGCAATATCCACAGATCCGCAAACTTCCGGGCA 681
|||
Qy 661 CAATCATCTTCTGGAGAGATTTGGAATGCAACAGAGTCTGCTGCTTGTTCAT 720
|||
Db 682 CAATCATCTTCTGGAGAGATTTGGAATGCAACAGAGTCTGCTGCTTGTTCAT 741
|||
Qy 721 GTGACTGATCCAGCCAGTGAAGCCATGAGCCATGAGCCATGAGCCATGAGCCAT 780
|||
Db 742 GTGACTGATCCAGCCAGTGAAGCCATGAGCCATGAGCCATGAGCCATGAGCCAT 801
|||
Qy 781 CTCTGA 786
|||
Db 802 CTCTGA 807
|||
RESULT 7
US-08-690-096-1
; Sequence 1, Application US/08690096
; Patent No. 5945513
; GENERAL INFORMATION:
; APPLICANT: ARUPPO, ALEJANDRO
; APPLICANT: HOLLENBAUGH, DIANE
; APPLICANT: LEDBETTER, JEFFREY A.
; TITLE OF INVENTION: SOLUBLE LIGANDS FOR CP40
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/690,096
; FILING DATE: 31-Jul-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/940,605
; FILING DATE: 04-SEP-1992

```

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; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 5624-184
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 840 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 22..807
; US-08-690-096-1
;
Query Match 98.8%; Score 776.4; DB 2; Length 840;
Best Local Similarity 99.2%; Pred. No. 2.ee-219;
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
;
Qy 1 ATGATCGAAACATACACCAAACTTCTCCCGATCTGCGGCACTGAGCTGCCATGAGC 60
Db 22 ATGATCGAAACATACACCAAACTTCTCCCGATCTGCGGCACTGAGCTGCCATGAGC 81
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Qy 61 ATGAAATTTTATGATTTTATCTTACTGTTTCTTATCAACCAATGATGATGATCTGTG 120
Db 82 ATGAAATTTTATGATTTTATCTTACTGTTTCTTATCAACCAATGATGATGATGATG 141
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Qy 121 CTTTTCGTGTATCTTCATAGAGGTTGACCAAGATAGAGATGAAAGATCTTCAT 180
Db 142 CTTTTCGTGTATCTTCATAGAGGTTGACCAAGATAGAGATGAAAGATCTTCAT 201
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Qy 181 GAAATTTTGTATGATGAAAGAGATGACATGACATGACATGACATGACATGACATG 240
Db 202 GAAATTTTGTATGATGAAAGAGATGACATGACATGACATGACATGACATGACATG 261
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Qy 241 TTAAGAACTGTGAGAGATTTAAAGCCAGTTTGAAGCTTTGGAAGATATATGTTA 300
Db 262 TTAAGAACTGTGAGAGATTTAAAGCCAGTTTGAAGCTTTGGAAGATATATGTTA 321
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Qy 301 AACAAAGAGAGACGAGAAAGAAACAGCTTTGAATGCAAAAAGGATGATGAAATCCT 360
Db 322 AACAAAGAGAGACGAGAAAGAAACAGCTTTGAATGCAAAAAGGATGATGAAATCCT 381
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Qy 361 CAAATTGGCGCACTGTCTAATGAGAGCCGACGATGAAACAACTCTGTGTTCAGTGG 420
Db 382 CAAATTGGCGCACTGTCTAATGAGAGCCGACGATGAAACAACTCTGTGTTCAGTGG 441
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Qy 421 GCTGAAAAGGATCTACACCATGAGCAACAGTTGTAACCTGGAATAATGGAAACAG 480
Db 442 GCTGAAAAGGATCTACACCATGAGCAACAGTTGTAACCTGGAATAATGGAAACAG 501
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Qy 481 CTGACCGTTAAAGACAGAGACTTATATATCTATGCCAAAGTCACTTCTGTTCAT 540
Db 502 CTGACCGTTAAAGACAGAGACTTATATATCTATGCCAAAGTCACTTCTGTTCAT 561
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Qy 541 CGGAGAGCTTGAGTCAAGCTCTATTTAGCAGAGCTCTGCTTAAAGTCCCGGTAGA 600
Db 562 CGGAGAGCTTGAGTCAAGCTCTATTTAGCAGAGCTCTGCTTAAAGTCCCGGTAGA 621
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Qy 601 TTGAGAGAACTTCTACAGAGCTGCAATATCCACAGATCCGCAAACTTCCGGGCA 660
Db 622 TTGAGAGAACTTCTACAGAGCTGCAATATCCACAGATCCGCAAACTTCCGGGCA 681
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Qy 661 CAAATTCATCTGAGAGAGATTTGGAATGCAACAGAGTCTGCTGCTTGTTCAT 720
Db 682 CAAATTCATCTGAGAGAGATTTGGAATGCAACAGAGTCTGCTGCTTGTTCAT 741
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Qy 721 GTGACTGATCCAGCCAGTGAAGCCATGAGCCATGAGCCATGAGCCATGAGCCAT 780

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Db 742 GTGACTGATCCAAAGCCAAAGTGAAGCATGGCACTGGCTTCAAGTCTTTGGCTTACTCAA 801
 Qy 781 CTCCTGA 786
 Db 802 CTCCTGA 807

RESULT 8

US-08-249-189-11
 ; Sequence 11, Application US/08249189
 ; Patent No. 5961974

GENERAL INFORMATION:

APPLICANT: ARMITAGE, RICHARD
 APPLICANT: FANSLAW, WILLIAM
 APPLICANT: SPRIGGS, MELANIE
 APPLICANT: SRINIVASAN, SUBHASHINI
 APPLICANT: GIBSON, MARYLOU
 TITLE OF INVENTION: NOVEL CYTOKINE
 NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: IMMUNEX CORPORATION
 STREET: 51 UNIVERSITY STREET
 CITY: SEATTLE
 STATE: WASHINGTON
 COUNTRY: USA
 ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: Apple Operating System 7.1
 SOFTWARE: Microsoft Word for Apple, version 5.1a
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/249,189
 FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/969,703
 FILING DATE: October 23, 1992

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/805,723
 FILING DATE: December 5, 1991

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/783,707
 FILING DATE: October 25, 1991

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia A.
 REGISTRATION NUMBER: 34,693
 REFERENCE/DOCKET NUMBER: 2802-C
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 2065870430
 TELEFAX: 2065870606

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 840 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHEICAL: NO
 ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

IMMEDIATE SOURCE:

CLONE: CD40-L
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 46..831

US-08-249-189-11

Query Match 98.8%; Score 776.4; DB 2; Length 840;
 Best Local Similarity 99.2%; Pred. No. 2,6e-219;
 Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy	1	ATGATCGAAATATCAACCAAACTTCTCCCGATCTGGCGGCGCATGACCTCCCATCAGC	60
Db	46	ATGATCGAAATATCAACCAAACTTCTCCCGATCTGGCGGCGCATGACCTCCCATCAGC	105
Qy	61	ATGAAATTTTATGATTTTATTTTCTGTTTCTTATCAACCAATGATGATCTGTG	120
Db	106	ATGAAATTTTATGATTTTATTTTCTGTTTCTTATCAACCAATGATGATGATCTGTG	165
Qy	121	CTTTTGTGTGATCTTCATAGAGGTGGCAAGATGAGATGAGAAAGAAATCTTAT	180
Db	166	CTTTTGTGTGATCTTCATAGAGGTGGCAAGATGAGATGAGAAAGAAATCTTAT	225
Qy	181	GAAGATTTTGTATTCATGAAAACGATACAGATGACACACAGAGAAAGATCTTATCC	240
Db	226	GAAGATTTTGTATTCATGAAAACGATACAGATGACACACAGAGAAAGATCTTATCC	285
Qy	241	TTACTGAATGTGAGAGATTTAAAGCAAGTTTGAAGCTTGTGAAGATATATGTTA	300
Db	286	TTACTGAATGTGAGAGATTTAAAGCAAGTTTGAAGCTTGTGAAGATATATGTTA	345
Qy	301	AACAAAG	360
Db	346	AACAAAG	405
Qy	361	CAATTTGGGCGCATGCTATTAAGTGGCGAGAGAGAGAGAGAGAGAGAGAGAGAG	420
Db	406	CAATTTGGGCGCATGCTATTAAGTGGCGAGAGAGAGAGAGAGAGAGAGAGAGAG	465
Qy	421	GCTGAAAAGAGATATCAACCAAGTGAAGCAAACTTGTATCCCTGGAAAATGGAAACAG	480
Db	466	GCTGAAAAGAGATATCAACCAAGTGAAGCAAACTTGTATCCCTGGAAAATGGAAACAG	525
Qy	481	CTGACCGTTAAAGACAGAGACTATTTATATCTATGCCAAGTCACTTGTGTTCAAT	540
Db	526	CTGACCGTTAAAGACAGAGACTATTTATATCTATGCCAAGTCACTTGTGTTCAAT	585
Qy	541	CGGAAAGCTTCAGTCAAGCTCCATTTATGAGCCAGCTCCCTGAAAGTCCCGGTGGA	600
Db	586	CGGAAAGCTTCAGTCAAGCTCCATTTATGAGCCAGCTCCCTGAAAGTCCCGGTGGA	645
Qy	601	TTGAGAGAAATCTTACTCAAGCTGCAAAATACCAAGTCCGCAAACTTGGCGGCA	660
Db	646	TTGAGAGAAATCTTACTCAAGCTGCAAAATACCAAGTCCGCAAACTTGGCGGCA	705
Qy	661	CAATCAATCACTTGGAGAGATTTTGAATTTGCAACAGGTCTTGGTGTTCAT	720
Db	706	CAATCAATCACTTGGAGAGATTTTGAATTTGCAACAGGTCTTGGTGTTCAT	765
Qy	721	GTGACTGATCCAAAGCCAAAGTGAAGCATGGCTTCAAGTCTTGGCTTACTCAA	780
Db	766	GTGACTGATCCAAAGCCAAAGTGAAGCATGGCTTCAAGTCTTGGCTTACTCAA	825
Qy	781	CTCCTGA 786	
Db	826	CTCCTGA 831	

RESULT 9

US-08-484-624A-11
 ; Sequence 11, Application US/08484624A
 ; Patent No. 5962406

GENERAL INFORMATION:

APPLICANT: ARMITAGE, RICHARD
 APPLICANT: FANSLAW, WILLIAM
 APPLICANT: SPRIGGS, MELANIE
 APPLICANT: SRINIVASAN, SUBHASHINI
 APPLICANT: GIBSON, MARYLOU
 APPLICANT: MORRIS, ARVIA E.
 APPLICANT: MCGREW, JEFFERY

```

TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNE CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,624A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/477,733
FILING DATE: June 07, 1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,703
FILING DATE: October 23, 1992
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/805,723
FILING DATE: December 5, 1991
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/783,707
FILING DATE: October 25, 1991
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870606
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHEetical: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46..831
US-08-484-624A-11
Query Match 98.8% Score 776.4; DB 2; Length 840;
Best Local Similarity 99.2%; Pred. No. 2.6e-219;
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 ATGATCGAAGACATCAACCAAACTTCTCCCGATCTGCGGCACTGACCTGCCATCAGC 60
DB 46 ATGATCGAAGACATCAACCAAACTTCTCCCGATCTGCGGCACTGACCTGCCATCAGC 105
QY 61 ATGAAATTTTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 120
DB 106 ATGAAATTTTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 165
QY 121 CTTTTCCTGTATCTTCAATGAAAGTTGACAAAGATGAAGATGAAGATCTTCAT 180

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DB 166 CTTTTCCTGTATCTTCAATGAAAGTTGACAAAGATGAAGATGAAGATCTTCAT 225
QY 181 GAAGATTTGATTCATGAAAGACATTAAGATGACCAACAGAGAAAGATCTTATCC 240
DB 226 GAAGATTTGATTCATGAAAGACATTAAGATGACCAACAGAGAAAGATCTTATCC 285
QY 241 TTACTGACCTGTGAGAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
DB 286 TTACTGACCTGTGAGAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 345
QY 301 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
DB 346 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 405
QY 361 CAAATTCGCGCATGATCATTAAGTACGCGCAGCGTAAACAAATCTGTGTACAGTGG 420
DB 406 CAAATTCGCGCATGATCATTAAGTACGCGCAGCGTAAACAAATCTGTGTACAGTGG 465
QY 421 GCTGAAAAGATTAATCAACATGACCAAACTTGGTAACTCGGAAAATGGGAAACAG 480
DB 466 GCTGAAAAGATTAATCAACATGACCAAACTTGGTAACTCGGAAAATGGGAAACAG 525
QY 481 CTGACCGTTAAAGACAAAGACCTCTATTAATTAATTAATTAATTAATTAATTAATTA 540
DB 526 CTGACCGTTAAAGACAAAGACCTCTATTAATTAATTAATTAATTAATTAATTAATTA 585
QY 541 CCGGAGAGCTTCAGTCAAGCTCCATTTAAGCAGCCTCTGCTTAAAGTCCCGGATGA 600
DB 586 CCGGAGAGCTTCAGTCAAGCTCCATTTAAGCAGCCTCTGCTTAAAGTCCCGGATGA 645
QY 601 TTGAGAGAAATTTTACTGAGAGCTGCAAAATCCCAAGCTTCCGAAACCTTGGGGGCA 660
DB 646 TTGAGAGAAATTTTACTGAGAGCTGCAAAATCCCAAGCTTCCGAAACCTTGGGGGCA 705
QY 661 CAATCAATCACTTGGAGAGAGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 720
DB 706 CAATCAATCACTTGGAGAGAGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 765
QY 721 GTGACGATTCAGAGCAAGTACGACATGACATGCGCTTACGCTTGGCTTACTCAAA 780
DB 766 GTGACGATTCAGAGCAAGTACGACATGACATGCGCTTACGCTTGGCTTACTCAAA 825
QY 781 CTCTGA 786
DB 826 CTCTGA 831
RESULT 10
US-08-477-733B-11
Sequence 11, Application US/08477733B
Patent No. 5981724
GENERAL INFORMATION:
APPLICANT: ARMSTRONG, RICHARD
APPLICANT: FANSLAW, WILLIAM
APPLICANT: SPRIGGS, MELANIE
APPLICANT: SRINIVASAN, SUBHASHINI
APPLICANT: GIBSON, MARYLOU
APPLICANT: MORRIS, ARVIA E.
APPLICANT: MCGREW, JEFFERY
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNE CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1

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;; CURRENT APPLICATION DATA:
 ;; APPLICATION NUMBER: US/08/477,733B
 ;; FILING DATE: June 07, 1995
 ;; CLASSIFICATION: 435

;; PRIOR APPLICATION DATA:
 ;; APPLICATION NUMBER: 08/249,189
 ;; FILING DATE: May 24, 1994
 ;; CLASSIFICATION: 435

;; PRIOR APPLICATION DATA:
 ;; APPLICATION NUMBER: 07/969,703
 ;; FILING DATE: October 23, 1992
 ;; CLASSIFICATION: 435

;; PRIOR APPLICATION DATA:
 ;; APPLICATION NUMBER: 07/805,723
 ;; FILING DATE: December 5, 1991
 ;; CLASSIFICATION: 435

;; PRIOR APPLICATION DATA:
 ;; APPLICATION NUMBER: 07/783,707
 ;; FILING DATE: October 25, 1991
 ;; CLASSIFICATION: 435

;; ATTORNEY/AGENT INFORMATION:
 ;; NAME: Perkins, Patricia A.
 ;; REGISTRATION NUMBER: 34,693
 ;; REFERENCE/DOCKET NUMBER: 2802-D
 ;; TELECOMMUNICATION INFORMATION:
 ;; TELEPHONE: 2065870430
 ;; TELEFAX: 2065870606

;; INFORMATION FOR SEQ ID NO: 11:
 ;; SEQUENCE CHARACTERISTICS:
 ;; LENGTH: 840 base pairs
 ;; TYPE: nucleic acid
 ;; STRANDEDNESS: single
 ;; TOPOLOGY: linear

;; MOLECULE TYPE: CDNA
 ;; HYPOTHETICAL: NO
 ;; ANTI-SENSE: NO
 ;; ORIGINAL SOURCE:
 ;; ORGANISM: Homo sapiens
 ;; IMMEDIATE SOURCE:
 ;; CLONE: CD40-L
 ;; FEATURE:
 ;; NAME/KEY: CDS
 ;; LOCATION: 46..831
 ;; US-08-477-733B-11

Query Match 98.8%; Score 776.4; DB 2; Length 840;
 Best Local Similarity 99.2%; Pred. No. 2,6e-219;
 Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY 1 ATGATCGAACAATCAACCAAACTTCTCCCGATCTGCGGCACTGAGTCCCATCAGC 60
Db 46 ATGATCGAACAATCAACCAAACTTCTCCCGATCTGCGGCACTGAGTCCCATCAGC 105
QY 61 ATGAAAATTTTATGATTTTACTCTGTTTCTTCTTATCAACCAATGATTCATCTG 120
Db 106 ATGAAAATTTTATGATTTTACTCTGTTTCTTCTTATCAACCAATGATTCATCTG 165
QY 121 CTTTTCCTGCTGATCTTCTTCAAGAGTTGACAAAGTAAAGATGAAGAACTTCAT 180
Db 166 CTTTTCCTGCTGATCTTCTTCAAGAGTTGACAAAGTAAAGATGAAGAACTTCAT 225
QY 181 GAAGATTTTGTATTCATGAAAGCATACAGAGATGCAACAGAGAAATCTTATTC 240
Db 226 GAAGATTTTGTATTCATGAAAGCATACAGAGATGCAACAGAGAAATCTTATTC 285
QY 241 TTAAGTCTGTGAGAGATTAAGGCAAGTTGAAGCTTTGTGAAGATATATATGTTA 300
Db 286 TTAAGTCTGTGAGAGATTAAGGCAAGTTGAAGCTTTGTGAAGATATATATGTTA 345
QY 301 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Db 346 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 405

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QY 361 CAATTTGGGCAATGTCTATAGTAGAGGCGACAGAGTAAACAACTGTGTATACAGTG 420
Db 406 CAATTTGGGCAATGTCTATAGTAGAGGCGACAGAGTAAACAACTGTGTATACAGTG 465
QY 421 GCTGAAAAAGATCTACACCATGAGCAACAACCTGGTAACTGGGAAAAATGGGAAACG 480
Db 466 GCTGAAAAAGATCTACACCATGAGCAACAACCTGGTAACTGGGAAAAATGGGAAACG 525
QY 481 CTGACCTTTAAAGACAAAGACTCTATATATCTATGAGCCAAATGACCTTCTGTTCAAT 540
Db 526 CTGACCTTTAAAGACAAAGACTCTATATATCTATGAGCCAAATGACCTTCTGTTCAAT 585
QY 541 CGGAAAGCTTGAAGTCAAGCTCCATTTATAGCCAGGCTGTGCTAAAGTCCCGGTAGA 600
Db 586 CGGAAAGCTTGAAGTCAAGCTCCATTTATAGCCAGGCTGTGCTAAAGTCCCGGTAGA 645
QY 601 TTGAGAGAAATCTTACTCAGAGCTGCAAAATCCCAAGTTCCGCCAAACCTTGCGGCA 660
Db 646 TTGAGAGAAATCTTACTCAGAGCTGCAAAATCCCAAGTTCCGCCAAACCTTGCGGCA 705
QY 661 CAATCATTCACTTGGAGAGATATTTGAATTGCAACAGAGTGTGCTGCTGTTTGCAT 720
Db 706 CAATCATTCACTTGGAGAGATATTTGAATTGCAACAGAGTGTGCTGCTGTTTGCAT 765
QY 721 GTGACTGATCCAGCCAAAGTGAAGCCATGCGCATGCGCTTCAAGTCTTGTACTCAAA 780
Db 766 GTGACTGATCCAGCCAAAGTGAAGCCATGCGCATGCGCTTCAAGTCTTGTACTCAAA 825
QY 781 CTCTGA 786
Db 826 CTCTGA 831

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RESULT 11
 US-08-763-995-1
 ; Sequence 1, Application US/08763995
 ; Patent No. 6017527
 ; GENERAL INFORMATION:
 ; APPLICANT: MARASKOVSKY, EUGENE
 ; TITLE OF INVENTION: METHOD OF ACTIVATING DENDRITIC CELLS
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: IMMUNEX CORPORATION
 ; STREET: 51 UNIVERSITY STREET
 ; CITY: SEATTLE
 ; STATE: WASHINGTON
 ; COUNTRY: USA
 ; ZIP: 98101
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Power Macintosh 7200/90
 ; OPERATING SYSTEM: Apple Operating System 7.5.5
 ; SOFTWARE: Microsoft Word for Macintosh, Version #6.0.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/763,995
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: USN 08/677,762
 ; FILING DATE: 10 JUL 1996
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Perkins, Patricia A.
 ; REGISTRATION NUMBER: 34,693
 ; REFERENCE/DOCKET NUMBER: 2845-A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206)587-0430
 ; TELEFAX: (206)213-0644
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 840 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46..831
US-08-763-995-1

Query Match 98.8%; Score 776.4; DB 3; Length 840;
Best Local Similarity 99.2%; Pred. No. 2.6e-219;
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy 1 ATGATCGAAACATACAAACCAACCTTCCCGGATCTGGCGGACATGGACCTCCCATACG 60
Db 46 ATGATCGAAACATACAAACCAACCTTCCCGGATCTGGCGGACATGGACCTCCCATACG 105
Qy 61 ATGAAATTTTATGATTTTACTTACTGTTTCTTATCCCAATGATGGATCTGTG 120
Db 106 ATGAAATTTTATGATTTTACTTACTGTTTCTTATCCCAATGATGGATCTGTG 165
Qy 122 CTTTTCCTGCTGATCTTCTATGAAAGTTGGAACAATGAAAGTGAAGATCTTCAT 180
Db 166 CTTTTCCTGCTGATCTTCTATGAAAGTTGGAACAATGAAAGTGAAGATCTTCAT 225
Qy 181 GAAATTTTATGATTTTATGAAAGTTGGAACAATGAAAGTGAAGATCTTCAT 240
Db 226 GAAATTTTATGATTTTATGAAAGTTGGAACAATGAAAGTGAAGATCTTCAT 285
Qy 241 TTAATGAACTGTGAGGAGATTTAAAGCCAGTTGGAAGCTTTGGAAGATTAATGTTA 300
Db 286 TTAATGAACTGTGAGGAGATTTAAAGCCAGTTGGAAGCTTTGGAAGATTAATGTTA 345
Qy 301 AACAAAGAGAGACGAAAGAAAGAAACGCTTGAATGCAAAAAGTATCGAATCTT 360
Db 346 AACAAAGAGAGACGAAAGAAAGAAACGCTTGAATGCAAAAAGTATCGAATCTT 405
Qy 361 CAAATTTGGGACATGTCATTAAGTGGCCAGAGTAAACAATCTGTGTACAGTGG 420
Db 406 CAAATTTGGGACATGTCATTAAGTGGCCAGAGTAAACAATCTGTGTACAGTGG 465
Qy 421 GCTGAAAAAGATCTACACCTAGCAACAACCTTGTAACTGGTGAAGTGGAAAAAG 480
Db 466 GCTGAAAAAGATCTACACCTAGCAACAACCTTGTAACTGGTGAAGTGGAAAAAG 525
Qy 481 CTGACCGTTAAAGACAAAGACCTATATATCTATGCCCAAGTCACTTCTGTCAAT 540
Db 526 CTGACCGTTAAAGACAAAGACCTATATATCTATGCCCAAGTCACTTCTGTCAAT 585
Qy 541 CGGGAAGCTTGAAGTCAAGTCCATTTTAAAGCCCTCTGCTTAAGTCCCGGTTAA 600
Db 586 CGGGAAGCTTGAAGTCAAGTCCATTTTAAAGCCCTCTGCTTAAGTCCCGGTTAA 645
Qy 601 TTGAGAGAACTTACTCAGAGCTCAATATCCCAAGTTCGCCAAACCTTGGGGCA 660
Db 646 TTGAGAGAACTTACTCAGAGCTCAATATCCCAAGTTCGCCAAACCTTGGGGCA 705
Qy 661 CAATCATTTCACTGGAGAGAGATTTGAATTGGAACGAGGTGCTTGGGTTTGTCAAT 720
Db 706 CAATCATTTCACTGGAGAGAGATTTGAATTGGAACGAGGTGCTTGGGTTTGTCAAT 765
Qy 721 GTGACTGATCCAGCCAAAGTGAAGCCATGGCACTGGCTTCACTTGTGCTTAA 780
Db 766 GTGACTGATCCAGCCAAAGTGAAGCCATGGCACTGGCTTCACTTGTGCTTAA 825
Qy 781 CTCTGA 786
Db 826 CTCTGA 831
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RESULT 12
US-09-088-913A-11
Sequence 11, Application US/09088913A

Patent No. 6087329
GENERAL INFORMATION:

APPLICANT: ARMITAGE, RICHARD
APPLICANT: FANSLAW, WILLIAM

APPLICANT: SPRIGGS, MELANIE
APPLICANT: SRINIVASAN, SUBHASHINI

APPLICANT: GIBSON, MARYLOU
APPLICANT: MORRIS, ARVIA E.

APPLICANT: MCGREW, JEFFERY
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40

NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:

ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET

CITY: SEATTLE
STATE: WASHINGTON

COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk

COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5

SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/088,913A
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/484,624
FILING DATE:

APPLICATION NUMBER: 08/477,733
FILING DATE:

APPLICATION NUMBER: June 07, 1995
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/969,703
FILING DATE:

APPLICATION NUMBER: October 23, 1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/805,723
FILING DATE:

APPLICATION NUMBER: December 5, 1991
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/783,707
FILING DATE:

APPLICATION NUMBER: October 25, 1991
ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2802-D
TELECOMMUNICATION INFORMATION:

TELEPHONE: 2065870430
TELEFAX: 2065870606

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:

LENGTH: 840 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: cDNA
HYPOTHETICAL: NO

ANTI-SENSE: NO
ORIGINAL SOURCE:

ORGANISM: Homo sapiens
IMMEDIATE SOURCE:

CLONE: CD40-L
FEATURE:
NAME/KEY: CDS

LOCATION: 46..831
US-09-088-913A-11

Query Match 98.8%; Score 776.4; DB 3; Length 840;
Best Local Similarity 99.2%; Pred. No. 2.6e-219;
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;


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Db 466 GCTGAAAAAGATCTACACCACTGAGCAACAACCTTGTAACCTTGAAAAATGGAAAAACG 525
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Db 646 TTGAGAGAACTTACTCAGAGCTGCAAAATCCACAGTTCCGCAAAACCTTGCGGGCA 705
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Db 706 CAATCATTTCACTTGGAGAGATTTTGAATTGCAACAGTGTCTGGGTGTTGTCAAT 765
Qy 721 GTGACTGATCCAGCAAGTGAAGCCAGTGGCTTCAAGTCTCTTGTGCTTACTCAAA 780
Db 766 GTGACTGATCCAGCAAGTGAAGCCAGTGGCTTCAAGTCTCTTGTGCTTACTCAAA 825
Qy 781 CTCTGA 786
Db 826 CTCTGA 831

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RESULT 14

US-08-769-819-11

Sequence 11, Application us/08769819

Patent No. 6264851

GENERAL INFORMATION:

APPLICANT: ARMSTRONG, RICHARD

APPLICANT: FANSLAW, WILLIAM

APPLICANT: SPRINGS, MELANIE

APPLICANT: SRINIVASAN, SUBHASHINI

APPLICANT: GIBSON, MARYLOU

TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESSES:

ADDRESSEE: IMMUNEX CORPORATION

STREET: 51 UNIVERSITY STREET

CITY: SEATTLE

STATE: WASHINGTON

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: Apple Macintosh

SOFTWARE: Microsoft Word for Apple, version 5.1a

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/769,819

FILING DATE: 19-DEC-1996

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/484,624

FILING DATE: 07-JUN-1995

APPLICATION NUMBER: 08/249,189

FILING DATE: May 24, 1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/969,703

FILING DATE: October 23, 1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/805,723

FILING DATE: December 5, 1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/783,707

FILING DATE: October 25, 1991

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia A.

REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2802-B

TELECOMMUNICATION INFORMATION:

TELEPHONE: 2065870430

TELEFAX: 2065870606

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 840 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

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ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

IMMEDIATE SOURCE:

CLONE: CD40-L

FEATURE:

NAME/KEY: CDS

LOCATION: 46..831

US-08-769-819-11

Query Match

Best Local Similarity 99.2%; Pred. No. 2,66-219;

Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Db 46 ATGATGAAACATACACCAAACTTCTCCCGATCTGGGCGCTGAGTCCCGCATACG 105
Qy 61 ATGAAATTTTATGATTTTCTTACTCTGTTTCTTTATCAACCAATGATGATCTGTG 120
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 Db 706 CAATCATTCACCTGGAGAGATTTGATTCACACAGCTCTTGGTGTTCAT 765
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 Db 766 GTGACTGATCCAAAGCAAGTGAAGCCATGCACTGGCTTCACTGCTTACTCAAA 825
 Qy 781 CTCCTGA 786
 Db 826 CTCCTGA 831

RESULT 15 us-08-770-974-11

Sequence 11, Application US/08770974
 Patent No. 6290972

GENERAL INFORMATION:

APPLICANT: ARMITAGE, RICHARD
 APPLICANT: FANSLON, WILLIAM
 APPLICANT: SPRIGGS, MELANIE
 APPLICANT: SRINIVASAN, SUBHASHINI
 APPLICANT: GIBSON, MARYLOU
 TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
 NUMBER OF SEQUENCES: 24
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: IMMUNEX CORPORATION
 STREET: 51 UNIVERSITY STREET
 CITY: SEATTLE
 STATE: WASHINGTON
 COUNTRY: USA
 ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: Apple Operating System 7.1
 SOFTWARE: Microsoft Word for Apple, version 5.1a
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/770,974
 FILING DATE: 20-DEC-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/477,733
 FILING DATE: 02-AUG-1995
 APPLICATION NUMBER: 08/249,189
 FILING DATE: May 24, 1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/969,703
 FILING DATE: October 23, 1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/805,723
 FILING DATE: December 5, 1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/783,707
 FILING DATE: October 25, 1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Perkins, Patricia A.
 REGISTRATION NUMBER: 34,693
 REFERENCE/DOCKET NUMBER: 2802-D
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 2065870430
 TELEFAX: 2065870606
 INFORMATION FOR SEQ ID NO: 11:

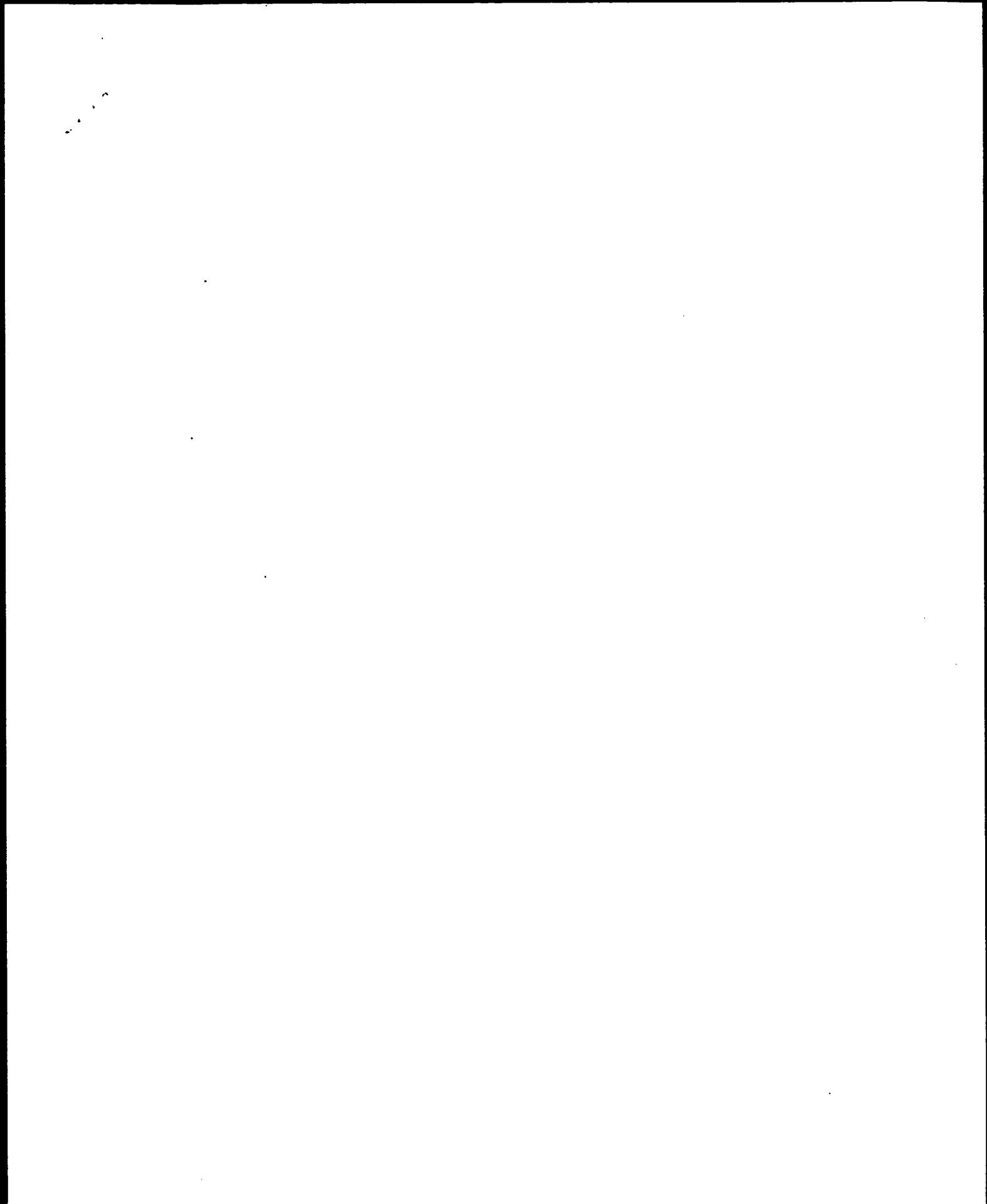
SEQUENCE CHARACTERISTICS:
 LENGTH: 840 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:

ORGANISM: Homo sapiens
 IMMEDIATE SOURCE:
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 FEATURE:
 NAME/KEY: CDS
 LOCATION: 46..831
 us-08-770-974-11

Query Match 98.8%; Score 776.4; DB 4; Length 840;
 Best Local Similarity 99.2%; Pred. No. 2,6e-219;
 Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ATGATCGAATACATACCAACCAATCTTCCCGATGCGGCGCATGAGCTGCCATCAGC 60
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 Qy 61 ATGAAATTTTATGATTTTACTTACTGTTTCTTATCACCATAATGATGATCTGTG 120
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 Qy 541 CGGAAAGCTTCCAGTCAAGCTTCAATTAATGAGCAAGCTTCAAGTCCCGGTGAG 600
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 Qy 601 TTGAGAGAAATCTTACTGAGCTGCAAAATACCAAGTTCCGCAAAAGCTTCCGAGAA 660
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 Qy 661 CAATCCATTCATCTGGAGAGATTTGAAATGCAACAGAGTCCGATGATTTTCTCAT 720
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 Db 766 GTGACTGATCCAAAGCAAGTGAAGCCATGCACTGGCTTCACTGCTTACTCAAA 825
 Qy 781 CTCCTGA 786
 Db 826 CTCCTGA 831

Search completed: March 9, 2003, 04:46:12
 Job time : 36.6448 secs



GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: March 8, 2003, 18:35:23 ; Search time 2040.79 Seconds

(without alignments)
1166.008 Million cell updates/sec

Title: US-08-982-272-5

Perfect score: 783

Sequence: 1 ATGATCGAACAATACCA.....TTGGCTTACTCAACTCTGA 783

Scoring table: IDENTITY NUC

Gapop 10⁻⁰, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : GenEmbl.1.*
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2: gb_hcg.*
3: gb_in.*
4: gb_on.*
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6: gb_pat.*
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8: gb_pl.*
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14: gb_vt.*
15: em_da.*
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17: em_hum.*
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38: em_ay.*
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41: em_hugo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	760.6	97.1	818 6	AR044778
2	760.6	97.1	818 6	AR171646
3	760.6	97.1	1250 6	AX208160
4	759	96.9	783 6	AR076918
5	759	96.9	783 6	AR078308
6	759	96.9	783 6	AR085411
7	759	96.9	783 6	AR103367
8	759	96.9	783 6	AR169224
9	759	96.9	783 6	187865
10	759	96.9	1250 10	NMCD40
11	687	87.7	783 10	AF013985
12	683.8	87.3	783 10	AF116582
13	631.4	80.6	878 6	AR076933
14	631.4	80.6	878 6	AR078323
15	631.4	80.6	878 6	AR085426
16	631.4	80.6	878 6	AR103382
17	631.4	80.6	878 6	AR169239
18	582.8	74.4	786 6	187864
19	582.8	74.4	840 6	AR044779
20	582.8	74.4	840 6	AR076926
21	582.8	74.4	840 6	AR078316
22	582.8	74.4	840 6	AR085419
23	582.8	74.4	840 6	AR103375
24	582.8	74.4	840 6	AR106246
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28	582.8	74.4	840 6	127345
29	582.8	74.4	840 6	167828
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36	573.2	73.2	1058 9	AF344859
37	567.6	72.5	839 9	HACD40L
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45	446.2	57.0	1425 6	AR076929

ALIGNMENTS

RESULT 1
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LOCUS AR044778 818 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1 from patent US 5817516.
ACCESSION AR044778
VERSION AR044778.1 GI:5966243
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 818)
AUTHORS Kehly,M. and Castle,B.
TITL Methods for proliferating and differentiating B cells with high
JOURNAL density membrane CD40 ligand
Patent: US 5817516-A 1 06-Oct-1998;

FEATURES

Location/Qualifiers

source

1. .818

/organism="unknown"

BASE COUNT 249 a 170 c 186 g 213 t

ORIGIN

Query Match 97.1%; Score 760.6; DB 6; Length 818;

Best Local Similarity 98.2%; Pred. No. 1.4e-190;

Matches 769; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGATGAAACATACCAACCAATTCCTCCCGATCTGCGGCACTGAGTCCCATCAGC 60
 DB 13 ATGATGAAACATACCAACCAATTCCTCCCGATCTGCGGCACTGAGTCCCATCAGC 72
 QY 61 ATGAAATTTTATGATTTTACTTACTGTTTCTTATCCCAATGATGATCTGTG 120
 DB 73 ATGAAATTTTATGATTTTACTTACTGTTTCTTATCCCAATGATGATCTGTG 132
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 QY 781 TGA 783
 DB 793 TGA 795

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 818)

AUTHORS Kehry, M. and Caetle, B.

TITLE B cell culture system comprising high density membrane bound CD40 ligand

JOURNAL Patent: US 6297052-A 1 02-OCT-2001;

FEATURES

Location/Qualifiers

source

1. .818

/organism="unknown"

BASE COUNT 249 a 170 c 186 g 213 t

ORIGIN

Query Match 97.1%; Score 760.6; DB 6; Length 818;

Best Local Similarity 98.2%; Pred. No. 1.4e-190;

Matches 769; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGATGAAACATACCAACCAATTCCTCCCGATCTGCGGCACTGAGTCCCATCAGC 60
 DB 13 ATGATGAAACATACCAACCAATTCCTCCCGATCTGCGGCACTGAGTCCCATCAGC 72
 QY 61 ATGAAATTTTATGATTTTACTTACTGTTTCTTATCCCAATGATGATCTGTG 120
 DB 73 ATGAAATTTTATGATTTTACTTACTGTTTCTTATCCCAATGATGATCTGTG 132
 QY 121 CTTTTCCTGCTGATCTTCTCAATGAAATGATGATGAAAGATTAACCTTCAT 180
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 QY 601 GAGAGATCTTACTCAAGGCGGCAATACCAAGTTCCTCCCACTTGGAGAGAGAG 660
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 QY 721 ACTGAAGCAAGCAAGTATCAAGAGTGTGCTTCACTTTTGGCTTCAAACTC 780
 DB 733 ACTGAAGCAAGCAAGTATCAAGAGTGTGCTTCACTTTTGGCTTCAAACTC 792
 QY 781 TGA 783
 DB 793 TGA 795

RESULT 2

AR171646

LOCUS

818 bp

DNA

linear

PAT 17-DEC-2001

DEFINITION

Sequence 1 from patent US 6297052.

AR171646

AR171646.1

GI:17910596

VERSION

Db 793 TGA 795

RESULT 3

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LOCUS AX208160 1250 bp DNA linear PAT 31-AUG-2001

DEFINITION Sequence 1 from Patent WO0156602.

ACCESSION AX208160

VERSION AX208160.1 GI:15422583

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLES

JOURNAL

FEATURES

source

BASE COUNT

ORIGIN

Query Match

Best local similarity

Matches 769; Conservative

0; Mismatches 14; Indels 0; Gaps 0;

97.1%; Score 760.6; DB 6; Length 1250;

98.2%; Pred. No. 1.4e-190;

0; Mismatches 14; Indels 0; Gaps 0;

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61 ATGAAATTTTATGATTTACTACTGTTTCTTATCAACCAAGATTTGATGATCTG 120

73 ATGAAATTTTATGATTTACTACTGTTTCTTATCAACCAAGATTTGATGATCTG 132

121 CTTTTCGCTGTATCTTCAATGAAAGTTGATGATGATGATGATGATGATGATG 180

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181 GAAGATTTTATGATTTATGATTTATGATTTATGATTTATGATTTATGATTTATG 240

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253 TTGCTGAACGTGTAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 312

301 AACAAAG 360

313 AACAAAG 372

361 ATTGAGACACGTTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420

373 ATTGAGACACGTTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 432

421 AAGAAAGATTTATGATTTATGATTTATGATTTATGATTTATGATTTATGATTTATG 480

433 AAGAAAGATTTATGATTTATGATTTATGATTTATGATTTATGATTTATGATTTATG 492

481 ACGTTTAAAG 540

493 ACGTTTAAAG 552

541 GAGCTTGAAGTCAAGCCCATTCATCGTGGCTTGGCTGAAGAGAGAGAGAGAGAGAG 600

553 GAGCTTGAAGTCAAGCCCATTCATCGTGGCTTGGCTGAAGAGAGAGAGAGAGAGAG 612

601 GAGAGATCTTACTCAAG 660

613 GAGAGATCTTACTCAAG 672

Qy 661 TCTGTTCACTTGGCGAGTGTGTTGATTAACAAGCTGCTGCTGCTGCTGCTGCTGCTG 720

Db 673 TCTGTTCACTTGGCGAGTGTGTTGATTAACAAGCTGCTGCTGCTGCTGCTGCTGCTG 732

Qy 721 ACTGAAGCAAGCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780

Db 733 ACTGAAGCAAGCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 792

Qy 781 TGA 783

Db 793 TGA 795

RESULT 4

AR076918

LOCUS AR076918

DEFINITION Sequence 1 from patent US 5961974.

ACCESSION AR076918

VERSION AR076918.1 GI:10003664

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLES

JOURNAL

FEATURES

source

BASE COUNT

ORIGIN

Query Match

Best local similarity

Matches 768; Conservative

0; Mismatches 15; Indels 0; Gaps 0;

96.9%; Score 759; DB 6; Length 783;

98.1%; Pred. No. 3.7e-190;

0; Mismatches 15; Indels 0; Gaps 0;

1 ATGATCGAAACATTCACCAACTCTCCCGATCTGCGGCACTGACCTCCCATCAGC 60

1 ATGATCGAAACATTCACCAACTCTCCCGATCTGCGGCACTGACCTCCCATCAGC 60

61 ATGAAATTTTATGATTTATGATTTATGATTTATGATTTATGATTTATGATTTATG 120

61 ATGAAATTTTATGATTTATGATTTATGATTTATGATTTATGATTTATGATTTATG 120

121 CTTTTCGCTGTATCTTCAATGAAAGTTGATGATGATGATGATGATGATGATGATG 180

121 CTTTTCGCTGTATCTTCAATGAAAGTTGATGATGATGATGATGATGATGATGATG 180

121 CTTTTCGCTGTATCTTCAATGAAAGTTGATGATGATGATGATGATGATGATGATG 180

181 GAAGATTTTATGATTTATGATTTATGATTTATGATTTATGATTTATGATTTATG 240

181 GAAGATTTTATGATTTATGATTTATGATTTATGATTTATGATTTATGATTTATG 240

241 TTGCTGAACGTGTAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 300

241 TTGCTGAACGTGTAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 300

301 AACAAAG 360

301 AACAAAG 360

361 ATTGAGACACGTTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420

361 ATTGAGACACGTTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420

421 AAGAAAGATTTATGATTTATGATTTATGATTTATGATTTATGATTTATGATTTATG 480

421 AAGAAAGATTTATGATTTATGATTTATGATTTATGATTTATGATTTATGATTTATG 480

481 ACGTTTAAAG 540

Db 481 ACGGTTAAAGAAAGACTATATATCTCACTCAAGTCACTTCTGCTTATCCG 540
 Qy 541 GAGCTTCGATCAACGCCATTCATCGTGGCCCTCTGGCTGAAGCCGACATGGATCT 600
 Db 541 GAGCTTCGATCAACGCCATTCATCGTGGCCCTCTGGCTGAAGCCGACATGGATCT 600
 Qy 601 GAGGATCTTACTCAAGGCGGCAATATCCACATCTCCAGCTTTGGCAGCAG 660
 Db 601 GAGGATCTTACTCAAGGCGGCAATATCCACATCTCCAGCTTTGGCAGCAG 660
 Qy 661 TCTGTTCACTTGGCGGAGTGTGAATTAACAAGTGTCTCTGTGTTTCAACGTG 720
 Db 661 TCTGTTCACTTGGCGGAGTGTGAATTAACAAGTGTCTCTGTGTTTCAACGTG 720
 Qy 721 ACTGAAGCAAGCAAGTATCCACAGAGTGGCTTCTCATCTTTGGCTTACTCAATC 780
 Db 721 ACTGAAGCAAGCAAGTATCCACAGAGTGGCTTCTCATCTTTGGCTTACTCAATC 780
 Qy 781 TGA 783
 Db 781 TGA 783

RESULT 5
 AR078308 783 bp DNA linear PAT 31-AUG-2000
 LOCUS AR078308
 DEFINITION Sequence 1 from patent US 5962406.
 ACCESSION AR078308
 VERSION AR078308.1 GI:10005054
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 783)
 AUTHORS Armitage,R.J., Fanslow,M.C., Spriggs,M.K., Srinivasan,S.,
 Gibson,M.G., Morris,A.E. and McGrew,J.T.
 TITLE Recombinant soluble CD40 ligand and polypeptide and pharmaceutical
 composition containing the same
 JOURNAL Patent: US 5962406-A 1 05-OCT-1999;
 FEATURES
 source 1..783
 location/Qualifiers
 BASE COUNT 243 a 159 c 178 g 203 t
 ORIGIN

Query Match 96.9%; Score 759; DB 6; Length 783;
 Best Local Similarity 98.1%; Pred. No. 3,7e-190;
 Matches 768; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1 ATGATCGAAACATACCAACCACTTCTCCCGATCTGCGGCACTGATGCCATCAGC 60
 Db 1 ATGATCGAAACATACCAACCACTTCTCCCGATCTGCGGCACTGATGCCATCAGC 60
 Qy 61 ATGAAATTTTATGATTTTACTTACTGTTTCTTATCAACCAATGATTTGATCTG 120
 Db 61 ATGAAATTTTATGATTTTACTTACTGTTTCTTATCAACCAATGATTTGATCTG 120
 Qy 121 CTTTTCGTGTATCTTCAATAGATTTGATTAAGTGAAGAGAACTTATTCAT 180
 Db 121 CTTTTCGTGTATCTTCAATAGATTTGATTAAGTGAAGAGAACTTATTCAT 180
 Qy 181 GAAATTTTGTATTCATTAAGAAAGCTTAAGATGCAACAAAGAGAAAGATCTTATCC 240
 Db 181 GAAATTTTGTATTCATTAAGAAAGCTTAAGATGCAACAAAGAGAAAGATCTTATCC 240
 Qy 241 TTGCTGAAGTGTGAGAGATGAGAAAGCAATTTGAAGACTTGTCAAGATATAGCTTA 300
 Db 241 TTGCTGAAGTGTGAGAGATGAGAAAGCAATTTGAAGACTTGTCAAGATATAGCTTA 300
 Qy 301 AACAAAG 360
 Db 301 AACAAAG 360

Qy 361 ATTGCAGACAGCTTTGTAAGCGAAGCAAGTAATGACATCCGTTCTACAGTGGGCC 420
 Db 361 ATTGCAGACAGCTTTGTAAGCGAAGCAAGTAATGACATCCGTTCTACAGTGGGCC 420
 Qy 421 AAGAAAGATTTTATCATGAAAGCAACTTGGTATGCTTGAATATGGGAAACGCTG 480
 Db 421 AAGAAAGATTTTATCATGAAAGCAACTTGGTATGCTTGAATATGGGAAACGCTG 480
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 Db 481 ACGGTTAAAGAGAGACTTATATGATCTTCACTCAAGTCACTTGTGCTTAATCCG 540
 Qy 541 GAGCTTCGATCAACGCCATTCATCGTGGCCCTCTGGCTGAAGCCGACATGGATCT 600
 Db 541 GAGCTTCGATCAACGCCATTCATCGTGGCCCTCTGGCTGAAGCCGACATGGATCT 600
 Qy 601 GAGAGATCTTACTCAAGGCGGCAATATCCACAGTCTCTCCAGCTTTGGCAGCAG 660
 Db 601 GAGAGATCTTACTCAAGGCGGCAATATCCACAGTCTCTCCAGCTTTGGCAGCAG 660
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 Db 661 TCTGTTCACTTGGCGGAGTGTGAATTAACAAGTGTCTCTGTGTTTCAACGTG 720
 Qy 721 ACTGAAGCAAGCAAGTATCCACAGAGTGGCTTCTCATCTTTGGCTTACTCAATC 780
 Db 721 ACTGAAGCAAGCAAGTATCCACAGAGTGGCTTCTCATCTTTGGCTTACTCAATC 780
 Qy 781 TGA 783
 Db 781 TGA 783

RESULT 6
 AR085411 783 bp DNA linear PAT 01-SEP-2000
 LOCUS AR085411
 DEFINITION Sequence 1 from patent US 5981724.
 ACCESSION AR085411
 VERSION AR085411.1 GI:10012180
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 783)
 AUTHORS Armitage,R.J., Fanslow,M.C., Spriggs,M.K., Srinivasan,S.,
 Gibson,M.G., Morris,A.E. and McGrew,J.T.
 TITLE DNA encoding CD40 ligand, a cytokine that binds CD40
 JOURNAL Patent: US 5981724-A 1 09-NOV-1999;
 FEATURES
 source 1..783
 location/Qualifiers
 BASE COUNT 243 a 159 c 178 g 203 t
 ORIGIN

Query Match 96.9%; Score 759; DB 6; Length 783;
 Best Local Similarity 98.1%; Pred. No. 3,7e-190;
 Matches 768; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1 ATGATCGAAACATACCAACCACTTCTCCCGATCTGCGGCACTGATGCCATCAGC 60
 Db 1 ATGATCGAAACATACCAACCACTTCTCCCGATCTGCGGCACTGATGCCATCAGC 60
 Qy 61 ATGAAATTTTATGATTTTACTTACTGTTTCTTATCAACCAATGATTTGATCTG 120
 Db 61 ATGAAATTTTATGATTTTACTTACTGTTTCTTATCAACCAATGATTTGATCTG 120
 Qy 121 CTTTTCGTGTATCTTCAATAGATTTGATTAAGTGAAGAGAACTTATTCAT 180
 Db 121 CTTTTCGTGTATCTTCAATAGATTTGATTAAGTGAAGAGAACTTATTCAT 180
 Qy 181 GAAATTTTGTATTCATTAAGAAAGCTTAAGATGCAACAAAGAGAGAGATCTTATCC 240
 Db 181 GAAATTTTGTATTCATTAAGAAAGCTTAAGATGCAACAAAGAGAGAGATCTTATCC 240

QY	241	TTCTGGAAC	CTGTGAGGAGATGAGAGCAATTGTAAGACCTGTGCAAGAGATTAACGTTA	300
DB	241	TTCTGGAAC <th>CTGTGAGGAGATGAGAGCAATTGTAAGACCTGTGCAAGAGATTAACGTTA</th> <td>300</td>	CTGTGAGGAGATGAGAGCAATTGTAAGACCTGTGCAAGAGATTAACGTTA	300
QY	301	AACAAAGAGAGAAAAAGAAAA	CAAGCTTTGAATGCGAAGAGTGATGAGATCTCTCA	360
DB	301	AACAAAGAGAGAAAAAGAAAA	CAAGCTTTGAATGCGAAGAGTGATGAGATCTCTCA	360
QY	361	ATTGCGACACAGCTGTGTAAGCGAAGCCAA	CAGTAAATGACATCGCTTCAAGTGGGCC	420
DB	361	ATTGCGACACAGCTGTGTAAGCGAAGCCAA	CAGTAAATGACATCGCTTCAAGTGGGCC	420
QY	421	AAGAAAGAGATTTATACCTTGAAGCACTTG	GGTATGCTTGAATATGGGAAACAGCTTG	480
DB	421	AAGAAAGAGATTTATACCTTGAAGCACTTG	GGTATGCTTGAATATGGGAAACAGCTTG	480
QY	481	ACGGTTAAAAAGAGAGACCTCTAATTAATG	CTCACTCACTCAAGCTTCCTGCTCTAATCGG	540
DB	481	ACGGTTAAAAAGAGAGACCTCTAATTAATG	CTCACTCACTCAAGCTTCCTGCTCTAATCGG	540
QY	541	GAGCCTTGAGATCAAGCCCAATATATGTCG	AGCCCTGCGGCGTGAAGCCAGCATTTGGATCT	600
DB	541	GAGCCTTGAGATCAAGCCCAATATATGTCG	AGCCCTGCGGCGTGAAGCCAGCATTTGGATCT	600
QY	601	GAGAGATATCTTACTCAAGGCGGCAATAT	CCCAAGTTCTCTCCAGCTTTGGGAGCAGAG	660
DB	601	GAGAGATATCTTACTCAAGGCGGCAATAT	CCCAAGTTCTCTCCAGCTTTGGGAGCAGAG	660
QY	661	TCGTTCACCTTGGGCGGAGTGTGTTGAAT	TACAAGCTGGTGTCTTGTTGTCACACGGT	720
DB	661	TCGTTCACCTTGGGCGGAGTGTGTTGAAT	TACAAGCTGGTGTCTTGTTGTCACACGGT	720
QY	721	ACGGAAGAGACCCAGTATATCCACAGATTT	GCGCTTCTCATCTTTGGCTTACCTCAACTC	780
DB	721	ACGGAAGAGACCCAGTATATCCACAGATTT	GCGCTTCTCATCTTTGGCTTACCTCAACTC	780
QY	781	TEA	783	
DB	781	TEA	783	
RESULT 7				
LOCUS	AR103367		783 bp	DNA
DEFINITION	Sequence 1 from patent US 6087329.			linear
ACCESSION	AR103367			
VERSION	AR103367.1		GI:12814955	
KEYWORDS	Unknown.			
SOURCE	Unknown.			
ORGANISM	Unclassified.			
REFERENCE	1 (bases 1 to 783)			
AUTHORS	Armitage,R.J., Fanslow,W.C. and Spriggs,M.K.			
TITLE	CD40 ligand polypeptide			
JOURNAL	Patent: US 6087329-A 1 11-JUN-2000;			
FEATURES	Location/Qualifiers			
source	1..783			
BASE COUNT	243 a	159 c	178 g	203 t
ORIGIN				
Query Match				
		96.9%	Score 759,	DB 6;
		Best Local Similarity 98.1%;	Pred. No. 3.7e-190;	Length 783;
		Matches 768; Conservative 0;	Mismatches 15;	Indels 0;
				Gaps 0;
QY	1	ATGATCGAAACATACACCAAACTTCTCCCG	ATCTCGGCACTGACATGACCTGCCCATCAGC	60
DB	1	ATGATAGAAACATACACCAAACTTCTCCCG	ATCTCGGCACTGACATGACCTGCCCATCAGC	60
QY	61	ATGAAATATTTATATATTAATTAATTAATTA	ATTAATTAATTAATTAATTAATTAATTAATTA	120
DB	61	ATGAAATATTTATATATTAATTAATTAATTA	ATTAATTAATTAATTAATTAATTAATTAATTA	120

QY	121	CTTTTGTGTGTATCTTCATATAGAAATTTGGATTAAGTGGAAAGAAAGTAAACCTTCAT	180
Db	121	CTTTTGTGTGTATCTTCATATAGAAATTTGGATTAAGTGGAAAGAAAGTAAACCTTCAT	180
QY	181	GAGATTTTGTATTCATATATAAAAGCTTAAGAGATGACACAAAGAGAGAGATCTTATCC	240
Db	181	GAGATTTTGTATTCATATATAAAAGCTTAAGAGATGACACAAAGAGAGAGATCTTATCC	240
QY	241	TTGCTGAACGTGAGAGATGAGATGAGAGCAATTTAABACCTTGTCATAGATATTAACGTTA	300
Db	241	TTGCTGAACGTGAGAGATGAGATGAGAGCAATTTAABACCTTGTCATAGATATTAACGTTA	300
QY	301	AACAAAGAGAGAAAAAGAAAAACAGCTTTGAAATGCAAAAGGTGATGAGATCCTCAA	360
Db	301	AACAAAGAGAGAAAAAGAAAAACAGCTTTGAAATGCAAAAGGTGATGAGATCCTCAA	360
QY	361	ATTGACAGACAGCTGTGAAGCAAGCCACAGTAAATGACATCCGTTCTACAGTGGGCC	420
Db	361	ATTGACAGACAGCTGTGAAGCAAGCCACAGTAAATGACATCCGTTCTACAGTGGGCC	420
QY	421	AAGAAAGATTTATTCATATGAAAGCAACTTGTTAATGCTGAAATGAGAAACAGCTG	480
Db	421	AAGAAAGATTTATTCATATGAAAGCAACTTGTTAATGCTGAAATGAGAAACAGCTG	480
QY	481	ACGGTTAAAAAGAGAGACTTATTAATGCTACACTAGTACACTTCTGCTTAATCGG	540
Db	481	ACGGTTAAAAAGAGAGACTTATTAATGCTACACTAGTACACTTCTGCTTAATCGG	540
QY	541	GAGCCTTCAGATCAAGCCATTCATCGTGGCCTCTGGCTTAAGCCACATTTGATCT	600
Db	541	GAGCCTTCAGATCAAGCCATTCATCGTGGCCTCTGGCTTAAGCCACATTTGATCT	600
QY	601	GAGAGATCTTAATCTCAAGCGGCAATAACCAAGTTCCTCCACATTTGCGAGCAGAG	660
Db	601	GAGAGATCTTAATCTCAAGCGGCAATAACCAAGTTCCTCCACATTTGCGAGCAGAG	660
QY	661	TCTGTCACTGGGCGAGGTTTGAATTAACAACGTGGGCTTCGTTTGTGCAACGTG	720
Db	661	TCTGTCACTGGGCGAGGTTTGAATTAACAACGTGGGCTTCGTTTGTGCAACGTG	720
QY	721	ACTGAAACAGCCACAGATGATCCACAGAGTTGGCTTCTCATCTTTGGCTTAATCAATC	780
Db	721	ACTGAAACAGCCACAGATGATCCACAGAGTTGGCTTCTCATCTTTGGCTTAATCAATC	780
QY	781	TGA 783	
Db	781	TGA 783	
RESULT 8			
LOCUS	ARI69224		
DEFINITION	Sequence 1 from patent US 6290972.	783 bp	DNA linear PAT 17-DEC-2001
ACCESSION	ARI69224		
VERSION	ARI69224.1	GI:17907035	
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 783)		
TITLE	Armitage,R.J., Fanslow,W.C., Spriggs,M.K., Srinivasan,S. and Gibson,M.G.		
JOURNAL	Method of augmenting a vaccine response by administering CD40 ligand		
FEATURES	Patent: US 6290972-A 1 18-SEP-2001;		
FEATURES	Location/Qualifiers		
source	1..783		
BASH COUNT	243 a 159 c 178 g	203 t	
ORIGIN	/organism="unknown"		
Query Match	96.9%; Score 759; DB 6; Length 783;		

Best Local Similarity 98.1%; Pred. No. 3.7e-190;
Matches 768; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACACCAACCTTCTCCCGACTGCGGCACTGAGTCCCATCAGC 60
Db 1 ATGATGAAACATACACCAACCTTCTCCCGACTGCGGCACTGAGTCCCATCAGC 60
QY 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCACCAATGATGATCTGTG 120
Db 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCACCAATGATGATCTGTG 120
QY 121 CTTTTCGTGTATCTTATGAAAGTGGATAGTGAAGAGAGTAACTTAT 180
Db 121 CTTTTCGTGTATCTTATGAAAGTGGATAGTGAAGAGAGTAACTTAT 180
QY 181 GAAGATTTTGTATCTATTAAGAAAGTGAAGTGAACAAAGAGAGATTTATCC 240
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QY 241 TTGCTGAACCTGTGAGAGATGAAAGCAATTTGAAGCTTTGTCAAGATTAACGTTA 300
Db 241 TTGCTGAACCTGTGAGAGATGAAAGCAATTTGAAGCTTTGTCAAGATTAACGTTA 300
QY 301 AACAAAG 360
Db 301 AACAAAG 360
QY 361 ATTGACAGACAGTTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Db 361 ATTGACAGACAGTTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
QY 421 AAGAAAGATTTATATCATGAAAGCACTTGTATGCTTGAAGAGAGAGAGAGAG 480
Db 421 AAGAAAGATTTATATCATGAAAGCACTTGTATGCTTGAAGAGAGAGAGAGAG 480
QY 481 ACGGTTAAAG 540
Db 481 ACGGTTAAAG 540
QY 541 GAGCCTTGAAGTCAAGCCATTCATCGTGGGCTGTGGCTGAAGCCACATTTGATCT 600
Db 541 GAGCCTTGAAGTCAAGCCATTCATCGTGGGCTGTGGCTGAAGCCACATTTGATCT 600
QY 601 GAGAGATCTTACTCAAGGCGGCAATACCAAGTCTTCCAGCTTGGCGAGAGAG 660
Db 601 GAGAGATCTTACTCAAGGCGGCAATACCAAGTCTTCCAGCTTGGCGAGAGAG 660
QY 661 TCTGTTCACTTGGCGGAGTGTGATTAACAAGCTGTGCTTCTGTGTGTCAACGTG 720
Db 661 TCTGTTCACTTGGCGGAGTGTGATTAACAAGCTGTGCTTCTGTGTGTCAACGTG 720
QY 721 ACTGAAG 780
Db 721 ACTGAAG 780
QY 781 TGA 783
Db 781 TGA 783

RESULT 9
LOCUS 187865 783 bp DNA linear PAT 10-AUG-1998
DEFINITION Sequence 5 from patent US 5716805.
ACCESSION 187865
VERSION 187865.1 GI:3407805
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 783)
AUTHORS Sriniivasan, S. and Springs, M.K.
TITLE Methods of preparing soluble, oligomeric proteins

JOURNAL Patent: US 5716805-A 5 10-FEB-1998;

FEATURES
Source Location/Qualifiers
BASE COUNT 243 a 159 c 178 g 203 t
ORIGIN

Query Match 96.9%; Score 759; DB 6; Length 783;
Best Local Similarity 98.1%; Pred. No. 3.7e-190;
Matches 768; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 ATGATGAAACATACACCAACCTTCTCCCGACTGCGGCACTGAGTCCCATCAGC 60
Db 1 ATGATGAAACATACACCAACCTTCTCCCGACTGCGGCACTGAGTCCCATCAGC 60
QY 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCACCAATGATGATCTGTG 120
Db 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCACCAATGATGATCTGTG 120
QY 121 CTTTTCGTGTATCTTATGAAAGTGGATAGTGAAGAGAGTAACTTAT 180
Db 121 CTTTTCGTGTATCTTATGAAAGTGGATAGTGAAGAGAGTAACTTAT 180
QY 181 GAAGATTTTGTATCTATTAAGAAAGTGAAGTGAACAAAGAGAGATTTATCC 240
Db 181 GAAGATTTTGTATCTATTAAGAAAGTGAAGTGAACAAAGAGAGATTTATCC 240
QY 241 TTGCTGAACCTGTGAGAGATGAAAGCAATTTGAAGCTTTGTCAAGATTAACGTTA 300
Db 241 TTGCTGAACCTGTGAGAGATGAAAGCAATTTGAAGCTTTGTCAAGATTAACGTTA 300
QY 301 AACAAAG 360
Db 301 AACAAAG 360
QY 361 ATTGACAGACAGTTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Db 361 ATTGACAGACAGTTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
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Db 421 AAGAAAGATTTATATCATGAAAGCACTTGTATGCTTGAAGAGAGAGAGAGAG 480
QY 481 ACGGTTAAAG 540
Db 481 ACGGTTAAAG 540
QY 541 GAGCCTTGAAGTCAAGCCATTCATCGTGGGCTGTGGCTGAAGCCACATTTGATCT 600
Db 541 GAGCCTTGAAGTCAAGCCATTCATCGTGGGCTGTGGCTGAAGCCACATTTGATCT 600
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Db 601 GAGAGATCTTACTCAAGGCGGCAATACCAAGTCTTCCAGCTTGGCGAGAGAG 660
QY 661 TCTGTTCACTTGGCGGAGTGTGATTAACAAGCTGTGCTTCTGTGTGTCAACGTG 720
Db 661 TCTGTTCACTTGGCGGAGTGTGATTAACAAGCTGTGCTTCTGTGTGTCAACGTG 720
QY 721 ACTGAAG 780
Db 721 ACTGAAG 780
QY 781 TGA 783
Db 781 TGA 783

RESULT 10
LOCUS MIMC40 1250 bp mRNA linear ROD 26-APR-2001
DEFINITION MIMC40
AUTHORS M. musculus mRNA for CD40 ligand.
ACCESSION X65453


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VERSION X65453.2 GI:13872516
KEYWORDS CD4 antigen.
SOURCE house mouse.
ORGANISM Mus musculus.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1250)
Armitage, R., Fanslow, M., Sato, T. A., Clifford, K. N., Strockbine, L.,
Macduff, B. M., Anderson, D. M., Gimpel, S. D., Davis-Smith, T.,
Maliszewski, C. R., Clark, E. A., Smith, C. A., Grabstein, K. H., Cosman, D.
and Spriggs, M. K.
Molecular and biological characterization of a murine ligand for
CD40
JOURNAL Nature 357 (6373), 80-82 (1992)
MEDLINE 92244364
PUBMED 1374165
REFERENCE 2 (bases 1 to 1250)
AUTHORS Spriggs, M. K.
TITLE Direct Submission
JOURNAL Submitted (07-APR-1992) M. K. Spriggs, Immunex Research &
Development, Molecular Biology, 51 University Street, Seattle,
Washington, 98101, USA
REMARK revised by (3)
AUTHORS 3 (bases 1 to 1250)
TITLE Direct Submission
JOURNAL Submitted (24-APR-2001) Strockbine, L. Immunex Research &
Development, Molecular Biology, 51 University Street, Seattle,
Washington, 98101, USA
On Apr 27, 2001 this sequence version replaced gi:50351.
COMMENT Location/Qualifiers
FEATURES
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1..1250
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/db_xref="taxon:10090"
13..795
/gene="CD40L"
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CDS
13..795
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/protein_id="CAA6448.2"
/db_xref="GI:13872517"
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/translation="MIETSGPSVAVNG;PASMKIEMVLTIVFLITOMIGSVLNAV
YLHRLDKVEEVNLDHPVPIKIKCKKCKEGLSLINCEMRQFEDLVKDTLTK
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TVKREGLVTVTVTFCSNREPSQPPFVGLWLPKPSGSERIILKANTHSSSOLCE
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BASE COUNT 379 a 273 c 286 g 312 t
ORIGIN
Query Match 96.9%; Score 759; DB 10; Length 1250;
Best Local Similarity 98.1%; Pred. No. 3.8e-190;
Matches 768; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 1 ATGATCGAAACATACCAAACTTCCCGATCTGCGGCACTGAGCTGCCATCAGC 60
DB 13 ATGATGAAACATACCAAGCACTTCCCGATCGTGGCACTGAGCTGCCAGAAC 72
QY 61 ATGAAATTTTATGATTTACTCTACTGTTTCCCTATCAACCAAGATTTGATCTG 120
DB 73 ATGAAATTTTATGATTTACTCTACTGTTTCCCTATCAACCAAGATTTGATCTG 132
QY 121 CTTTGTCTGTATCTTCAATGAAGATTTGATGAAGTGAAGAGTAACTTCAT 180
DB 133 CTTTGTCTGTATCTTCAATGAAGATTTGATGAAGTGAAGAGTAACTTCAT 192
QY 181 GAAGATTTTATGATTTATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 240
DB 193 GAAGATTTTATGATTTATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 252
QY 241 TTGCTGAACGTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 300
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DB 253 TTGCTGAACGTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 312
QY 301 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
DB 313 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 372
QY 361 ATTGAGACACGTTGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 373 ATTGAGACACGTTGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 432
QY 421 AAGAAAGATTTATACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
DB 433 AAGAAAGATTTATACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 492
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QY 541 GAGCTTCAGTCAAGCGCCATTCATGTCGCGCTTCGAGAGAGAGAGAGAGAGAG 600
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QY 601 GAGAGATCTTACTCAAGGCGGCAAAATACCAAGTCTCCAGCTTTCGAGAGAGAG 660
DB 613 GAGAGATCTTACTCAAGGCGGCAAAATACCAAGTCTCCAGCTTTCGAGAGAGAG 672
QY 661 TCTGTTCACTTGGGCGAGAGTTTGAATTAAGAGCTGCTTCTGTTTTCACAGTG 720
DB 673 TCTGTTCACTTGGGCGAGAGTTTGAATTAAGAGCTGCTTCTGTTTTCACAGTG 732
QY 721 ACTGAACAGCAAGCAAGTATCAGAGAGTTCATCTTTCGCTTTCAGTCAAGTTC 780
DB 733 ACTGAACAGCAAGCAAGTATCAGAGAGTTCATCTTTCGCTTTCAGTCAAGTTC 792
QY 781 TGA 783
DB 793 TGA 795

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```

RESULT 11
LOCUS AF013985 783 bp mRNA linear ROD 26-JAN-1999
DEFINITION Rattus norvegicus CD40 ligand mRNA, complete cds.
ACCESSION AF013985
VERSION AF013985.1 GI:4102613
KEYWORDS
SOURCE
Rattus norvegicus.
Rattus norvegicus.
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 783)
Daniel, K. C., Foss, Y., Mousavi, A., Macary, P., Kemeny, D. M.,
Farzaneh, F. and Gaken, J. A.
Cloning and sequencing of rat CD40 ligand
Unpublished
2 (bases 1 to 783)
Daniel, K. C., Foss, Y., Mousavi, A., Macary, P., Kemeny, D. M.,
Farzaneh, F. and Gaken, J. A.
Direct Submission
Submitted (14-JUL-1997) Immunology, King's College School of
Medicine and Dentistry, 123 Coldharbour Lane, London SE5 9NU, United
Kingdom
FEATURES
Source
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 OOSIHGVEILOAGASVFNVTBASQVHIGIFSISGLKL"
 BASE COUNT 236 a 152 c 189 g 206 t
 ORIGIN

Query Match 87.7%; Score 687; DB 10; Length 783;
 Best Local Similarity 92.3%; Pred. No. 4,4e-171;
 Matches 723; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACACCAAACTTCTCCCGATCGGCGCACTGACATGCCATCAGC 60
 DB 1 ATGATAGAAACATACAGCCACTTCTCCCATCTGTGGCTTCCAGCGAGC 60
 QY 61 ATGAAATTTTATGATTTACTTACCTTTTCTTATCACCAGATTTGGTCGGTG 120
 DB 61 ATGAAATTTTATGATTTACTTACCTTTTCTTATCACCAGATTTGGTCGGTG 120
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 DB 121 CTTTTCGTGTATCTTATAGAAATGATGATGAGAGAGAAATTAACCTTCAT 180
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 QY 241 TTGCTGAACCTGTAGAGAGATGAGAGAAATTAACCTTCATGATATATCTTAA 300
 DB 241 TTGCTGAACCTGTAGAGAGATGAGAGAAATTAACCTTCATGATATATCTTAA 300
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 QY 481 ACGTTAAAG 540
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 DB 721 ACTGAAGCAAGCCAGATGATCAAGAGATGAGCTTCTTATGAGTTATCAATCT 780
 QY 781 TGA 783
 DB 781 TGA 783
 RESULT 12
 AF116582
 LOCUS AF116582 783 bp mRNA linear ROD 12-JUL-2000

DEFINITION Rattus norvegicus CD40 ligand mRNA, complete cds.

ACCESSION AF116582 GI:4545249

VERSION AF116582.1

KEYWORDS

SOURCE

ORGANISM

Rattus norvegicus.

Rattus norvegicus.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

REFERENCE 1 (bases 1 to 783)

AUTHORS Hallett K.M. and Oake M.K.

TITLE Nucleotide sequence of the rat CD40 ligand

JOURNAL DNA Seq. 10 (6), 405-406 (2000)

REFERENCE 2 (bases 1 to 783)

AUTHORS Hallett K.M. and Oake M.K.

TITLE Direct Submission

JOURNAL Submitted (24-DEC-1998) Transplant Research, St. Luke's Medical

Center, 2900 W. Oklahoma Ave., Milwaukee, WI 53215, USA

FEATURES

source

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/strain="Sprague Dawley"

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 OOSIHGVEILOAGASVFNVTBASQVHIGIFSISGLKL"

BASE COUNT 237 a 153 c 189 g 204 t

ORIGIN

Query Match 87.3%; Score 683.8; DB 10; Length 783;
 Best Local Similarity 92.1%; Pred. No. 3.1e-170;
 Matches 721; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACACCAAACTTCTCCCGATCGGCGCACTGACATGCCATCAGC 60
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 DB 121 CTTTTCGTGTATCTTATAGAAATGATGATGAGAGAGAAATTAACCTTCAT 180
 QY 181 GAAATTTTGTATCTTATAGAAATGATGATGAGAGAGAAATTAACCTTCAT 240
 DB 181 GAAATTTTGTATCTTATAGAAATGATGATGAGAGAGAAATTAACCTTCAT 240
 QY 241 TTGCTGAACCTGTAGAGAGATGAGAGAAATTAACCTTCTTATGAGTTATCAATCT 300
 DB 241 TTGCTGAACCTGTAGAGAGATGAGAGAAATTAACCTTCTTATGAGTTATCAATCT 300
 QY 301 AACAAAG 360
 DB 301 AACAAAG 360
 QY 361 ATTGACAGACAGCTTGTAAAGCAAGATGACATCTGTTCTTACATGAGGCGC 420
 DB 361 ATTGACAGACAGCTTGTAAAGCAAGATGACATCTGTTCTTACATGAGGCGC 420
 QY 421 AAGAAAGATTTATACATGAAAGCACTGTATCTTGAAGAGAGAGAGAGAGAG 480

Db 421 AAGAAAGATATTATACATGATAAAGCACTTGTAGTGGGAAAATGGGAGACAACCTG 480
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 QY 781 TGA 783
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RESULT 13
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 DEFINITION Sequence 22 from patent US 5961974.
 ACCESSION AR076933
 VERSION AR076933.1 GI:10003679
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 878)
 AUTHORS Armitage, R.J., Fanslow, W.C. and Spriggs, M.K.
 TITLE Monoclonal antibodies to CD40 ligand, pharmaceutical composition
 JOURNAL comprising the same and hybridomas producing the same
 FEATURES Patent: US 5961974-A 22 05-OCT-1999;
 Location/Qualifiers
 source 1..878
 /organism="unknown"

BASE COUNT 277 a 178 c 203 g 220 t
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 Query Match 80.6%; Score 631.4; DB 6; Length 878;
 Best Local Similarity 99.8%; Pred. No. 2,3e-156;
 Matches 632; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 151 GATAAGTCGAAGAGAGAAAGTAACTTCATGAAGATTTTGTATTAATAAAGCTAAAG 210
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 Db 285 AGATGCAACAAAGAGAGATCTTTATCTTCTGTAAGTGAAGATGAGAGCA 344
 QY 271 TTGGAAGACTTGTCAAGATATTAAGTAAACAAAGAGAGAGAGAGAGAGAGAGAG 330
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 DEFINITION Sequence 22 from patent US 5962406.
 ACCESSION AR078323
 VERSION AR078323.1 GI:10005069
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 878)
 AUTHORS Armitage, R.J., Fanslow, W.C., Spriggs, M.K., Srinivasan, S.,
 Gibson, M.G., Morris, A.E. and McGrew, J.T.
 TITLE Recombinant soluble CD40 ligand and polypeptide and pharmaceutical
 JOURNAL composition containing the same
 FEATURES Patent: US 5962406-A 22 05-OCT-1999;
 Location/Qualifiers
 source 1..878
 /organism="unknown"

BASE COUNT 277 a 178 c 203 g 220 t
 ORIGIN
 Query Match 80.6%; Score 631.4; DB 6; Length 878;
 Best Local Similarity 99.8%; Pred. No. 2,3e-156;
 Matches 632; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 151 GATAAGTCGAAGAGAGAAAGTAACTTCATGAAGATTTTGTATTAATAAAGCTAAAG 210
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QY 511 TACACTCAAGTCACTTCTGCTTAATCGGAGCCTTCGAGTCAAGCCCATTCATGTC 570
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 QY 631 CACAGTCTCCAGCTTTGCGAGCAGTCTGTTCACTTGGCGGAGTGTGAATTA 690
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RESULT 15

AR085426 878 bp DNA linear PAT 01-SEP-2000
 LOCUS AR085426
 DEFINITION Sequence 22 from patent US 5981724.
 ACCESSION AR085426
 VERSION AR085426.1 GI:10012195
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE

1 (bases 1 to 878)
 Armitage, R.J., Fanslow, W.C., Spriggs, M.K., Srinivasan, S.,
 Gibson, M.G., Morris, A.E. and McGraw, J.T.

TITLE DNA encoding CD40 ligand, a cytokine that binds CD40

JOURNAL Patent: US 5981724-A 22 09-NOV-1999;
 FEATURES
 source 1..878
 Location/Qualifiers
 BASE COUNT 277 a 178 c 203 g 220 t

ORIGIN

Query Match 80.6%; Score 631.4; DB 6; Length 878;
 Best Local Similarity 99.8%; Pred. No. 2,3e-156;

Matches 632; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 151 GATAAGTCAAGAGAGAGTAAGTAACTTCATGAAGATTTGATTCATTAAGCTTAAG 210
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 QY 331 GAAATGCAAGAGAGTATAGAGATCTCAAAATTCGACACAGTTGTAAGAGAGCAAC 390
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DB 585 TACACTCAAGTCACTTCTGCTTAATCGGAGCCTTCGAGTCAAGCCCATTCATGTC 644
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 DB 705 CACAGTCTCCAGCTTTGCGAGCAGTCTGTTCACTTGGCGGAGTGTGAATTA 764
 QY 691 CAAGCTGATCTGATGTTGTTGTTCAAGTGAAGCAAGCCCAAGTATCCACAGATT 750
 DB 765 CAAGCTGATCTGATGTTGTTGTTGTTCAAGTGAAGCAAGCCCAAGTATCCACAGATT 824
 QY 751 GGCTTCTCATCTTTGGCTTACTCAAACTCTGA 783
 DB 825 GGCTTCTCATCTTTGGCTTACTCAAACTCTGA 857

Search completed: March 9, 2003, 02:11:31
 Job time : 2042.79 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: March 8, 2003, 21:32:03 ; Search time 1286.6 Seconds
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Title: US-08-982-272-5

Perfect score: 783

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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 100%

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26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	248.4	31.7	398	10	AM486605 75217 MAR
3	72.8	9.3	638	9	AI982044 pat.PK007
4	55.8	7.1	997	17	CNS005TE
5	52.8	6.7	797	9	AL534423
6	51.2	6.5	1043	17	CNS0145P

7	51	6.5	1038	17	CNS0108N	AL098657 Drosophila
8	49.8	6.4	878	17 <td>CNS0187R <td>AL108993 Drosophila</td> </td>	CNS0187R <td>AL108993 Drosophila</td>	AL108993 Drosophila
9	47.2	6.3	1101	17 <td>CNS0039G <td>AL063921 Drosophila</td> </td>	CNS0039G <td>AL063921 Drosophila</td>	AL063921 Drosophila
10	47.6	6.1	920	17 <td>AZ691914 <td>ENTM126TR</td> </td>	AZ691914 <td>ENTM126TR</td>	ENTM126TR
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13	45.6	5.8	802	17 <td>CNS0383B <td>AL232112 Tetraodon</td> </td>	CNS0383B <td>AL232112 Tetraodon</td>	AL232112 Tetraodon
14	45.6	5.8	828	17 <td>CNS011TX <td>AL100719 Drosophila</td> </td>	CNS011TX <td>AL100719 Drosophila</td>	AL100719 Drosophila
15	45.2	5.8	458	9 <td>AL514085 <td>AL514085 Tetraodon</td> </td>	AL514085 <td>AL514085 Tetraodon</td>	AL514085 Tetraodon
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19	44.6	5.7	529	9 <td>AL514657 <td>AL514657 Drosophila</td> </td>	AL514657 <td>AL514657 Drosophila</td>	AL514657 Drosophila
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22	44.4	5.7	814	17 <td>AZ203738 <td>SP_0084_A</td> </td>	AZ203738 <td>SP_0084_A</td>	SP_0084_A
23	44.2	5.6	633	9 <td>AL513979 <td>AL513979 Drosophila</td> </td>	AL513979 <td>AL513979 Drosophila</td>	AL513979 Drosophila
24	44.2	5.6	938	17 <td>CNS006TV <td>AL065906 Drosophila</td> </td>	CNS006TV <td>AL065906 Drosophila</td>	AL065906 Drosophila
25	43.8	5.6	330	9 <td>AL513817 <td>AL513817 Drosophila</td> </td>	AL513817 <td>AL513817 Drosophila</td>	AL513817 Drosophila
26	43.8	5.6	799	17 <td>CNS011SA <td>AL100660 Drosophila</td> </td>	CNS011SA <td>AL100660 Drosophila</td>	AL100660 Drosophila
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28	43.8	5.6	1101	17 <td>CNS0182P <td>AL108811 Drosophila</td> </td>	CNS0182P <td>AL108811 Drosophila</td>	AL108811 Drosophila
29	43.6	5.6	588	17 <td>AQ451757 <td>AQ451757 HS_5184_B</td> </td>	AQ451757 <td>AQ451757 HS_5184_B</td>	AQ451757 HS_5184_B
30	43.6	5.6	828	17 <td>CNS018PA <td>AL109264 Drosophila</td> </td>	CNS018PA <td>AL109264 Drosophila</td>	AL109264 Drosophila
31	43.4	5.5	625	17 <td>CNS036A2 <td>AL229763 Tetraodon</td> </td>	CNS036A2 <td>AL229763 Tetraodon</td>	AL229763 Tetraodon
32	43.2	5.5	870	17 <td>CNS060VZ <td>AL416517 T7 end of</td> </td>	CNS060VZ <td>AL416517 T7 end of</td>	AL416517 T7 end of
33	43	5.5	468	9 <td>AL514541 <td>AL514541 Tetraodon</td> </td>	AL514541 <td>AL514541 Tetraodon</td>	AL514541 Tetraodon
34	43	5.5	548	10 <td>BE022382 <td>BE022382 sm5b02.Y</td> </td>	BE022382 <td>BE022382 sm5b02.Y</td>	BE022382 sm5b02.Y
35	43	5.5	642	13 <td>BJ086288 <td>BJ086288 B096268</td> </td>	BJ086288 <td>BJ086288 B096268</td>	BJ086288 B096268
36	42.8	5.4	807	17 <td>CNS0119V <td>AL099997 Drosophila</td> </td>	CNS0119V <td>AL099997 Drosophila</td>	AL099997 Drosophila
37	42.6	5.4	415	14 <td>R41111 <td>AL1111 HK372-F Adu</td> </td>	R41111 <td>AL1111 HK372-F Adu</td>	AL1111 HK372-F Adu
38	42.6	5.4	595	17 <td>AQ521025 <td>AQ521025 HS_5212_B</td> </td>	AQ521025 <td>AQ521025 HS_5212_B</td>	AQ521025 HS_5212_B
39	42.6	5.4	744	17 <td>AG043338 <td>AG043338 Pan trog1</td> </td>	AG043338 <td>AG043338 Pan trog1</td>	AG043338 Pan trog1
40	42.6	5.4	805	9 <td>AI557564 <td>AI557564 pt2.1-1.A</td> </td>	AI557564 <td>AI557564 pt2.1-1.A</td>	AI557564 pt2.1-1.A
41	42.6	5.4	959	17 <td>CNS00655 <td>AL062806 Drosophila</td> </td>	CNS00655 <td>AL062806 Drosophila</td>	AL062806 Drosophila
42	42.6	5.4	1007	17 <td>CNS06X8S <td>AL419462 T3 end of</td> </td>	CNS06X8S <td>AL419462 T3 end of</td>	AL419462 T3 end of
43	42.4	5.4	634	9 <td>AL514497 <td>AL514497 Tetraodon</td> </td>	AL514497 <td>AL514497 Tetraodon</td>	AL514497 Tetraodon
44	42.4	5.4	918	17 <td>CNS006W <td>AL065768 Drosophila</td> </td>	CNS006W <td>AL065768 Drosophila</td>	AL065768 Drosophila
45	42.2	5.4	431	17 <td>CNS0406O <td>AL293145 Tetraodon</td> </td>	CNS0406O <td>AL293145 Tetraodon</td>	AL293145 Tetraodon

ALIGNMENTS

RESULT 1
BF599437 492 bp mRNA linear EST 25-APR-2001
263218 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.

BF599437
BF599437.1 GI:11695919
EST.
COW.
BOS taurus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.

REFERENCE

Smith, T.P.L., Grose, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
1 (bases 1 to 492)
Casas, E., Way, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett,
G.L., Heaton, M.P., Jaeger, W.M., Rohrer, G.A., Chitko-McKown, C.G.,
Peters, G., Holt, I., Karaycheva, S., Liang, F., Quackenbush, J. and
Keele, J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)

TITLE

JOURNAL MEDLINE
COMMENT

USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smtl@mail.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred

v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.

PCR primers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCAGTCAGCAGC
Plate: 33 row: N column: 5
Seq primer: ATTAGTGACACTATAG.

FEATURES
source
1..492
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 380V"
/issue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendinosus muscle, and fetal
longissimus muscle."

BASE COUNT 163 a 103 c 104 g 122 t
ORIGIN

Query Match 39.1%; Score 305.8; DB 12; Length 492;

Best Local Similarity 82.0%; Pred. No. 4,4e-58;
Matches 365; Conservative 0; Mismatches 77; Indels 3; Gaps 1;

QY 1 ATGATCGAAACATACACCAAACTTCCCGGATCGGCGCACTGACCTGCCCATCAGC 60
DB 46 ATGATCGAAACATACACCTCTCCCGGATCGGCGCACTGACCTGCCCATCAGT 105
QY 61 ATGAAATTTTATGATATTTACTTACTGCTTTTCTTATCACTCAACCAATGATGATCTGTG 120
DB 106 ATGAAATTTTATGATATTTACTTACTGCTTTTCTTATCACTCAACCAATGATGATGATGAGG 165
QY 121 CTTTTCCTGTATCTTCTAGAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
DB 166 CTTTTCCTGTATCTTCTAGAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 225
QY 181 GAAGATTTTGTTCATGAAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
DB 226 GAAGATTTTGTTCATGAAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 285
QY 241 TTGCTGAACCTGTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
DB 286 TTACTGAACTGTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 345
QY 301 AACAAAGAG--AGAAAAAGAAACGCTTTGAATGCAAGAGGATGATGATGATGATGATGATGATGAT 357
DB 346 AACAAAGAGTAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 405
QY 358 CAATTTGAGCAGCAGCTTTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 417
DB 406 CAGATAGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 465
QY 418 GCCAAGAAAGATTTTATCATGA 442
DB 466 GCCCCAAAGATTTATCAACCTTAA 490

RESULT 2
AM486605 398 bp mRNA linear EST 25-APR-2001
LOCUS
DEFINITION 75217 MARC 180V Bos taurus cDNA 5', mRNA sequence.
ACCESSION AM486605
VERSION AM486605.1 GI:7056711
KEYWORDS
SOURCE
ORGANISM

REFERENCE
Smith,T.P.L., Grose,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett

G.L., Heaton,M.P., Laegreid,W.M., Rohrer,G.A., Chitko-McKown,C.G.,
Peters,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
Keefe,J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
21180013

COMMENT

USDA, ARS US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 20
and -minmatch 12 options.

PCR primers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCAGTCAGCAGC
Plate: 34 row: F column: 23
Seq primer: ATTAGTGACACTATAG.
Location/Qualifiers

FEATURES
source

1..398
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 180V"
/issue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from lymph node, ovary,
fat, hypothalamus, and pituitary."

BASE COUNT 134 a 77 c 82 g 105 t
ORIGIN

Query Match 31.7%; Score 248.4; DB 10; Length 398;

Best Local Similarity 84.4%; Pred. No. 2.9e-45;
Matches 292; Conservative 0; Mismatches 51; Indels 3; Gaps 1;

QY 1 ATGATCGAAACATACACCAAACTTCCCGGATCGGCGCACTGACCTGCCCATCAGC 60
DB 53 ATGATCGAAACATACACCTCTCCCGGATCGGCGCACTGACCTGCCCATCAGT 112
QY 61 ATGAAATTTTATGATATTTACTTACTGCTTTTCTTATCACTCAACCAATGATGATCTGTG 120
DB 113 ATGAAATTTTATGATATTTACTTACTGCTTTTCTTATCACTCAACCAATGATGATGATGATGAT 172
QY 121 CTTTTCCTGTATCTTCTAGAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
DB 173 CTTTTCCTGTATCTTCTAGAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 232
QY 181 GAAGATTTTGTTCATGAAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
DB 233 GAAGATTTTGTTCATGAAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 292
QY 241 TTGCTGAACCTGTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
DB 293 TTACTGAACTGTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 352
QY 301 AACAAAGAG--AGAAAAAGAAACGCTTTGAATGCAAGAGGATGATGATGATGATGATGATGATGAT 343
DB 353 AACAAAGAGTAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 398

RESULT 3
A1982044 638 bp mRNA linear EST 07-MAY-2001
LOCUS
DEFINITION pat.pK0072.c9.f chicken activated T cell cDNA Gallus gallus cDNA
ACCESSION A1982044
VERSION A1982044.1 GI:5885072
KEYWORDS
SOURCE
ORGANISM

Gallus gallus

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
COMMENT

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianidae; Gallus.
1 (bases 1 to 638)
Tirumagaru, V.G., Sofer, L., Cui, J. and Burnside, J.
An expressed sequence tag database of T-cell-enriched activated
chicken splenocytes: sequence analysis of 5251 clones
Genomics 66 (2), 144-151 (2000)
20318616
Contact: Joan Burnside
Molecular Endocrinology
University of Delaware
40 Townsend Hall, Newark, DE 19717, USA
Tel: 302 831-1345
Fax: 302-831-3411
Email: joan@udel.edu, www.chickest.udel.edu
Seq primer: T7.

FEATURES
source
Location/Qualifiers

1..638
/organism="Gallus gallus"
/db_xref="taxon:9031"
/clone="pat.PK0072.c9.f"
/clone_1lb="Chicken activated T cell cDNA"
/sex="male"
/cell_type="Con A-activated splenic T cell"
/lab_host="E.coli TOP10 F"
/note="Vector: pCDNA3"

BASE COUNT 132 a 171 c 151 g 180 t 4 others
ORIGIN
Query Match 9.3%; Score 72.8; DB 9; Length 638;
Best Local Similarity 58.3%; Pred. No. 3.7e-06;
Matches 169; Conservative 0; Mismatches 112; Indels 9; Gaps 2;

Qy 495 AGAAGCTATTTATGCTACACTGAAGACCTTCTGCTTAATGGAGACCTTGAAGCA 554
Db 2 AGGCTCTACTACTACTACTCAAGTCAAGCTTCTGACCAAGCGCGCTTCG----- 56
Qy 555 AGGCCATTCATCTGCTGGCCTCTGCTGAAGCCAGCATTTGATCTGAGAGATTTACT 614
Db 57 -GCCCATTCACCTCTATTTATTTGTAACCTCCCACTGAAGAGACCGGCTCTGAT 115
Qy 615 CAAGCGGCGCAATATCCAGTTCCTCCGCG---CTTTGGAGAGAGAGCTGTTCACTT 671
Db 116 GAAGGAGCTTGACAGCAGACACTTCCAGCGCTCTCTGAGCTCAATTCATCCGGA 175
Qy 672 GGGCGAGTGTGTAATTACAGCTGCTCTCTGTTTGTCAAGTGAAGCAAG 721
Db 176 GGGCGGTGCTTCAAGCTGCGGAGGCGACATGCTTTGTCAATGTGACGACTCAAC 235
Qy 732 CCAAGTATCCAGAGTTCCTTCATCTTTGGCTTACTCAAACTCT 781
Db 236 AGCAGTAACTGAACCTTGGCAACACTTCTTGGCATTTCAAGCTGT 285

RESULT 4
CNS005TE/c 997 bp DNA linear GSS 03-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence TET3 end of BAC #
DEFINITION BAC12K22 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL060767 GI:4943573
VERSION AL060767
KEYWORDS GSS.
SOURCE Drosophila melanogaster.
ORGANISM Drosophila melanogaster.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 997)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

COMMENT
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org> The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mammoler in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
P1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES
source
Location/Qualifiers

1..997
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="BAC12K22"
/clone_1lb="RPCI-98"
/note="end : TET3"

BASE COUNT 89 a 99 c 13 g 258 t 538 others
ORIGIN
Query Match 7.1%; Score 55.8; DB 17; Length 997;
Best Local Similarity 19.5%; Pred. No. 0.021;
Matches 69; Conservative 131; Mismatches 153; Indels 0; Gaps 0;

Qy 140 ATAGAAGATTGATAGTGAAGAGAAACCTTCATTAAGATTGTATTCATTA 199
Db 881 ARARARRARARARARARRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 822
Qy 200 AAAAGTTAAGATGCAACAAAGAGAGATTTATCTTCTGTAACCTGAGAGA 259
Db 821 RAGAARARRRRRRARARARRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 762
Qy 260 TGAGAGCAATTTGAAGACCTTTCAGATATTAAGTTAAACAAAGAGAAAAAG 319
Db 761 ARARARARARARARARRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 702
Qy 320 AAAAGCTTTGAATGCAAGAGGTGATGATCTTCAATTCACACACGTTGTA 379
Db 701 GAGAARRRRRRGAGARRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 642
Qy 380 GCGAAGCCAGATGATGACATCCGTTTACAGTGGCGCAAGAAAGATATTATCA 439
Db 641 RRARARR 582
Qy 440 TGAAGCACTTGTAAATGCTTGAATGGAAGACGCTGACGGTTAAAGA 492
Db 581 GAGARR 529

RESULT 5
AL534423 797 bp mRNA linear EST 13-FEB-2001
LOCUS AL534423 LIT_F1013_FBrn1 Homo sapiens cDNA clone CS00P004YD24 5
DEFINITION prlme, mRNA sequence.
ACCESSION AL534423 GI:12797916
VERSION AL534423
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 797)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polajsek, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope

COMMENT

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - <http://www.edgp.ebi.ac.uk> - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.

FEATURES

source

Location/Qualifiers
1..1038
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="BACN03101"
/clone_lib="DrosBAC"
/plasmid="pBelobAC11"
/note="end : Sp6"

BASE COUNT 372 a 6 c 119 g 219 t 322 others
ORIGIN

Query Match

Best Local Similarity 35.0%; Score 51; DB 17; Length 1038;
Matches 157; Conservative 20; Mismatches 271; Indels 0; Gaps 0;

Qy 72 TAGTATTTACTTACTGTTTCTTATCAACCAATGATGATGCTGCTTTGCTGT 131
Db 37 TTTNNNTTTNNNNNTTTGTTWANNACYTATTTATTTTATTTATTTTATTTT 96
Qy 132 GTATCTTCATAGAGATTGATAGGTCAGAGAGTAACCTTCATGAAAGATTTCG 191
Db 97 TTATTAAGTCAC 156
Qy 192 ATTCAATTAAGTAAAGATGACAAAGAGAGAGATCTTATCTTCTGTAAGT 251
Db 157 TTTNNNTTTNNNNNTTTGTTWANNACYTATTTATTTTATTTTATTTTATTT 216
Qy 252 TGAGAGATGAGAGAGATTTGAGACCTGTCAGAGATATATGCTTAAACAAGAG 311
Db 217 NNNNTTANNNTTAAABAAAATTTATTAATTAATTAATTAATTAATTAATTA 276
Qy 312 GAAAAAGAAAAAGCCTTGAATGAAAGAGATGAGATCTCAATTTGACAGCA 371
Db 277 AAAAAAGAAAAAGCCTTGAATGAAAGAGATGAGATCTCAATTTGACAGCA 336
Qy 372 CGTTGAGAGAGAGCAAGTATGACAGATCGCTCTCACTGGCCAGAGAGAT 431
Db 337 AAAAAAGAAAAAGCCTTGAATGAAAGAGATGAGATCTCAATTTGACAGCA 396
Qy 432 TTATACCATGAAAGCACTGTAATGCTTGAATGAGAAACAGCTGACGTTAAAG 491
Db 397 TAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 456
Qy 492 AGAAGACTTATATGCTTACACTCA 519
Db 457 AAAAAAAAAAATWDTGKGAASAAA 484

RESULT 8

CNS0187R

LOCUS

DEFINITION

CNS0187R 878 bp DNA linear GSS 26-JUL-1999
Drosophila melanogaster genome survey sequence Sp6 end of BAC
BACN04E04 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

GSS:

Drosophila melanogaster.

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

REFERENCE

AUTHORS

Genoscope.

1 (bases 1 to 878)

TITLE

Direct Submission

JOURNAL

Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

COMMENT

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - <http://www.edgp.ebi.ac.uk> - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.

FEATURES

source

Location/Qualifiers
1..878
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="BACN04E04"
/clone_lib="DrosBAC"
/plasmid="pBelobAC11"
/note="end : Sp6"

BASE COUNT 279 a 132 c 120 g 182 t 165 others
ORIGIN

Query Match

Best Local Similarity 25.1%; Score 49.8; DB 17; Length 878;
Matches 60; Conservative 81; Mismatches 98; Indels 0; Gaps 0;

Qy 257 AGATGAGAGCAATTTGAAGACCTTGCAAGATTAACGTTAAACAAGAGAGAAA 316
Db 88 AAAAAAAGAAAAAGCAATTTGAAGACCTTGCAAGATTAACGTTAAACAAGAGAGAAA 147
Qy 317 AAAAAAGCACTTGAATGAAAGAGATGAGATGAGATGAGATGAGATGAGATGAG 376
Db 148 AAAAAAGCACTTGAATGAAAGAGATGAGATGAGATGAGATGAGATGAGATGAG 207
Qy 377 TAAGGAGCAAGATTAAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 436
Db 208 WAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 267
Qy 437 CCATGAAGAGCACTTGAATGCTTGAATGAGGAGGAGGAGGAGGAGGAGGAGGAG 495
Db 268 WAAAAAAGCAATTTGAAGACCTTGCAAGATTAACGTTAAACAAGAGAGAAA 326

RESULT 9

CNS0039G/c

LOCUS

DEFINITION

CNS0039G 1101 bp DNA linear GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

GSS:

Drosophila melanogaster.

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

REFERENCE

AUTHORS

Genoscope.

1 (bases 1 to 1101)

TITLE

Direct Submission

JOURNAL

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

COMMENT

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org>. The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Oseguwa and
Aaron Mammosser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the

JOURNAL COMMENT

plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0229 row: 1 column: 06
Seq primer: CTTGTAAACGACGCCACGT
Class: plasmid ends
High quality sequence stop: 423.

FEATURES

SOURCE

1. 423
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M229106"
/clone_1lb="Mouse 10kb plasmid UUCG1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

119 a 90 c 40 g 174 t

Query Match

Best Local Similarity 50.4%; Score 46.8; DB 17; Length 423;
Matches 114; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

QY 100 ACCCAATGATGATCTGCTGCTTTCCTGATCATAGAGATTGAGTAAGTGC 159
Db 423 ACTGAGCTGCTGATTTGATTTAGAACATATGATTAATTTCTTCACTATT 364
QY 160 GAAGAGAGTAACCTTCATGAGATTTGATCAATAAAGCTTAAGAGTCAAC 219
Db 363 GACTATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 304
QY 220 AAAGAGAGAGATTTTATCTGCTGAATCTGAGAGATGAGAGCAATTGGAAGC 279
Db 303 ATAGAGAGAGATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 244
QY 280 CTTGTCAAGATTAACGTTAAACAAAGAGAGAGAGAGAGAGAGAGAGAGAG 325
Db 243 CTTGAAAATTAAGAAATTAATTAATTAATTAATTAATTAATTAATTAAT 198

RESULT 12

AL514085/c

LOCUS AL514085 LTI NF1006 PL2 Homo sapiens cDNA clone CLOB0404ZE10 3
DEFINITION prime, mRNA sequence.

ACCESSION

AL514085

VERSION

AL514085.1 GI:12777579

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS

Li W.B., Gruber C., Jeesee J. and Polayes D.

TITLE

Full-length cDNA libraries and normalization

JOURNAL

Unpublished (2001)

COMMENT

Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr.

FEATURES

source

1. 458
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CLOB0404ZE10"
/clone_1lb="LTI NF1006 PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: filiang@lifetech.com URL: http://fulllength.invitrogen.com"

BASE COUNT

186 a 13 c 3 g 207 t 49 others

Query Match

Best Local Similarity 42.5%; Score 46.8; DB 9; Length 458;
Matches 117; Conservative 14; Mismatches 144; Indels 0; Gaps 0;

QY 68 TTTTATGATTTACTTACTGCTTTCCTTCAACCCCAATGATGATCGTCTTTTG 127
Db 304 TTTTATGATTTACTTACTGCTTTCCTTCAACCCCAATGATGATCGTCTTTTG 245
QY 128 CTGTGATCTTCATAGAGATTGATTAAGTGCAGAGAGAGTAACCTTCATGAAGT 187
Db 244 TTTTATGATTTACTTACTGCTTTCCTTCAACCCCAATGATGATCGTCTTTTG 185
QY 188 TTTGATTCATTAATAAAGCTTAAGAGATGCAAGAGAGATCTTATCTGCTGA 247
Db 184 ATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 125
QY 248 ACTGAGAGAGATGAGAGAGATTTGAGAGATCTTCAAGATATTAAGTCAAG 307
Db 124 AAA 65
QY 308 AAG 342
Db 64 AAA 30

RESULT 13

CNS0383B/c

LOCUS CNS0383B 802 bp DNA linear GSS 15-MAY-2000
DEFINITION Tetradon nigroviridis genome survey sequence PUC-ori end of clone 004012 of library G from Tetradon nigroviridis, genomic survey sequence.

ACCESSION

AL232112

VERSION

GI:7891247

KEYWORDS

GSS: genome survey sequence.

SOURCE

Tetradon nigroviridis.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Genoscope - Centre National de Séquençage
BP 191 91006 EVRY cedex - France

FEATURES Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
source 1. 458

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CLOBA004ZE10"
/clone_1b="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: PCWVSPORT 6; Site 1: NotI; 1st strand cDNA was primed with a NotI-oligo(drf) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the PCWVSPORT 6 vector. Library was normalized. Library was constructed by a division of Invitrogen 9800 Medical Center Drive, Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : filang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 186 a 13 c 3 g 207 t 49 others
ORIGIN

Query Match 5.8%; Score 45.2; DB 9; Length 458;
Best Local Similarity 41.1%; Pred. No. 5.6;

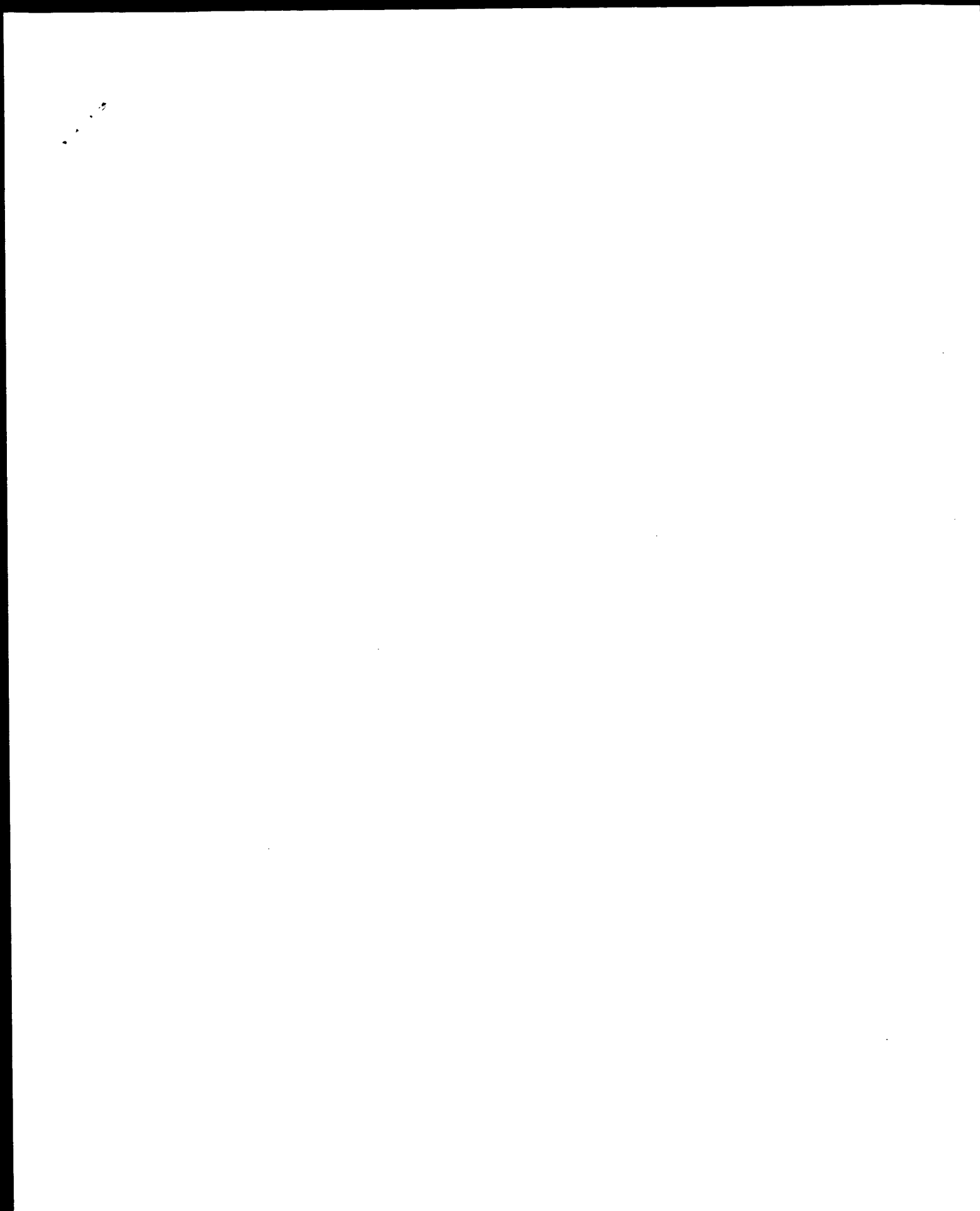
Matches 113; Conservative 18; Mismatches 144; Indels 0; Gaps 0;

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Db 162 TTTTATGTAATTAAGTCTTACTGTTTCTTATCACCAGATGATTGGATCTGAGCTTTTG 221
    ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
QY 128 CTGTGATCTTCATGAGAGATGATGATGAGTGAAGAGAGATGAACCTTCATGAAGATT 187
    ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db 222 CACCTTGCTTTAATAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAA 281
    ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
QY 188 TTGTATTCATAAAGAGCTTAAGAGATGCAACAAGAGAGAGATCTTTATCTTGCTGA 247
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Db 282 AAGAAATTTAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAA 341
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QY 248 ACTGTAGAGAGATGAGAGCAATTTGAAGACTTGTCAGAGATTAACGTTAAACAAAG 307
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Search completed: March 9, 2003, 04:42:19
Job time : 1291.6 secs



GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: March 8, 2003, 18:30:53 ; Search time 163.589 Seconds
(without alignments)
10778.963 Million cell updates/sec

Title: US-08-982-272-5

Perfect score: 783
Sequence: 1 ATGATCGAACAATACACCA.....TTGGCTTACTCAACTCTGA 783

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/NA1981.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	783	100.0	783	19	AAV39001
2	773.4	98.8	783	19	AAV38999
3	760.6	97.1	783	19	AAV38998
4	760.6	97.1	818	19	AAV61062
5	759	96.9	783	15	AAO63960
6	759	96.9	783	19	AAV12853
7	759	96.9	783	20	AAZ27524
8	754.8	96.4	782	14	AAQ41507
9	645.2	82.4	1477	22	AAH25527

10	642.2	82.0	818	16	AAU05762	Murine CD40 ligand
11	639	81.6	783	19	AAV42184	Exemplary nucleic
12	631.4	80.6	878	20	AAZ27538	Mouse trimethyl CD4
13	592.4	75.7	786	19	AAV39000	Exemplary CD40 lig
14	582.8	74.4	786	15	AAO63959	Human CD40-L type
15	582.8	74.4	786	19	AAV89997	CD40 ligand gene u
16	582.8	74.4	786	19	AAV12852	CD40 ligand coding
17	582.8	74.4	840	14	AAO41506	CD40-L DNA. Homo
18	582.8	74.4	840	15	AAO67123	CD40 ligand gene.
19	582.8	74.4	840	16	AAU05763	Human CD40 ligand
20	582.8	74.4	840	18	AAV93782	CDNA of CD40L, a n
21	582.8	74.4	840	19	AAV61063	Human CD40-L ligand
22	582.8	74.4	840	20	AAZ27525	Human CD40-L codin
23	582.8	74.4	879	22	AAE55539	Nucleotide sequenc
24	582.8	74.4	1816	21	AA51745	Human CD40 ligand
25	582.8	74.4	1816	23	AA586571	DNA encoding novel
26	581.4	74.3	840	18	AAU58122	Human CD40L nucleic
27	579.6	74.0	840	15	AAO37884	Genomic sequence o
28	578	73.8	840	16	AAO94091	Human CD40-L CDNA.
29	570	72.8	786	19	AAV39003	Exemplary CD40 lig
30	560.4	71.6	786	19	AAV39002	Exemplary CD40 lig
31	534.8	68.3	864	19	AAV39004	CD40 ligand gene u
32	525.4	67.1	885	21	AAZ55540	Feline CD154 CDNA.
33	525.4	67.1	885	21	AAZ55541	Feline CD154 CDNA.
34	522.4	66.7	780	21	AAZ55542	Feline CD154 CDNA.
35	522.4	66.7	780	21	AAZ55543	Feline CD154 CDNA.
36	522.2	66.7	1878	21	AAZ55534	Canine CD154 CDNA.
37	522.2	66.7	1878	21	AAZ55535	Canine CD154 CDNA.
38	519.2	66.3	780	21	AAZ55536	Canine CD154 CDNA.
39	519.2	66.3	780	21	AAZ55537	Canine CD154 CDNA.
40	454.6	58.1	1552	22	AAZ55525	Nucleotide sequenc
41	449.2	57.4	865	22	AAH29332	HIV-1 gp120 V3 100
42	449.2	57.4	906	22	AAH29332	HIV-1 gp120 V3 100
43	449.2	57.4	2209	22	AAH82829	HIV-1 gp120-human
44	449.2	57.4	2252	22	AAH82828	HIV-1 gp120-human
45	446.2	57.0	1425	14	AAQ41516	Human CD40-L/Fc fu

ALIGNMENTS

RESULT 1	AAV39001	standard; DNA; 783 BP.
XX	AAV39001;	
XX	23-SEP-1998	(first entry)
XX	Exemplary CD40 ligand gene used in the course of the invention.	
XX	CD40 ligand; alteration; immunoreactivity; human cell;	
XX	accessory molecule ligand; AMU; gene therapy; treatment; neoplasia;	
XX	autoimmune disorder; rheumatoid arthritis; vaccine; chimera; ss.	
OS	Chimeric - Mus sp.	
OS	Chimeric - Homo sapiens.	
XX	WO9826061-A2.	
XX	18-JUN-1998.	
XX	08-DEC-1997;	97WO-US22740.
XX	01-DEC-1997;	97US-0982272.
XX	09-DEC-1996;	96US-0032145.
XX	(REBC) UNIV CALIFORNIA.	
XX	Cantwell M, Krips TV, Sharma S;	
XX	WPI, 1998-348521/30.	

Db	61	ATGAAAATTTTATGATTAATTACTAGTGTTCCTTATCAACCCAGATGATGGGTCAACA	120
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Qy	181	GGAATTTTGTATTCATAAAAAGCTAAAGATGCAACAAGAGAGATCTTTATCC	240
Db	181	GGAATTTTGTATTCATAAAAAGCTAAAGATGCAACAAGAGAGATCTTTATCC	240
Qy	241	TTCGTGAACGTGTAGAGATGGAAGCATTTGGAAGCTTGTCAAGATATTAAGTTA	300
Db	241	TTCGTGAACGTGTAGAGATGGAAGCATTTGGAAGCTTGTCAAGATATTAAGTTA	300
Qy	301	AACAAAGAGAAAAAAGAAAAACAGCTTTGAATGCCAAGAGTGAATGAGATCTTCA	360
Db	301	AACAAAGAGAAAAAAGAAAAACAGCTTTGAATGCCAAGAGTGAATGAGATCTTCA	360
Qy	361	ATTGACAGACCGTTGATAGAGCAACCAAGATATGACAGATCCGTTCAAGTGGGCC	420
Db	361	ATTGACAGACCGTTGATAGAGCAACCAAGATATGACAGATCCGTTCAAGTGGGCC	420
Qy	421	AAGAAAGATATTAATCCATGAAAGCAACTTGTATGCTTGAATATGGAAACAGCTG	480
Db	421	AAGAAAGATATTAATCCATGAAAGCAACTTGTATGCTTGAATATGGAAACAGCTG	480
Qy	481	ACGGTTAAAAAGAGAGACTCATATATGTCTCAACATCAAGTCACTTGTCTTAATCG	540
Db	481	ACGGTTAAAAAGAGAGACTCATATATGTCTCAACATCAAGTCACTTGTCTTAATCG	540
Qy	541	GAGCCTTGACATCAAGCCCATTCATCGTGGCCTTGAGTGAAGCCACAGATGATCT	600
Db	541	GAGCCTTGACATCAAGCCCATTCATCGTGGCCTTGAGTGAAGCCACAGATGATCT	600
Qy	601	GAGAGATCTTACTCAAGGCGGCAATCCCAAGTCTCCCAAGCTTTGCCAGACAG	660
Db	601	GAGAGATCTTACTCAAGGCGGCAATCCCAAGTCTCCCAAGCTTTGCCAGACAG	660
Qy	661	TCTGTCACTTGCGGCGAGTGTGTAATTAACAAGTGTGTCTGTGTGTCAAGTGG	720
Db	661	TCTGTCACTTGCGGCGAGTGTGTAATTAACAAGTGTGTCTGTGTGTCAAGTGG	720
Qy	721	ACTGAAGACCAAGATGATCCACAGATGGCTTCATCTTTTGGCTTACTCAATC	780
Db	721	ACTGAAGACCAAGATGATCCACAGATGGCTTCATCTTTTGGCTTACTCAATC	780
Qy	781	TGA TGA 783	
Db	781	TGA 783	
RESULT 3			
AAV38998			
ID	AAV38998	standard; DNB; 783 BP.	
XX	AAV38998;		
XX	23-SEP-1998	(first entry)	
XX	CD40 ligand gene used in the course of the invention.		
XX	CD40 ligand; alteration; immunoreactivity; human cell;		
XX	accessory molecule ligand; AML; gene therapy; treatment; neoplasia;		
XX	autoimmune disorder; Rheumatoid arthritis; vaccine; ss.		
XX	Homo sapiens.		
XX	MO9826061-A2.		
XX	18-JUN-1998.		
XX	08-DEC-1997;	97MO-US22740.	

[illegible]

Db 601 GAGAGATCTTACTCAGGCGCAATACCCAGTTCTCCAGCTTTGGAGCAGCAG 660
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 Db 661 TCTGTCACTTGGCGGAGTGTGTAATTAACAGCTGTCTTGTGTGTCAAGTG 720
 Qy 721 ACTGAAGCAAGCAAGTATCAAGAGTGTGCTTCTCATCTTTGGCTTACTCAATC 780
 Db 721 ACTGAAGCAAGCAAGTATCAAGAGTGTGCTTCTCATCTTTGGCTTACTCAATC 780
 Qy 781 TGA 783
 Db 781 TGA 783
 RESULT 4
 AAV61062
 ID AAV61062 standard; DNA; 818 BP.
 AC AAV61062;
 XX 08-DEC-1998 (first entry)
 DT
 DE Murine CD40 ligand encoding DNA sequence.
 XX
 KM Murine; mouse; CD40 ligand; TNF receptor family; activated T cell;
 KW type 2 membrane glycoprotein; cell proliferation; differentiation;
 XX B cell; ds.
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT CDS 13..795
 FT /*tag= a
 FT /product= "CD40 ligand"
 XX
 PN US5817516-A.
 XX 06-OCT-1998.
 FD
 XX 28-APR-1995; 95US-0431055.
 PF
 XX 28-APR-1995; 95US-0431055.
 PR 28-APR-1995; 95US-0431055.
 PR 28-APR-1994; 94US-0234580.
 XX
 PA (BOEH) BOEHRINGER INGELHEIM PHARM INC.
 XX
 PI Castle B, Kehrly M;
 XX
 DR WPI; 1998-556393/47.
 DR P-PSDB; AAW71750.
 XX
 PT Increased proliferation of B cells in culture - by incubating them
 XX in the presence of membrane-bound CD40 ligand
 PS
 XX Example 2; Fig 1; 37pp; English.
 CC The present sequence encodes murine CD40 ligand which is used in the
 CC method of the invention. The method has been developed for proliferating
 CC B cells to increase their number at least 100-fold. The method
 CC comprises: (a) providing high density, membrane bound CD40 ligand; and
 CC (b) culturing one or more B cells in the presence of this ligand. The
 CC culture results in a proliferation in the number of B cells of at least
 CC 100 fold. Also described is a method as above where the B cells are
 CC induced to differentiate into antibody-producing cells in the presence
 CC of one or more cytokines. The method can be used for stimulating B-cell
 CC proliferation in vitro or in vivo, e.g. for treating conditions in which
 CC B-cell proliferation and activation is suppressed. Eight rounds of
 CC division over six days can be achieved, corresponding to a 256-fold
 CC increase in cell numbers, which is a vast increase compared to previous
 CC culturing methods.
 CC
 XX

SQ Sequence 818 BP; 249 A; 170 C; 186 G; 213 T; 0 other;
 Query Match 97.1%; Score 760.6; DB 19; Length 818;
 Best Local Similarity 98.2%; P-Id. No. 7,36-202;
 Matches 769; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
 Qy 1 ATGATCGAAACATACCAACCAATCTTCCCGATCTGGGCGACCTGACCTGCCATCAGC 60
 Db 13 ATGATGAAACATACCAACCAATCTTCCCGATCTGGGCGACCTGACCTGCCATCAGC 72
 Qy 61 ATGAAATTTTATGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATGAT 120
 Db 73 ATGAAATTTTATGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATGAT 132
 Qy 121 CTTTGTGTGTATCTTCAATGAAAGTATGATGATGATGATGATGATGATGATGATGAT 180
 Db 133 CTTTGTGTGTATCTTCAATGAAAGTATGATGATGATGATGATGATGATGATGATGAT 192
 Qy 181 GAAATTTTGTATTTCAATGAAAGTATGATGATGATGATGATGATGATGATGATGAT 240
 Db 193 GAAATTTTGTATTTCAATGAAAGTATGATGATGATGATGATGATGATGATGATGAT 252
 Qy 241 TTGCTGAACTGTGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAG 300
 Db 253 TTGCTGAACTGTGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAG 312
 Qy 301 AACAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 360
 Db 313 AACAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 372
 Qy 361 ATTGCAAGACAGCTTGTAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 420
 Db 373 ATTGCAAGACAGCTTGTAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 432
 Qy 421 AAGAAAGATATTTATCCATGAAAGCACTTGTATGATGATGATGATGATGATGATGAT 480
 Db 433 AAGAAAGATATTTATCCATGAAAGCACTTGTATGATGATGATGATGATGATGATGAT 492
 Qy 481 ACGTTTAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 540
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 Qy 541 GAGCTTCAAGTCAAGCCCAATGATGATGATGATGATGATGATGATGATGATGATGAT 600
 Db 553 GAGCTTCAAGTCAAGCCCAATGATGATGATGATGATGATGATGATGATGATGATGAT 612
 Qy 601 GAGAAATCTTACTCAAGGCGCAATATCCACAGTCTCTCCAGCTTTGCGAGCAGCAG 660
 Db 613 GAGAAATCTTACTCAAGGCGCGCAATATCCACAGTCTCTCCAGCTTTGCGAGCAGCAG 672
 Qy 661 TCTGTCACTTGGCGGAGTGTGTAATTAACAGCTGTCTTGTGTGTCAAGTG 720
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 Qy 721 ACTGAAGCAAGCAAGTATCAAGAGTGTGCTTCTCATCTTTGGCTTACTCAATC 780
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 Qy 781 TGA 783
 Db 793 TGA 795
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 ID AA063960 standard; cDNA to mRNA; 783 BP.
 AC AA063960;
 XX
 DT 12-JAN-1995 (first entry)
 XX
 DE Mouse CD40-L type II transmembrane protein coding sequence.
 XX

KM Leucine zipper; trimerisation; trimeric CD40-L; fusion protein;
 KW hetero-oligomer; homo-oligomer; type II transmembrane protein;
 XX soluble CD40-L; tumour necrosis factor family; ss.
 OS Mus musculus.

Key Location/Qualifiers
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 FT /tag= a
 FT /product= mouse CD40-L
 FT /note= "nucleotides 148-780 code for the
 extracellular region (amino acids 50-260)"

W09410308-A.

11-MAY-1994.

20-OCT-1993; 93WO-US10034.

23-OCT-1992; 92US-0969703.

13-AUG-1993; 93US-0107353.

(IMMV) IMMUNEX CORP.

Spriggs MK, Srinivasan S;

WPI; 1994-167465/20.

P-RSDB; AARS3970.

Pren. of soluble oligomeric mammalian proteins - using host
 cells to express a fusion protein comprising a leucine zipper
 domain and a heterologous mammalian protein

Example 1; Page 25-26; 35pp; English.

A DNA fragment encoding the extracellular (soluble) region of mouse
 CD40-L was ligated to a synthetic oligonucleotide sequence coding
 for a leader peptide, a 33 amino acid leucine zipper sequence
 (AARS3968) and the Flag (RTM) linker sequence. Cells expressing the
 fusion construct are grown to accumulate oligomeric, soluble CD40-L
 in the supernatant. The leucine zipper sequence spontaneously
 trimerises in solution and fusion proteins comprising
 the sequence fused to a heterologous mammalian protein also form
 oligomers.

Sequence 783 BP; 243 A; 159 C; 178 G; 203 T; 0 other;

Query Match 96.9%; Score 759; DB 15; Length 783;

Best Local Similarity 98.1%; Pred. No. 2e-201;

Matches 768; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 ATGATGAAACATACACCAAACTTCCCGATCGCGCCACATGATCCCATCAGC 60
 DB 1 ATGATGAAACATACACCACTTCCCGATCGCGCCACATGATCCCATCAGC 60
 QY 61 ATGAAATTTTATGATTTACTTACTCTTTTCTTATCCCAATGATGATCTG 120
 DB 61 ATGAAATTTTATGATTTACTTACTCTTTTCTTATCCCAATGATGATCTG 120
 QY 121 CTTTTCGTGATCTTCTTATGAGATTTGATGATGATGATGATGATGATGAT 180
 DB 121 CTTTTCGTGATCTTCTTATGAGATTTGATGATGATGATGATGATGATGAT 180
 QY 181 GAAGATTTTATGATTTATGATGATGATGATGATGATGATGATGATGATGAT 240
 DB 181 GAAGATTTTATGATTTATGATGATGATGATGATGATGATGATGATGATGAT 240
 QY 241 TTGCTGAAGCTGTGAGAGATGAGAGCAATTTGAGAGCTTGTCAAGGATTA 300
 DB 241 TTGCTGAAGCTGTGAGAGATGAGAGCAATTTGAGAGCTTGTCAAGGATTA 300
 QY 301 AACAAAG 360
 DB 301 AACAAAG 360

DB 301 AACAAAG 360
 QY 361 ATTGAGACACAGTTGTAAGCAGAACCAAGTATGACAGATCCGTTTACAGTGG 420
 DB 361 ATTGAGACACAGTTGTAAGCAGAACCAAGTATGACAGATCCGTTTACAGTGG 420
 QY 421 AAGAAAGATTTTATGATTTATGATGATGATGATGATGATGATGATGATGAT 480
 DB 421 AAGAAAGATTTTATGATTTATGATGATGATGATGATGATGATGATGATGAT 480
 QY 481 ACGGTTAAAG 540
 DB 481 ACGGTTAAAG 540
 QY 541 GAGCCTTGAGTCAAGCCCATTCATGCTGAGCTCTGAGCTGAGCCAGATGAT 600
 DB 541 GAGCCTTGAGTCAAGCCCATTCATGCTGAGCTCTGAGCTGAGCCAGATGAT 600
 QY 601 GAGAGATCTTACTCAAGCGGCAAAATACCAAGTTCCTCCAGCTTTCGAGCAG 660
 DB 601 GAGAGATCTTACTCAAGCGGCAAAATACCAAGTTCCTCCAGCTTTCGAGCAG 660
 QY 661 TCGTTCACTTGGCGGAGTGTGAAATTAAGCTGCTGCTGCTTGTCAAGCTG 720
 DB 661 TCGTTCACTTGGCGGAGTGTGAAATTAAGCTGCTGCTGCTTGTCAAGCTG 720
 QY 721 ACTGAAGCAAGCCAGATGATCCACAGAGTTCCTCATCTTTGGCTTACTCAATC 780
 DB 721 ACTGAAGCAAGCCAGATGATCCACAGAGTTCCTCATCTTTGGCTTACTCAATC 780
 QY 781 TGA 783
 DB 781 TGA 783

RESULT 6
 AA12853
 ID AA12853 standard; cDNA to mRNA; 783 BP.
 XX
 AC AA12853;
 XX
 DT 13-MAY-1998 (first entry)
 XX
 DE CD40 ligand coding sequence.
 XX
 KW Leucine zipper; fusion protein production; soluble oligomeric protein;
 KW heterologous mammalian type II transmembrane protein; activated T cell;
 KW heterologous mammalian type I transmembrane protein; antibody production;
 KW CD40-L; B-cell proliferation; CD27-L; lymphocyte antigen; ss.
 OS Mus sp.
 FH Key Location/Qualifiers
 FT CDS 1..783
 FT /tag= a
 PN US5716805-A.
 PD 10-FEB-1998.
 PF 18-MAY-1995; 95US-0446922.
 PR 18-MAY-1995; 95US-0446922.
 PR 25-OCT-1991; 91US-0763707.
 PR 05-DEC-1991; 91US-0805723.
 PR 23-OCT-1992; 92US-0969703.
 PR 13-AUG-1993; 93US-0107353.
 PA (IMMV) IMMUNEX CORP.
 XX Spriggs MK, Srinivasan S;
 PI WPI; 1998-144799/13.
 XX

DR P-85DB; AAM41179.

XX Soluble oligomeric fusion proteins - comprising leucine zipper fused
PT to extracellular region of transmembrane protein

XX Example 1; column 23-24; 21pp; English.

XX This sequence is the coding sequence for the mouse CD40 ligand (CD40-L).
CC The encoded protein can be used in a fusion protein produced using the
CC method of the invention. The method is for preparing soluble oligomeric
CC protein by culturing a host cell transfected with a vector for the
CC fusion protein. The soluble oligomeric proteins comprise a leucine zipper
CC fused to the N terminus of the extracellular region of a heterologous
CC mammalian type II transmembrane protein or to the C terminus of the
CC extracellular region of a heterologous mammalian type I transmembrane
CC protein, where the leucine zipper is a peptide comprising at least part
CC of AAM41171 or AAM41172, optionally with conservative amino acid
CC substitutions, provided that the peptide trimerizes in solution. A
CC soluble fusion protein comprising the leucine zipper of AAM41171 linked
CC to the extracellular region of CD40-L (a type II transmembrane protein
CC that is found on activated T cells and acts as a ligand for the B-cell
CC antigen CD40) stimulates B-cell proliferation and antibody production in
CC a similar manner to membrane-bound CD40-L. A soluble fusion protein
CC comprising the leucine zipper of AAM41172 linked to the extracellular
CC region of CD27-L (a type II transmembrane protein that binds to the
CC lymphocyte antigen CD27) inhibits binding of CD27c (a fusion protein
CC comprising the extracellular region of CD27 and a human IgG1 Fc region)
CC to EBV-transformed B cells expressing CD27-L.

XX Sequence 783 BP; 243 A; 159 C; 178 G; 203 T; 0 other;

XX Query Match 96.9%; Score 759; DB 19; Length 783;

XX Best Local Similarity 98.1%; Pred. No. 2e-201;

XX Matches 768; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACCAACCACTCTCCCGATCGCGCGCATGACATGCCATCAGC 60
DB 1 ATGATAGAAACATACCAACCACTCTCCCGATCGCGCGCATGACATGCCATCAGC 60
QY 61 ATGAAATTTTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 120
DB 61 ATGAAATTTTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 120
QY 121 CTTTTCGTCGTATCTTCTATGAAAGATTTGATTAAGTGAAGAGAGAGAGAGAGAG 180
DB 121 CTTTTCGTCGTATCTTCTATGAAAGATTTGATTAAGTGAAGAGAGAGAGAGAG 180
QY 181 GAAATTTTGTATTCATTAATAAAGCTAAAGATGCAACAAGAGAGAGATCTTATCC 240
DB 181 GAAATTTTGTATTCATTAATAAAGCTAAAGATGCAACAAGAGAGAGATCTTATCC 240
QY 241 TTGCTGAACGTGAGAGATGAGAGAGATTTGAGAGACCTTGTCAAGATATTAAGTTA 300
DB 241 TTGCTGAACGTGAGAGATGAGAGAGATTTGAGAGACCTTGTCAAGATATTAAGTTA 300
QY 301 AACAAAG 360
DB 301 AACAAAG 360
QY 361 ATTGAG 420
DB 361 ATTGAG 420
QY 421 AAGAAAGATTTATTCATTAATAAAGCTTGAATGCTTGAATAAGGAGAGAGAGAGAG 480
DB 421 AAGAAAGATTTATTCATTAATAAAGCTTGAATGCTTGAATAAGGAGAGAGAGAGAG 480
QY 481 ACGGTTAAAG 540
DB 481 ACGGTTAAAG 540
QY 541 GAGCTTGAGTCAAGCCCATTCATCTGCGCTCTGGGTGAAGCCCAAGATTTGAGATCT 600
DB 541 GAGCTTGAGTCAAGCCCATTCATCTGCGCTCTGGGTGAAGCCCAAGATTTGAGATCT 600

DB 541 GAGCTTGAGTCAAGCCCATTCATCTGCGCTCTGGGTGAAGCCCAAGATTTGAGATCT 600

QY 601 GAGAGATCTTATCTCAAG 660

DB 601 GAGAGATCTTATCTCAAG 660

QY 661 TCTGTTCACTTGGGCGAGAGTGTGTAATTAACAAGCTGTGCTTGTGTTGTCACAGTG 720

DB 661 TCTGTTCACTTGGGCGAGAGTGTGTAATTAACAAGCTGTGCTTGTGTTGTCACAGTG 720

QY 721 ACTGAAGCAAGCAAGATGATTCACAGAGTGGCTTCTCATCTTTGGCTTACTCAACTC 780

DB 721 ACTGAAGCAAGCAAGATGATTCACAGAGTGGCTTCTCATCTTTGGCTTACTCAACTC 780

QY 781 TGA 783

DB 781 TGA 783

DE Mouse CD40-L coding sequence.

DE RESULT 7
AA227524
ID AA227524 standard; cDNA; 783 BP.

AC AA227524;

XX 13-DEC-1999 (first entry)

XX Mouse CD40-L coding sequence.

KW CD40-L; CD40 receptor ligand; anti-human CD40-L monoclonal antibody;

KW binding inhibitor; trimeric CD40-L; anti-immunoglobulin M;

KW peripheral blood B cell; proliferation inhibitor; 88.

XX Mus sp.

XX US5961974-A.

XX 24-MAY-1994; 94US-0249189.

XX 25-OCT-1991; 91US-0783707.

XX 05-DEC-1991; 91US-0805723.

XX 23-OCT-1992; 92US-0969703.

XX (IMMV) IMMUNEX CORP.

PI Spriggs MK, Fanslow WC, Armistage RJ;

DR WPI; 1999-579604/49.

DR P-85DB; AAY39937.

XX Anti-human CD40-Ligand monoclonal antibodies -

XX Disclosure; Fig 1; 59pp; English.

XX This sequence encodes the mouse CD40 receptor ligand (CD40-L). The

XX invention relates to anti-human CD40-L monoclonal antibodies M90 secreted

XX by hybridoma hCD40L-M90 (ATCC HB-12055) and M91 secreted by hybridoma

XX hCD40L-M91 (ATCC HB-12056). M90 and M91 inhibit CD40-L binding to CD40

XX CC and the ability of trimeric CD40-L and anti-immunoglobulin M to induce

XX CC proliferation of peripheral blood B cells.

QY 1 ATGATCGAAACATACCAACCACTCTCCCGATCGCGCGCATGACATGCCATCAGC 60

DB 1 ATGATAGAAACATACCAACCACTCTCCCGATCGCGCGCATGACATGCCATCAGCAGC 60

QY 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATCAACCAATGATTTGATCTGTG 120
 DB 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATCAACCAATGATTTGATCTGTG 120
 QY 121 CTTTGGCTGTGATCTTCAATGAAGATTTGATGATGATGATGATGATGATGATGAT 180
 DB 121 CTTTGGCTGTGATCTTCAATGAAGATTTGATGATGATGATGATGATGATGATGAT 180
 QY 181 GAAGATTTTATGATTTATGATTTATGATTTATGATTTATGATTTATGATTTATGATTT 240
 DB 181 GAAGATTTTATGATTTATGATTTATGATTTATGATTTATGATTTATGATTTATGATTT 240
 QY 241 TTGCTGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
 DB 241 TTGCTGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
 QY 301 AACAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 360
 DB 301 AACAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 360
 QY 361 ATTGACGACACGCTGTGATGACGACGACGACGACGACGACGACGACGACGACGACGAC 420
 DB 361 ATTGACGACACGCTGTGATGACGACGACGACGACGACGACGACGACGACGACGACGAC 420
 QY 421 AAGAAAGATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 480
 DB 421 AAGAAAGATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 480
 QY 481 ACGGTTAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 540
 DB 481 ACGGTTAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 540
 QY 541 GAGCTTTGAGTCAAGCCGATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
 DB 541 GAGCTTTGAGTCAAGCCGATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
 QY 601 GAGAGATCTTTACTCAAGGCGGCAATACCAAGCTTCCCTCCCACTTTGGAGACGACG 660
 DB 601 GAGAGATCTTTACTCAAGGCGGCAATACCAAGCTTCCCTCCCACTTTGGAGACGACG 660
 QY 661 TCTGTTCACTTGGCGGAGTGTGTAATTAACAAGCTGTGCTGTGTTGTGCAACGCTG 720
 DB 661 TCTGTTCACTTGGCGGAGTGTGTAATTAACAAGCTGTGCTGTGTTGTGCAACGCTG 720
 QY 721 ACTGAAGCAAGCCAAAGTATCCACAGAGTTGGCTTCATCTTTGGCTTACCAATC 780
 DB 721 ACTGAAGCAAGCCAAAGTATCCACAGAGTTGGCTTCATCTTTGGCTTACCAATC 780
 QY 781 TGA 783
 DB 781 TGA 783
 RESULT 8
 AAQ41507
 ID AAQ41507 standard; DNA; 782 BP.
 AC AAQ41507;
 DT 12-AUG-1993 (first entry)
 DE Murine CD40-L DNA.
 XX Human; CD40-L; CD40; type II; membrane; polypeptide; extracellular;
 KM transmembrane; region; intracellular; soluble; activity; B cell;
 KM proliferation; induction; antibody; secretion; IGB; agonist;
 KM antagonist; binding assay; ss.
 OS Mus musculus.
 OS W09308207-A.
 PN W09308207-A.
 XX 29-APR-1993.
 PD

XX 23-OCT-1992; 92MO-US08990.
 PF 25-OCT-1991; 91US-0783707.
 PR 05-DEC-1991; 91US-0805723.
 PA (IMMW) IMMUNEX CORP.
 PI Armitage RJ, Fanslow WC, Spriggs MK;
 XX WPI; 1993-152417/18.
 DR P-PSDB; AAR6702.
 XX
 PT New cytokine CD40-L as CD40 agonist and antagonist - is used for
 PT treating allergies, lupus, rheumatoid arthritis,
 PT graft-versus-host disease and insulin-dependent diabetes mellitus
 PS Disclosure; Fig 1; 80pp; English.
 CC This sequence encodes a murine CD40-L polypeptide which binds to CD40.
 CC CD40-L is a type II membrane polypeptide which has an extracellular
 CC region at its C-terminus, a transmembrane region and an
 CC intracellular region at its N-terminus. A soluble form of CD40-L
 CC lacks the transmembrane domain. CD40-L activity is mediated by
 CC binding with CD40 and induces B cell proliferation and induction of
 CC antibody secretion, including IGB. Membrane bound CD40-L acts as a
 CC CD40 agonist and soluble CD40-L acts as a CD40 antagonist. CD40-L
 CC can be used in a binding assay to detect cells expressing CD40.
 SQ Sequence 782 BP; 242 A; 157 C; 180 G; 203 T; 0 other;
 Query Match 96.4%; Score 754.8; DB 14; Length 782;
 Best Local Similarity 97.8%; Pred. No. 3e-200;
 Matches 765; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
 QY 1 ATGATCAAAACATACCAACCAACTTCTCCCGATGCGGCGCACTGAGTCCCATCAGC 60
 DB 1 ATGATCAAAACATACCAACCAACTTCTCCCGATGCGGCGCACTGAGTCCCATCAGC 60
 QY 61 ATGAAATTTTATGATTTATGATTTATGATTTATGATTTATGATTTATGATTTATGATTT 120
 DB 61 ATGAAATTTTATGATTTATGATTTATGATTTATGATTTATGATTTATGATTTATGATTT 120
 QY 121 CTTTGGCTGTGATCTTCAATGAAGATTTGATGATGATGATGATGATGATGATGATGAT 180
 DB 121 CTTTGGCTGTGATCTTCAATGAAGATTTGATGATGATGATGATGATGATGATGATGAT 180
 QY 181 GAAGATTTTATGATTTATGATTTATGATTTATGATTTATGATTTATGATTTATGATTT 240
 DB 181 GAAGATTTTATGATTTATGATTTATGATTTATGATTTATGATTTATGATTTATGATTT 240
 QY 241 TTGCTGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
 DB 241 TTGCTGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
 QY 301 AACAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 360
 DB 301 AACAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 360
 QY 361 ATTGACGACACGCTGTGATGACGACGACGACGACGACGACGACGACGACGACGACGAC 420
 DB 361 ATTGACGACACGCTGTGATGACGACGACGACGACGACGACGACGACGACGACGACGAC 420
 QY 421 AAGAAAGATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 480
 DB 421 AAGAAAGATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 480
 QY 481 ACGGTTAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 540
 DB 481 ACGGTTAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 540
 QY 541 GAGCTTTGAGTCAAGCCGATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600

Accession	Sequence	Position
Dd	541 GACCTTGAGATCAAGCCCAATTCAATGCTGGGCTGTGGCTGAAAGCCCAAGTGAATCT	6000
Qy	601 GAGAGATCTTACTCAAGGGCGCAATATCCCAAGTCTTCCCAAGCTTTGGCAGCGAG	6600
Dd	601 GAGAGATCTTACTCAAGGGCGCAATATCCCAAGTCTTCCCAAGCTTTGGCAGCGAG	6600
Qy	661 TCTGTTCACTGGGCGAGGTTTGAATTACAAGCTGTGCTTCGTGTTGTCAACGTG	7200
Dd	661 TCTGTTCACTGGGCGAGGTTTGAATTACAAGCTGTGCTTCGTGTTGTCAACGTG	7200
Qy	721 ACTGAAGCAAGCCAAATGATCCACAGAGTTGGCTTCTCATCTTTGGCTTACTCAAACTC	7800
Dd	721 ACTGAAGCAAGCCAAATGATCCACAGAGTTGGCTTCTCATCTTTGGCTTACTCAAACTC	7800
Qy	781 TG 782	
Dd	781 TG 782	

AAH25527	standard; DNA; 1477 BP.
AAH25527;	
22-AUG-2001	(first entry)
Nucleotide sequence of surfactant protein D fused to CD40 ligand.	
Fusion protein; CD40 ligand; tumour necrosis factor; TNF; collectin;	
pulmonary surfactant protein D; SPD; immunocompetent cell;	
cell antigenicity; vaccine adjuvant; chimera; ss.	
Chimeric - Mus sp.	
Chimeric - Mus sp.	
Key	Location/Qualifiers
CDS	32..1444
FT	/*tag= a
FT	32..88
FT	/*tag= b
FT	/note= "signal peptide from murine surfactant protein D"
WO200142296-A1.	
14-JUN-2001.	
20-MAR-2000; 2000MO-US07380.	
09-DEC-1999; 99US-0454222.	
(KORN/) KORNBLUTH R S.	
Kornbluth RS;	
WPI; 2001-381642/40.	
P-PSDB; AAB84421.	
Producing tumor necrosis factor superfamily proteins as multimeric	
ligands fused onto collectin molecules e.g. pulmonary surfactant	
protein D, useful as vaccine adjuvants against infectious agents and	
tumours -	
Claim 1; Page 65-68; 74p; English.	
The present sequence encodes a fusion protein comprising the mature	
murine surfactant protein D (including hmb region, collagenous portion,	
and neck) fused to the murine CD40 ligand extracellular region (including	
stalk). The specification describes a method for constructing stable	
bioactive fusion proteins of the difficult to express tumor necrosis	
factor superfamily (TNFSF) proteins (especially CD40 ligand) as	
multimeric ligands fused onto branched protein backbones such as	
collectin molecules e.g. pulmonary surfactant protein D (SPD). The fusion	

proteins if the invention are useful for stimulating immune response in CC potentially immunocompetent cells (e.g., resting B cells). They are also useful for increasing antigenicity of cells such as tumor cells or human immunodeficiency virus (HIV) positive cells. They are also useful as a vaccine adjuvant since they stimulate B cells, macrophages and dendritic cells. Since the large size of the soluble fusion protein makes them less likely to diffuse into the circulation, they can be advantageously used as a vaccine adjuvant or tumor immunotherapy agent, injected locally to prevent them from diffusing away. Also, the TNF α -collectin fusion proteins present new possibilities for the expression of highly active, multimeric, soluble TNF α members. CD40L was a powerful stimulant for macrophages and dendritic cells.

CC a gene encoding an accessory molecule ligand (AML) into the cells so that
 CC the AML is expressed on the surface of the cells. Vectors containing the
 CC AML genes can be used in gene therapy for treating neoplasia or
 CC autoimmune disorders such as rheumatoid arthritis. They can also be
 CC used for vaccination to produce immunity against a virus cell,
 CC bacteria, protein, fungus or neoplasia.

XX Sequence 783 BP; 252 A; 167 C; 166 G; 198 T; 0 other;

Query Match 81.6%; Score 639; DB 19; Length 783;
 Best Local Similarity 88.5%; Pred. No. 5.6e-168;

Matches 693; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACCAACCACTTCTCCCGATCTGCGGCGCACTGATGCCCATCAGC 60
 DB 1 ATGATCGAAACATACCAACCACTTCTCCCGATCTGCGGCGCACTGATGCCCATCAGC 60
 QY 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCCAAATGATGATCTGTG 120
 DB 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCCAAATGATGATGATCTGTG 120
 QY 121 CTTTTCCTGTGATCTTATGAAAGATGATGATGATGATGATGATGATGATGATGAT 180
 DB 121 CTTTTCCTGTGATCTTATGAAAGATGATGATGATGATGATGATGATGATGATGAT 180
 QY 181 GAAATTTTGTATCTATAAAAGCTAAAGATGCAAAAGAGAGAGATCTTTATCC 240
 DB 181 GAAATTTTGTATCTATAAAAGCTAAAGATGCAAAAGAGAGATCTTTATCC 240
 QY 241 TTGCTGAACCTGTAGAGATGAGAAAGCAATTTGAAGCTTGTCAAGATATACGTTA 300
 DB 241 TTGCTGAACCTGTAGAGATGAGAAAGCAATTTGAAGCTTGTCAAGATATACGTTA 300
 QY 301 AACCAAG 360
 DB 301 AACCAAG 360
 QY 361 ATTGAGAGACAGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
 DB 361 ATTGAGAGACAGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
 QY 421 AAGAAAGATTTATACATCATGAAAGCACTTGATGCTTGAAGAGAGAGAGAGAGAG 480
 DB 421 AAGAAAGATTTATACATCATGAAAGCACTTGATGCTTGAAGAGAGAGAGAGAGAG 480
 QY 481 ACGGTTAAAG 540
 DB 481 ACGGTTAAAG 540
 QY 541 GAGCTTCAGATCAAGCCCATTCATCTGCGGCTGTGCTGAGAGAGAGAGAGAGAGAT 600
 DB 541 GAGCTTCAGATCAAGCCCATTCATCTGCGGCTGTGCTGAGAGAGAGAGAGAGAGAT 600
 QY 601 GAGAGATCTTACTCAAGCGGCAATACCAAGCTTCCGACCTTGGAGAGAGAGAGAG 660
 DB 601 GAGAGATCTTACTCAAGCGGCAATACCAAGCTTCCGACCTTGGAGAGAGAGAGAG 660
 QY 661 TCTGTTCACTTGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
 DB 661 TCTGTTCACTTGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
 QY 721 ACTGAAG 780
 DB 721 ACTGAAG 780
 QY 781 TGA 783
 DB 781 TGA 783

RESULT 12
 AA227538
 ID AA227538 standard; cDNA; 878 BP.

XX AA227538;
 AC 13-DEC-1999 (first entry)
 XX Mouse trimeric CD40-L coding sequence.
 DE CD40-L; CD40 receptor ligand; anti-human CD40-L monoclonal antibody;
 KW binding inhibitor; trimeric CD40-L; anti-immunoglobulin M;
 KW peripheral blood B cell; proliferation inhibitor; ss.
 XX Mus sp.
 OS US5961974-A.
 PN 05-OCT-1999.
 PD 24-MAY-1994; 94US-0249189.
 PF 25-OCT-1991; 91US-0783707.
 PR 05-DEC-1991; 91US-0805723.
 PR 23-OCT-1992; 92US-0969703.
 XX (IMV) IMMUNEX CORP.
 PA Spriggs MK, Fanelow WC, Armitage RJ;
 PI WPI; 1999-579604/49.
 DR P-PSDB; AAY39941.
 XX Anti-human CD40-L ligand monoclonal antibodies -
 PS Example 17; Column 69-72; 59pp; English.
 CC This sequence encodes the mouse trimeric CD40 receptor ligand (CD40-L).
 CC The invention relates to anti-human CD40-L monoclonal antibodies M90
 CC secreted by hybridoma hCD40L-M90 (ATCC HB-12055) and M91 secreted by
 CC hybridoma hCD40L-M91 (ATCC HB-12056). M90 and M91 inhibit CD40-L binding
 CC to CD40 and the ability of trimeric CD40-L and anti-immunoglobulin M to
 CC induce proliferation of peripheral blood B cells.
 XX
 SQ Sequence 878 BP; 277 A; 178 C; 203 G; 220 T; 0 other;

Query Match 80.6%; Score 631.4; DB 20; Length 878;
 Best Local Similarity 99.8%; Pred. No. 7.8e-166;
 Matches 632; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 151 GATAGAGTGAAG 210
 DB 225 GATAGAGTGAAG 284
 QY 211 AGATGCAACAAAG 270
 DB 285 AGATGCAACAAAG 344
 QY 271 TTGAAGACCTGTCAAGAGATATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 330
 DB 345 TTGAAGACCTGTCAAGAGATATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 404
 QY 331 GAAATGCAAG 390
 DB 405 GAAATGCAAG 464
 QY 391 AGTAATGCAAG 450
 DB 465 AGTAATGCAAG 524
 QY 451 TTGTAATGCTTGAAG 510
 DB 525 TTGTAATGCTTGAAG 584
 QY 511 TACACTGAAGTCACTTGTGCTTAATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 570

Db 585 TACACTCAAGTCACTTCTGCTTAATCGGAGACCTTCGAGTCAAGCCCATTCATGTC 644
 Qy 571 GGCTCTGCTGAAGCCAGATTTGATCTGAGAAATCTTACTCAAGCCGCAATTC 630
 Db 645 GGCCTCTGCTGAAGCCAGATTTGATCTGAGAAATCTTACTCAAGCCGCAATTC 704
 Qy 631 CACAGTTCTCCAGCTTTCGAGACAGAGTCTTTCACCTTGGCGAGTGTGAATTA 690
 Db 705 CACAGTTCTCCAGCTTTCGAGACAGAGTCTTTCACCTTGGCGAGTGTGAATTA 764
 Qy 691 CAAGCTGTGCTTCTGTGTGTTGCAAGTCAAGTCAAGCCAGTGTTCACAGAGTT 750
 Db 765 CAAGCTGTGCTTCTGTGTGTTGCAAGTCAAGTCAAGCCAGTGTTCACAGAGTT 824
 Qy 751 GGCTCTCACTTTTGGCTTACTCAAACTCTGA 783
 Db 825 GGCTCTCACTTTTGGCTTACTCAAACTCTGA 857

RESULT 13

ID AAV39000
 XX AAV39000 standard; DNA; 786 BP.

AC AAV39000;

DT 23-SEP-1998 (first entry)

DE Exemplary CD40 ligand gene used in the course of the invention.

KW CD40 ligand; alteration; immunoreactivity; human cell;

KW accessory molecule; ligand; AMU; gene therapy; treatment; neoplasia;

OS autoimmune disorder; rheumatoid arthritis; vaccine; chimera; ss.

OS Chimeric - Mus sp.

PN Chimeric - Homo sapiens.

XX MO826061-A2.

PD 18-JUN-1998.

PF 08-DEC-1997; 97MO-US22740.

PR 01-DEC-1997; 97US-0982272.

PR 09-DEC-1996; 96US-0032145.

PA (REGC) UNIV CALIFORNIA.

PI Cantwell M, Kipps TJ, Sharma S;

DR MPI; 1998-348521/30.

PT Vectors containing accessory molecule ligand genes - used for

PT altering immunoreactivity of cells, particularly for treatment of

PS neoplasia or autoimmune disorders, e.g. rheumatoid arthritis

XX Disclosure; Page 105; 167pp; English.

CC The present sequence represents an exemplary CD40 ligand gene,

CC comprising nucleotides encoding the extracellular domains (Domains III

CC and IV) of human CD40 ligand gene (AAV38998) are operatively linked to

CC nucleotides encoding the murine CD40 ligand transmembrane domain (Domain

CC I) (AAV38997) which is operatively linked to the human CD40 ligand gene

CC cytoplasmic domain (Domain I). The sequence is used to exemplify the

CC method of the invention. The specification describes a method for

CC altering the immunoreactivity of human cells which comprises introducing

CC a gene encoding an accessory molecule ligand (AMU) into the cells so that

CC the AMU is expressed on the surface of the cells. Vectors containing the

CC AMU genes can be used in gene therapy for treating neoplasia or

CC autoimmune disorders such as rheumatoid arthritis. They can also be used

CC for vaccination to produce immunity against a virus cell, bacteria,

CC protein, fungus or neoplasia.

CC Sequence 786 BP; 250 A; 168 C; 167 G; 201 T; 0 other;

Query Match 75.7%; Score 592.4; DB 19; Length 786;
 Best Local Similarity 85.5%; Pred. No. 5,5e-155;
 Matches 672; Conservative 0; Mismatches 111; Indels 3; Gaps 1;

Qy 1 ATGATGAAACATCAACCAACTTCTCCCGATCTGCGGCCATCTGAGTCCCATACG 60
 Db 1 ATGATGAAACATCAACCAACTTCTCCCGATCTGCGGCCATCTGAGTCCCATACG 60
 Qy 61 ATGAAATTTTATGATTTTACTTCTGTTTCTTATACCAATGATGATCTGTG 120
 Db 61 ATGAAATTTTATGATTTTACTTCTGTTTCTTATACCAATGATGATCTGTG 120
 Qy 121 CTTTGTGCTGTATCTTCAATGAGATTTGATTAAGTGTGAGAGAGAACTTTCAT 180
 Db 121 CTTTGTGCTGTATCTTCAATGAGATTTGATTAAGTGTGAGAGAGAACTTTCAT 180
 Qy 181 GAAATTTTGTATTCATTAATAAAGCTTAAGATGCAACAAAGAGAGATCTTATCC 240
 Db 181 GAAATTTTGTATTCATTAATAAAGCTTAAGATGCAACAAAGAGAGATCTTATCC 240
 Qy 241 TTGCTGAATCTGTGAGAGATGAGAGCAATTTGAAGACTTGTCAAGATTAAGTTA 300
 Db 241 TTGCTGAATCTGTGAGAGATGAGAGCAATTTGAAGACTTGTCAAGATTAAGTTA 300
 Qy 301 AACCAAGAGA--GAAAAAGAAACAGCTTTGAATGCAAAAGGTGATGAGATCCT 357
 Db 301 AACCAAGATCCT 360
 Qy 358 CAATTTGAGAGACAGCTTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 417
 Db 361 CAATTTGAG 420
 Qy 418 GCCAAGAAAGATTTATTCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 477
 Db 421 GCTGAAAAGAGATTCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
 Qy 478 CTGACGTTTAAAG 537
 Db 481 CTGACGTTTAAAG 540
 Qy 538 CGGAGAGCTTCAGATCAAGCCCATTCATGCTGCGCTCTGAGAGCCAGCATTTGA 597
 Db 541 CGGAGAGCTTCAGATCAAGCCCATTCATGCTGCGCTCTGAGAGCCAGCATTTGA 600
 Qy 598 TCTGAGAGATTTTACTCAAGCGGCAAAATCCACAGTCTGCCAGCTTTGGCAGAG 657
 Db 601 TCTGAGAGATTTTACTCAAGCGGCAAAATCCACAGTCTGCCAGCTTTGGCAGAG 660
 Qy 658 CAGTCTGTTCACTGGGCGGAGGTGTTGAATTAACAAGTGTGCTGTGTGTCAC 717
 Db 661 CAGTCTGTTCACTGGGCGGAGGTGTTGAATTAACAAGTGTGCTGTGTGTCAC 720
 Qy 718 GTGACTGAGCAAGCAAGTATCAAGAGTTGCTTCTCATCTTTTGGCTTACTCAA 777
 Db 721 GTGACTGATCAAGCAAGTATGAGCAATGACATGCTTCAAGTCTTGGCTTACTCAA 780
 Qy 778 CTCCTGA 783
 Db 781 CTCCTGA 786

RESULT 14

ID AA063959
 XX AA063959 standard; cDNA to mRNA; 786 BP.

AC AA063959;

DT 11-JAN-1995 (first entry)

DE Human CD40-L type II transmembrane protein coding sequence.

KW Leucine zipper; trimerisation; trimeric CD40-L; fusion protein;

KM hetero-oligomer; homo-oligomer; type II transmembrane protein;
 KM soluble CD40-L; tumour necrosis factor family; ss.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 PH 1.786
 FT CDS /tag= a
 FT /product= human CD40-L
 FT /note= "nucleotides 148-793 code for the
 FT extracellular region (amino acids 50-261)"
 XX
 XX MO9410308-A.
 XX PD 11-MAY-1994.
 XX PF 20-OCT-1993; 93WO-US10034.
 XX PR 23-OCT-1992; 92US-0969703.
 XX PR 13-AUG-1993; 93US-0107353.
 XX PA (IMV) IMMUNEX CORP.
 PI Spriggs MK, Srinivasan S;
 DR WPI; 1994-167465/20.
 DR P-PsDB; AARS3969.
 XX
 PT Prepn. of soluble oligomeric mammalian proteins - using host
 PT cells to express a fusion protein comprising a leucine zipper
 PT domain and a heterologous mammalian protein
 XX
 PS Example 1; Page 22-23; 35pp; English.
 CC A DNA fragment encoding the extracellular (soluble) region of human
 CC CD40-L was ligated to a synthetic oligonucleotide sequence coding
 CC for a leader peptide, a 33 amino acid leucine zipper sequence
 CC (AARS3968) and the Flag (RTM) linker sequence. Cells expressing the
 CC fusion construct are grown to accumulate oligomeric, soluble CD40-L
 CC in the supernatant. The leucine zipper sequence spontaneously
 CC trimerises in solution and fusion proteins comprising
 CC the sequence fused to a heterologous mammalian protein also form
 CC oligomers.
 XX
 SQ Sequence 786 BP; 250 A; 168 C; 168 G; 200 T; 0 other;
 Query Match 74.4%; Score 582.8; DB 15; Length 786;
 Best Local Similarity 84.7%; Pred. No. 2,6e-152;
 Matches 666; Conservative 0; Mismatches 117; Indels 3; Gaps 1;

QY 358 CAAATTGGAGCAGCGTTGGTAAAGCCAGCAAGTATGAGCATCGTGTCTACAGTGG 417
 DB 361 CAAATTGGAGCAGCGTTGGTAAAGCCAGCAAGTATGAGCATCGTGTCTACAGTGG 420
 QY 418 GCCAAGAAAGATTTATACATGAAAGCACTTGGTAAAGTAAAGGAAACAG 477
 DB 421 GCTGAAAAGAGATCTACACATGAGCAACCTTGGTAAAGTAAAGGAAACAG 480
 QY 478 CTGAGCGTTAAAGAGAGACTTATTTATGCTTACACTCAAGTCACTTGTCTTAAT 537
 DB 481 CTGAGCGTTAAAGAGAGACTTATTTATGCTTACACTCAAGTCACTTGTCTTAAT 540
 QY 538 CGGAGACCTTGAAGTCAAGCCCTTCACTCGTGGCTGAGCCAGCATTTGA 597
 DB 541 CGGAGACCTTGAAGTCAAGCCCTTCACTCGTGGCTGAGCCAGCATTTGA 600
 QY 598 TCTGAGAGATCTTACTCAAGCGGCAATACCAAGTTCTCTCCAGCTTGGAGCAG 657
 DB 601 TTGAGAGATCTTACTCAAGCGGCAATACCAAGTTCTCTCCAGCTTGGAGCAG 660
 QY 658 CAGTCTGTTCACTTGGCGGAGCTGTTGAATTACAGCTGGCTTCTGTGTGTCAAC 717
 DB 661 CAATCCATTCACCTTGGAGAGATTTGATTTGCAACAGAGTCTTCTGTGTGTCAAC 720
 QY 718 GTGACTGAAGCAAGCCAGTATCCACAGAGTTGCTTCTTGTGCTTACTCAAA 777
 DB 721 GTGACTGAATCCAAAGCAAGTATCCACAGAGTTGCTTCTTGTGCTTACTCAAA 780
 QY 778 CTCTGA 783
 DB 781 CTCTGA 786
 RESULT 15
 AAV38997
 ID AAV38997 standard; DNA; 786 BP.
 AC AAV38997;
 XX
 XX 23-SEP-1998 (first entry)
 DT
 DE CD40 ligand gene used in the course of the invention.
 XX
 XX CD40 ligand; alteration; immunoreactivity; human cell;
 KW accessory molecule ligand; AMU; gene therapy; treatment; neoplasia;
 KW autoimmune disorder; rheumatoid arthritis; vaccine; ss.
 XX
 OS Mus sp.
 XX
 PN WO9826061-A2.
 XX
 PD 18-JUN-1998.
 PF 08-DEC-1997; 97WO-US22740.
 XX
 PR 01-DEC-1997; 97US-0982272.
 PR 09-DEC-1996; 96US-0032145.
 XX
 PA (REGC) UNIV CALIFORNIA.
 PI Cantwell M, Klype TV, Sharma S;
 DR WPI; 1998-348521/30.
 XX
 PT Vectors containing accessory molecule ligand genes - used for
 PT altering immunoreactivity of cells, particularly for treatment of
 PT neoplasia or autoimmune disorders, e.g. Rheumatoid arthritis
 PS Disclosure; Page 104; 167pp; English.
 CC The present sequence represents the CD40 ligand gene. The sequence is
 CC used to exemplify the method of the invention. The specification

CC describes a method for altering the immunoreactivity of human cells
CC which comprises introducing a gene encoding an accessory molecule
CC ligand (AML) into the cells so that the AML is expressed on the surface
CC of the cells. Vectors containing the AML genes can be used in gene
CC therapy for treating neoplasia or autoimmune disorders such as rheumatoid
CC arthritis. They can also be used for vaccination to produce immunity
CC against a virus cell, bacteria, protein, fungus or neoplasia.
XX

Sequence 786 BP; 250 A; 168 C; 168 G; 200 T; 0 other;

Query Match 74.4%; Score 582.8; DB 19; Length 786;
Best Local Similarity 84.7%; Pred. No. 2.6e-152;
Matches 666; Conservative 0; Mismatches 117; Indels 3; Gaps 1;

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QY 1 ATGATGAAACATACCAACCAACTCTCCCGATCTGCGGCACTGAGTCCCATCAGC 60
Db 1 ATGATGAAACATACCAACCAACTCTCCCGATCTGCGGCACTGAGTCCCATCAGC 60
QY 61 ATGAAATTTTATGATTTTACTTACTGTTTCTTATGACCCAAATGATTTGATCTG 120
Db 61 ATGAAATTTTATGATTTTACTTACTGTTTCTTATGACCCAAATGATTTGATCTG 120
QY 121 CTTTTCCTGCTGATCTTCTATAGAGATTGATAGAGTCCAGAGAGAACTTATCC 180
Db 121 CTTTTCCTGCTGATCTTCTATAGAGATTGATAGAGTCCAGAGAGAACTTATCC 180
QY 181 GAAGATTTTGTATCATTAATAAGCTAAAGAGATGCAACAAAGAGAGATCTTATCC 240
Db 181 GAAGATTTTGTATCATTAATAAGCTAAAGAGATGCAACAAAGAGAGATCTTATCC 240
QY 241 TTCTGACTGTGAGAGATGAGAGAGCAATTGAGACCTTGTCAAGATATACGTTA 300
Db 241 TTCTGACTGTGAGAGATGAGAGAGCAATTGAGACCTTGTCAAGATATACGTTA 300
QY 301 AACAAAGAAGA--GAAAAAGAAAAGCTTTGAATGCAAGAGTGAAGATCTCT 357
Db 301 AACAAAGAAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATCTCT 357
QY 358 CAATTTGACAGCAGCTTTGAGCGAGCAAGTATGACAGATCCGTTTCAAGTGG 417
Db 358 CAATTTGACAGCAGCTTTGAGCGAGCAAGTATGACAGATCCGTTTCAAGTGG 417
QY 418 GCCAAGAAAGATATATACATGAAAGCAACTGTTAGTGTGATGTAATGGGAAACAG 477
Db 421 GCTGAAAAAGATATATACATGAAAGCAACTGTTAGTGTGATGTAATGGGAAACAG 477
QY 478 CTGAGGTTTAAAGAGAGACTTATATGTTTCACTCAAGTCACTTCTGCTTAAT 537
Db 481 CTGAGGTTTAAAGAGAGACTTATATGTTTCACTCAAGTCACTTCTGCTTAAT 537
QY 538 CGGAGCCTTGAAGTCAACGCCATTCACTGCGGCTGAGCTGAAGCCAGATTGGA 597
Db 541 CGGAGCCTTGAAGTCAACGCCATTCACTGCGGCTGAGCTGAAGCCAGATTGGA 597
QY 598 TCTGAGAGATCTTACTCAAGCGGCAATACCAAGTTCTCCAGCTTTGGAGCAG 657
Db 601 TCTGAGAGATCTTACTCAAGCGGCAATACCAAGTTCTCCAGCTTTGGAGCAG 657
QY 658 CAGTCTGTTCACTTGGCGGAGTGTGATTAACAAGTGTGCTTCTGATTTGTCAAC 717
Db 661 CAATCATTTCACTTGGAGAGATTTGAATGCAACAGTGTGCTTCTGATTTGTCAAC 717
QY 718 GTGACTGAGAGCAAGATCCAGAGATGAGTGTGCTTCTGATTTGTCAAC 777
Db 721 GTGACTGATCCAGAGCAAGTGTGAGTGTGCTTCTGATTTGTCAAC 777
QY 778 CTCTGA 783
Db 781 CTCTGA 786
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6.

7.

8.

9.

us-08-982-272-5.rnpb

Page 1

OM nucleic - nucleic search, using SW model

Run on: March 9, 2003, 02:11:48 ; Search time 54.0541 Seconds
(without alignments)
9675.146 Million cell updates/sec

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Perfect score:	783
Sequence:	1 ATGATCGAATACATCAACCA.....TTGGCTTACTCAAACTCTGA 783

Scoring table: IDENT111_noc
Gapop 10.0 , Gapext 1.0

Total number of hits satisfying chosen parameters: 957848

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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1: /cgn2_6/p1odata/2/pubnpna/P001_NEW PUB.seq: *
2: /cgn2_6/p1odata/2/pubnpna/P002_NEW PUB.seq: *
3: /cgn2_6/p1odata/2/pubnpna/US06_PUBCOMB.seq: *
4: /cgn2_6/p1odata/2/pubnpna/US07_NEW PUB.seq: *
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14: /cgn2_6/p1odata/2/pubnpna/US60_PUBCOMB.seq: *
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	
1	760.6	97.1	1250	9	US-10-182-093-1	Sequence 1, Appl1	
2	146.2	18.7	2395	9	US-09-875-453-9	Sequence 9, Appl1	
3	46	5.9	9121	10	US-09-070-9278-221	Sequence 221, Appl	
4	44	5.6	2220	10	US-09-897-214-15	Sequence 17, Appl	
c	4	5.2	176373	9	US-10-095-407-17	Sequence 17, Appl	
5	40.4	4.7	1424	10	US-09-960-352-11218	Sequence 11218, A	
6	37	4.7	1788	12	US-10-071-751-29	Sequence 29, Appl	
7	37	4.7	1788	12	US-09-813-158-196	Sequence 196, Appl	
c	8	4.6	381	10	US-09-919-580-896	Sequence 896, Appl	
9	36.2	4.6	262	10	US-09-105-696-1	Sequence 1, Appl1	
c	7	4.6	2430	9	US-10-105-552-1	Sequence 1, Appl1	
10	36.2	4.6	2430	9	US-09-747-521-1	Sequence 1, Appl1	
11	36.2	4.6	2430	10	US-10-106-014-1	Sequence 1, Appl1	
12	36.2	4.6	2430	10	US-09-772-1348-31	Sequence 31, Appl	
13	36.2	4.6	544	10	US-09-864-761-1124	Sequence 7124, Appl	
c	14	4.6	544	10	US-09-864-761-1124	Sequence 31, Appl	
c	15	35.6	4.5	736	10	US-09-772-1348-31	Sequence 607, Appl
c	16	35.6	4.5	24766	10	US-09-764-887-602	Sequence 1039, Ap
c	17	35.2	4.5	2000	9	US-09-938-8428-1039	Sequence 291, Appl
c	18	35.2	4.5	4956	10	US-09-070-9278-291	Sequence 2, Appl1
19	35.2	4.5	335913	9	US-09-754-853A-2	Sequence 2, Appl1	

ALIGNMENTS

C	45	33.6	4.3	340	10	US-09-919-580-765	Sequence 765, Appl
C	44	33.6	4.3	170	10	US-09-867-701-9094	Sequence 9094, Appl
C	42	33.8	4.3	1354	10	US-09-925-301-115	Sequence 315, Appl
C	43	34	4.3	1744	10	US-09-804-662-78	Sequence 78, Appl
C	41	34	4.3	1710	9	US-10-078-770-117	Sequence 117, Appl
C	40	34	4.3	765	9	US-10-125-258-1	Sequence 137, Appl
C	39	34	4.3	375	10	US-09-860-352-15014	Sequence 15014, A
C	38	34.2	4.4	20561	10	US-09-970-927A-292	Sequence 292, Appl
C	37	34.2	4.4	422	10	US-09-764-864-675	Sequence 675, Appl
C	36	33.6	4.4	341	10	US-09-960-352-12302	Sequence 12302, A
C	35	33.6	4.4	7205	12	US-10-002-769-4	Sequence 186, Appl
C	34	33.6	4.4	5048	9	US-09-981-353-186	Sequence 232, Appl
C	32	34.8	4.4	465237	10	US-09-912-943-232	Sequence 232, Appl
C	31	34.8	4.4	3303	10	US-09-933-667A-1	Sequence 186, Appl
C	30	34.8	4.4	555	9	US-09-849-656-380	Sequence 380, Appl
C	29	34.8	4.4	555	9	US-09-702-941-380	Sequence 380, Appl
C	28	34.8	4.4	555	9	US-09-833-190-421	Sequence 421, Appl
C	27	34.8	4.4	555	9	US-09-736-457-380	Sequence 380, Appl
C	26	34.8	4.4	431	10	US-09-960-352-3058	Sequence 3058, Appl
C	25	34.8	4.4	420	10	US-09-960-352-5558	Sequence 5558, Appl
C	24	34.8	4.4	404	10	US-09-960-352-9259	Sequence 9259, Appl
C	23	34.8	4.4	399	10	US-09-960-352-14574	Sequence 14574, A
C	22	34.8	4.4	337	10	US-09-960-352-11232	Sequence 14574, A
C	21	35	4.5	2272	10	US-09-873-438-1	Sequence 1, Appl
C	20	35.2	4.5	315913	9	US-09-754-853A-3	Sequence 3, Appl

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1
US-10-182-093-1
Sequence 1, Application US/10182093
Publication No. US2003021808A1
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as represented by
the Secretary, Department of Health and Human Services,
APPLICANT: The Secretary, Department of Health and Human Services,
APPLICANT: c/o Center for Disease Control and Prevention
APPLICANT: Tripp, Ralph
APPLICANT: Jones, Les
APPLICANT: Anderson, Larry
APPLICANT: Brown, Michael
APPLICANT: Brown, Michael
TITLE OF INVENTION: CP40 Island Adjuvant for Respiratory
Virus
TITLE OF INVENTION: Syncytial Virus
FILE REFERENCE: 14114.030102
CURRENT APPLICATION NUMBER: US/10/182,093
CURRENT FILING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: 60/179,905
PRIOR FILING DATE: 2000-02-02
NUMBER OF SEQ ID NOS: 1
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 1
LENGTH: 1250
TYPE: DNA
ORGANISM: Murine
US-10-182-093-1

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Query Match	97.1%;	Score 760.6;	DB 9;	Length 1250;
Best Local Similarity	98.2%;	Pred. No. 1.3e-195;		
Matches 769; Conservative	0;	Mismatches 14;	Indels 0;	Gaps

Dp

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Oy																																																				
	13	A	T	G	A	T	A	G	A	C	A	T	A	G	C	C	A	C	T	T	C	C	C	C	A	G	A	T	C	C	G	T	G	C	A	A	C	T	G	A	C	T	T	C	C	A	G	C	G	A	C	72

61 ATGAAATTTTATGATTACTTACTGTTTTCTTATCACCACCAATGATGGATCTGTC 120
 QY |||||
 73 ATGAAGTTTATGATTACTTACTGTTTTCTTATCACCACCAATGATGGATCTGTC 130
 75 |||||

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Qy 181 GAAGATTTTGTATTCATTAAGAGTAAAGAGTCAAGAGAGAGATCTTTATCC 240
Db 193 GAAGATTTTGTATTCATTAAGAGTAAAGAGTCAAGAGAGAGATCTTTATCC 252
Qy 241 TTGCTGAACCTGTGAGAGATGAGAGATTTGAGAGATTTGAGAGATTTATACGTTA 300
Db 253 TTGCTGAACCTGTGAGAGATGAGAGATTTGAGAGATTTGAGAGATTTATACGTTA 312
Qy 301 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
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Qy 361 ATTGAGACACAGCTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
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Qy 421 AAGAAAGATATATATATATATATATATATATATATATATATATATATATAT 480
Db 433 AAGAAAGATATATATATATATATATATATATATATATATATATATATATAT 492
Qy 481 ACGTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
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Qy 541 GAGCTTCAGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
Db 553 GAGCTTCAGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 612
Qy 601 GAGAGATCTTATCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
Db 613 GAGAGATCTTATCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 672
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Qy 721 ACTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
Db 733 ACTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 792
Qy 781 TGA 783
Db 793 TGA 795

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RESULT 2
US-09-875-453-9
/ Sequence 9, Application US/09875453
/ Publication No. US20030027320A1
GENERAL INFORMATION:
/ APPLICANT: Kim, Jungshuk P.
/ APPLICANT: Stair, Douglas B.
/ APPLICANT: Tam, Albert W.
/ APPLICANT: Laurence, Megan E.
/ APPLICANT: Michelotti, Emil F.
/ APPLICANT: Velligan, Mark D.
/ APPLICANT: Latour, Derek R.
/ APPLICANT: Thomas, Rita L.
/ APPLICANT: Kongsachath, Ana
/ APPLICANT: Sheppard, Liana T.
/ APPLICANT: Lim, Moon Young
/ APPLICANT: Bruce, Thomas W.
TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
FILE REFERENCE: 4600-0135.30
CURRENT APPLICATION NUMBER: US/09/875.453
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 60/209,549
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Seq-Seq for Windows Version 4.0
/ SEQ ID NO 9
/ LENGTH: 2395

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-875-453-9

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Query Match 18.7%; Score 146.2; DB 9; Length 2395;
Best Local Similarity 87.4%; Pred. No. 1.3e-29;
Matches 160; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

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Qy 1 ATGATGAAACATACACCAACTTCTCCCGATTCGGCCACTGAGACTGCCATCAGC 60
Db 1939 ATGATGAAACATACACCAACTTCTCCCGATTCGGCCACTGAGACTGCCATCAGC 1998
Qy 61 ATGAAATTTTATATATATATATATATATATATATATATATATATATATATAT 120
Db 1999 ATGAAATTTTATATATATATATATATATATATATATATATATATATATATAT 2058
Qy 121 CTTTTCGTGTATCTTCAAGAGATGATGATGAGAGAGAGAGAGAGAGAGAGAGAG 180
Db 2059 CTTTTCGTGTATCTTCAAGAGATGATGATGAGAGAGAGAGAGAGAGAGAGAGAG 2118
Qy 181 GAA 183
Db 2119 TAA 2121

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RESULT 3
US-09-070-927A-221
/ Sequence 221, Application US/09070927A
/ Patent No. US20020120116A1
GENERAL INFORMATION:
/ APPLICANT: Charles A. Kunsch
/ Patrick J. Dillon
/ Steven Barash
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptide
NUMBER OF SEQUENCES: 982
CORRESPONDENCE ADDRESS:
/ ADDRESS: Human Genome Sciences, Inc.
/ STREET: 9410 Key West Avenue
/ CITY: Rockville
/ STATE: Maryland
/ COUNTRY: USA
/ ZIP: 20850
COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
/ COMPUTER: HP Vectra 486/33
/ OPERATING SYSTEM: MSDOS version 6.2
/ SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/070.927A
/ FILING DATE: 04-May-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/046,655
/ FILING DATE: 1997-05-16
/ APPLICATION NUMBER: 60/044,031
/ FILING DATE: 1997-05-06
/ APPLICATION NUMBER: 60/066,009
/ FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
/ NAME: Kenley K. Hoover
/ REGISTRATION NUMBER: 40,302
/ REFERENCE/DOCKET NUMBER: PB369
TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (301) 309-8504
/ TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 221:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 9121 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ SEQUENCE DESCRIPTION: SEQ ID NO: 221:
US-09-070-927A-221

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Query Match 5.9%; Score 46; DB 10; Length 9121;

Best Local Similarity 52.6%; Pred. No. 0.0277; Mismatches 90; Indels 0; Gaps 0;

Matches 100; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

Db 161 AAGAGAGAGTAAACCTTCATGAGATTTTGTATTCATTAAGTAAAGATGACAA 220

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Db 221 AAGAGAGAGTAAACCTTCATGAGATTTTGTATTCATTAAGTAAAGATGACAA 280

Db 8814 AAGAGAGAGTAAACCTTCATGAGATTTTGTATTCATTAAGTAAAGATGACAA 8873

Db 281 TTGTCAAGATTAACCTTCATGAGATTTTGTATTCATTAAGTAAAGATGACAA 340

Db 8874 TTGTCAAGATTAACCTTCATGAGATTTTGTATTCATTAAGTAAAGATGACAA 8933

Db 341 GAGGTATGA 350

Db 8934 CAATGATTA 8943

RESULT 4
US-09-897-214-15/c
Sequence 15, Application US/09897214

Patent No. US2002007679A1

GENERAL INFORMATION:

APPLICANT: Thayer, Edward C.

APPLICANT: Sheppard, Paul O.

APPLICANT: Preenell, Scott R.

TITLE OF INVENTION: Leucine-Rich Repeat Proteins, Zlrr7,

TITLE OF INVENTION: Zlrr8, and Zlrr9

FILE REFERENCE: 01-27

CURRENT APPLICATION NUMBER: US/09/897,214

PRIOR FILING DATE: 2001-07-02

PRIOR APPLICATION NUMBER: 60/215,446

NUMBER OF SEQ ID NOS: 15

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 15

LENGTH: 2220

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(2220)

OTHER INFORMATION: n = A,T,C or G

US-09-897-214-15

Query Match 5.6%; Score 44; DB 10; Length 2220;

Best Local Similarity 25.3%; Pred. No. 0.049; Mismatches 212; Indels 1; Gaps 1;

Matches 96; Conservative 70; Mismatches 212; Indels 1; Gaps 1;

Db 262 AAGAGAGTAAACCTTCATGAGATTTTGTATTCATTAAGTAAAGATGACAA 321

Db 925 AAGAGAGTAAACCTTCATGAGATTTTGTATTCATTAAGTAAAGATGACAA 866

Db 322 AAGAGAGTAAACCTTCATGAGATTTTGTATTCATTAAGTAAAGATGACAA 380

Db 865 TACAGTAAACCTTCATGAGATTTTGTATTCATTAAGTAAAGATGACAA 806

Db 381 GAGAGAGTAAACCTTCATGAGATTTTGTATTCATTAAGTAAAGATGACAA 440

Db 805 GAGAGAGTAAACCTTCATGAGATTTTGTATTCATTAAGTAAAGATGACAA 746

Db 441 GAGAGAGTAAACCTTCATGAGATTTTGTATTCATTAAGTAAAGATGACAA 500

Db 745 AAGAGAGTAAACCTTCATGAGATTTTGTATTCATTAAGTAAAGATGACAA 666

Db 501 GAGAGAGTAAACCTTCATGAGATTTTGTATTCATTAAGTAAAGATGACAA 560

Db 685 TACAGTAAACCTTCATGAGATTTTGTATTCATTAAGTAAAGATGACAA 626

Db 561 ATTCAGTGGGCTGCTGAGTAAAGAGTAAAGATGACAA 620

Db 625 ATTCAGTGGGCTGCTGAGTAAAGAGTAAAGATGACAA 566

Db 621 GAGAGAGTAAACCTTCATGAGATTTTGTATTCATTAAGTAAAGATGACAA 639

Db 565 GAGAGAGTAAACCTTCATGAGATTTTGTATTCATTAAGTAAAGATGACAA 547

RESULT 5

US-10-095-407-17

Sequence 17, Application US/10095407

Patent No. US2002016430A1

GENERAL INFORMATION:

APPLICANT: Pan, Yang

APPLICANT: Yang, Yang

TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY

TITLE OF INVENTION: AND USES THEREOF

FILE REFERENCE: 09404/052001

CURRENT APPLICATION NUMBER: US/10/095,407

PRIOR FILING DATE: 2002-03-11

PRIOR APPLICATION NUMBER: US 60/091,650

PRIOR FILING DATE: 1998-07-02

PRIOR APPLICATION NUMBER: US 60/054,646

NUMBER OF SEQ ID NOS: 18

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 17

LENGTH: 176373

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(176373)

OTHER INFORMATION: n = A,T,C or G

US-10-095-407-17

Query Match 5.2%; Score 40.4; DB 9; Length 176373;

Best Local Similarity 48.3%; Pred. No. 3.4; Indels 0; Gaps 0;

Matches 113; Conservative 0; Mismatches 121; Indels 0; Gaps 0;

Db 213 ATTCAGTGGGCTGCTGAGTAAAGAGTAAAGATGACAA 272

Db 114639 ATTCAGTGGGCTGCTGAGTAAAGAGTAAAGATGACAA 114698

Db 273 TGAAGAGTAAACCTTCATGAGATTTTGTATTCATTAAGTAAAGATGACAA 332

Db 114699 AGAGAGTAAACCTTCATGAGATTTTGTATTCATTAAGTAAAGATGACAA 114758

Db 333 AATGAGAGTAAACCTTCATGAGATTTTGTATTCATTAAGTAAAGATGACAA 392

Db 114759 TGAAGAGTAAACCTTCATGAGATTTTGTATTCATTAAGTAAAGATGACAA 114818

Db 393 TGAAGAGTAAACCTTCATGAGATTTTGTATTCATTAAGTAAAGATGACAA 446

Db 114819 GATGAGAGTAAACCTTCATGAGATTTTGTATTCATTAAGTAAAGATGACAA 114872

RESULT 6

US-09-960-352-11218

Sequence 11218, Application US/09960352

Patent No. US20020137139A1

GENERAL INFORMATION:

APPLICANT: Warren, Wesley C.

APPLICANT: Tao, Mengling

APPLICANT: Mathialagan, Nagesan

TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND

TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION

FILE REFERENCE: 16511.006/37-21.102981C

CURRENT APPLICATION NUMBER: US/09/960,352

PRIOR FILING DATE: 2001-09-24

NUMBER OF SEQ ID NOS: 15112

SEQ ID NO 11218
 LENGTH: 424
 TYPE: DNA
 ORGANISM: Bos taurus
 OTHER INFORMATION: Clone ID: 48-LIB3058-026-Q1-K1-D12
 US-09-960-352-11218

Query Match 4.7%; Score 37; DB 10; Length 424;
 Best Local Similarity 49.4%; Pred. No. 1.8;
 Matches 126; Conservative 0; Mismatches 125; Indels 4; Gaps 1;

QY 68 TTTTATGATTTACTAGCTTTTCTTATCACCCTAAGATGAGATCTGCTTTTG 127
 Db 30 TTTTATGATTTACTAGCTTTTCTTATCACCCTAAGATGAGATCTGCTTTTG 89
 QY 128 CTGTGATCTTCATGAGATTGATGATGATGAGAGATTAACCTTCATGAGATT 187
 Db 90 TTTTATGATTTACTAGCTTTTCTTATCACCCTAAGATGAGATCTGCTTTTG 149
 QY 188 TTGTATTCATTAAGCTAAAGATGACACAGAGAGAGATCTTATCTTCTGCTGA 247
 Db 150 TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 209
 QY 248 ACTG---GAGAGATGAGAGAGATTTGAGACCTTGTCAAGATTAAGCTTAAC 303
 Db 210 AATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 269
 QY 304 AAAGAAG 318
 Db 270 AAAAAAAAAATGAAA 284

RESULT 7
 US-10-071-751-29

Sequence 29, Application US/10071751
 Patent No. US20020142352A1
 GENERAL INFORMATION:
 APPLICANT: Hunter, Shirley Wu
 Inventor: Sim, Gek-Ke

TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA PROTEINS AND
 APPARATUS TO COLLECT SUCH PROTEINS
 NUMBER OF SEQUENCES: 88
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SHERIDAN ROSS P.C.
 STREET: 1560 BROADWAY, SUITE 1200
 CITY: DENVER
 STATE: CO
 COUNTRY: U.S.A.

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/071,751
 FILING DATE: 07-Feb-2002
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/171,156
 FILING DATE: 1998-10-09
 ATTORNEY/AGENT INFORMATION:
 NAME: Connell, Gary U.

REGISTRATION NUMBER: 32,020
 REFERENCE/DOCKET NUMBER: 2618-17-C4-PUS
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 303/863-9700
 TELEFAX: 303/863-0223
 INFORMATION FOR SEQ ID NO: 29:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1758 base pairs
 TYPE: nucleic acid

STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1...1758
 FEATURE:
 NAME/KEY: M = A or T
 LOCATION: 1136
 SEQUENCE DESCRIPTION: SEQ ID NO: 29:
 US-10-071-751-29

Query Match 4.7%; Score 37; DB 12; Length 1758;
 Best Local Similarity 47.2%; Pred. No. 3.4;
 Matches 109; Conservative 1; Mismatches 121; Indels 0; Gaps 0;

QY 155 AGCTGAT 214
 Db 1043 AAGATGTGAT 1102
 QY 215 GCAACAAAGAT 274
 Db 1103 AAGAACTAAGAT 1162
 QY 275 AAGACCTTGTCAAGATTAAGCTTAAGCTTAAGCTTAAGCTTAAGCTTAAG 334
 Db 1163 ATACTGTTTACAGAT 1222
 QY 335 TGCAAG 385
 Db 1223 TTGAAGCTCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1273

RESULT 8

US-09-813-358-196/C
 Sequence 196, Application US/09813358
 Patent No. US20020048759A1
 GENERAL INFORMATION:
 APPLICANT: Xu, Jiangchun
 Inventor: Pyle, Ruth

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 OF INFECTIONS CAUSED BY THE PARASITE AND DIAGNOSIS OF OVARIAN AND ENDOMETRIAL CANCER
 FILE REFERENCE: 210121.501
 CURRENT APPLICATION NUMBER: US/09/813,358
 NUMBER OF SEQ ID NOS: 222
 CURRENT FILING DATE: 2001-03-21
 SOFTWARE: FastSeq for Windows Version 4.0

SEQUENCE ID NO 196
 LENGTH: 391
 TYPE: DNA
 ORGANISM: Homo sapien

FEATURE:
 NAME/KEY: misc.feature
 LOCATION: (1)...(391)
 OTHER INFORMATION: n = A,T,C or G
 US-09-813-358-196

Query Match 4.6%; Score 36.4; DB 10; Length 391;
 Best Local Similarity 51.0%; Pred. No. 2.5;
 Matches 79; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 68 TTTTATGATTTACTAGCTTTTCTTATCACCCTAAGATGAGATCTGCTTTTG 127
 Db 369 TTTTATGATTTACTAGCTTTTCTTATCACCCTAAGATGAGATCTGCTTTTG 310
 QY 128 CTGTGATCTTCATGAGATTGATGATGATGAGAGATTAACCTTCATGAGATT 187
 Db 309 TTTTATGATTTACTAGCTTTTCTTATCACCCTAAGATGAGATCTGCTTTTG 250
 QY 188 TTGTATTCATTAAGCTAAAGATGACACAGAGAGAGATCTTATCTTCTGCTGA 222
 Db 249 TTATATACAAAGAT 215

RESULT 9
US-09-919-580-896

/ Sequence 896, Application US/09919580
/ Patent No. US2002010832A1
/ GENERAL INFORMATION:
/ APPLICANT: Pyle, Ruth
/ APPLICANT: Xu, Jiangchun
/ APPLICANT: Secrist, Heather
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
/ FILE REFERENCE: 210121.552
/ CURRENT APPLICATION NUMBER: US/09/919, 580
/ CURRENT FILING DATE: 2001-07-30
/ NUMBER OF SEQ ID NOS: 934
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 896
/ LENGTH: 262
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ NAME/KEY: misc.feature
/ LOCATION: 58, 132, 133, 139, 140, 147, 262
/ OTHER INFORMATION: n = A,T,C or G
US-09-919-580-896

Query Match

Best Local Similarity 4.6%; Score 36.2; DB 10; Length 262;
Matches 92; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

Oy 135 TCTTCATGAGAGATTGATTAAGCTGAGAGAGATTAACCTTCATGAGATTGATT 194
Db 56 TTTTATGAGCTGCTACATTAATGAATGAATGAATGAATGAATGAATGAATGAAT 115
Oy 195 CATTAAGAGCTTAAGAGATGACAAAGAGAGAGATCTTTCTCTGCTGAACCTGCA 254
Db 116 ACTATCCAACTTATTTNNCTGCTNNCAAGTAAAGAACTTTATAGTCTTAATCATTAA 175
Oy 255 GAGATGAGAGAGCAATTTGAAGACCTTGTCAAGATTTAACTTTAAACAAAGAGAGAA 314
Db 176 ATATTAAGCAAGATTAATTAATAATTTGCTTTGTTAAAAAAGAAAAAAGAAAAA 235
Oy 315 AAAAGAAAAA 325
Db 236 AAAAAAAAAA 246

RESULT 10
US-10-105-695-1

/ Sequence 1, Application US/10105695
/ Publication No. US20020197272A1
/ GENERAL INFORMATION:
/ APPLICANT: Galloway, Darrel R.
/ APPLICANT: Mateczun, Alfred J.
/ TITLE OF INVENTION: Methods for Protection Against Lethal Infection with Bacillus Anthracis
/ FILE REFERENCE: 22727/04115
/ CURRENT APPLICATION NUMBER: US/10/105, 695
/ CURRENT FILING DATE: 2002-03-25
/ PRIOR APPLICATION NUMBER: US 09/747,521
/ PRIOR FILING DATE: 2000-12-21
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 1
/ LENGTH: 2430
/ TYPE: DNA
/ ORGANISM: Bacillus anthracis
/ NAME/KEY: CDS
/ LOCATION: (1)..(2430)
/ OTHER INFORMATION:
US-10-105-695-1

Query Match

Best Local Similarity 4.6%; Score 36.2; DB 9; Length 2430;
Matches 89; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

Oy 158 TCGAAGAGAGATTAACCTTCATGAGAGATTGTTATTCATTAATAAGCTTAAGATGCA 217
Db 1053 TCTAAAAAGATCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1112
Oy 218 ACAAGAGAGAGATCTTTATCTGCTGAACCTGAGAGATGAGAGCAATTTGAAG 277
Db 1113 AAAAAAGCTCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1172
Oy 278 ACCTTGCAAGATTAATACCTTTAAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 334
Db 1173 TAGAATACAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1229

RESULT 11
US-10-105-694-1

/ Sequence 1, Application US/10105694
/ Publication No. US20030003109A1
/ GENERAL INFORMATION:
/ APPLICANT: Galloway, Darrel R.
/ APPLICANT: Mateczun, Alfred J.
/ TITLE OF INVENTION: Methods for Protection Against Lethal Infection with Bacillus Anthracis
/ FILE REFERENCE: 22727/04116
/ CURRENT APPLICATION NUMBER: US/10/105, 694
/ CURRENT FILING DATE: 2002-03-25
/ PRIOR APPLICATION NUMBER: US 09/747,521
/ PRIOR FILING DATE: 2000-12-21
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 1
/ LENGTH: 2430
/ TYPE: DNA
/ ORGANISM: Bacillus anthracis
/ NAME/KEY: CDS
/ LOCATION: (1)..(2430)
/ OTHER INFORMATION:
US-10-105-694-1

Query Match

Best Local Similarity 4.6%; Score 36.2; DB 9; Length 2430;
Matches 89; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

Oy 158 TCGAAGAGAGATTAACCTTCATGAGAGATTGTTATTCATTAATAAGCTTAAGATGCA 217
Db 1053 TCTAAAAAGATCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1112
Oy 218 ACAAGAGAGAGATCTTTATCTGCTGAACCTGAGAGATGAGAGCAATTTGAAG 277
Db 1113 AAAAAAGCTCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1172
Oy 278 ACCTTGCAAGATTAATACCTTTAAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 334
Db 1173 TAGAATACAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1229

RESULT 12
US-09-747-521-1

/ Sequence 1, Application US/09747521
/ Patent No. US20020051791A1
/ GENERAL INFORMATION:
/ APPLICANT: Galloway, Darrel R.
/ APPLICANT: Mateczun, Alfred J.
/ TITLE OF INVENTION: Methods for Protection Against Lethal Infection with Bacillus Anthracis
/ FILE REFERENCE: 22727/04079
/ CURRENT APPLICATION NUMBER: US/09/747,521
/ CURRENT FILING DATE: 2000-12-21
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 1

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; LENGTH: 2430
; TYPE: DNA
; ORGANISM: Bacillus anthracis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) .. (2430)
US-09-747-521-1

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Query Match	4.6%;	Score 36.2;	DB 10;	Length 2430;
Best Local Similarity	50.3%;	Pred. No. 6.5;		
Matches	89;	Conservative	0;	Mismatches 88;
			Indels 0;	Gaps 0;

Oy	158	TCGAAGAGAAATGAAACCTTCATGAAATTTTGATTCATATATAAAAGCTAAAGATGCA	217
Db	1053	TCATAAAAGAAATCAAAATGAGAGTAGTAGATTTTATCTACAGGAAAAAGGTTTT	1112
Oy	218	ACAAAGAGAGAGATCTTTATCTCTTGCGAACCTGAGAGAGATGAGAGGGAATTTGAG	277
Db	1113	AAAAAGCTCAAAATGATATTTCTGATTTCTTATCTGAAAGAGAAAAAGAGCTTTAAA	1172
Oy	278	ACCTTGTCAAGATATACGTTAAAACAAGAGAGAAAAAGAAACGCTTTGAA	334
Db	1173	TGAAATACAGGTGATAGTAGTAATCCTTTATCTGAAAAAGAAAAAGGTTTTAAA	1229

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RESULT 13
US-10-106-014-1
; Sequence 1, Application US/10106014
; Patent No. US20020142002A1
; GENERAL INFORMATION:
; APPLICANT: Galloway, Darrel R.
; APPLICANT: Marecun, Alfred J.
; TITLE OF INVENTION: Methods for Protection Against Lethal Infection with Bacillus Anthracis
; FILE REFERENCE: 22727/04114
; CURRENT APPLICATION NUMBER: US/10/106, 014
; PRIORITY FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US 09/747,521
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2430
; TYPE: DNA
; ORGANISM: Bacillus anthracis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2430)
; OTHER INFORMATION:
US-10-106-014-1

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Query Match      4.6%; Score 36.2; DB 12; Length 2430;
Best Local Similarity 50.3%; Pred. No. 6.5;
Matches 89; Conservative 0; Mismatches 88; Indels 0; Gaps 0
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Qy	158	TCGAAGAGAACTTAACCTTCATGAAATTTGGTATCTATAAAAAGCTAAAGAGATGCA	217
Db	1053	TCATAAAGAAATCAAAATGATAGATGATTTTTTATCTACGAGAAAAAGAGTTTTT	1112
Qy	218	ACAAAGAGAAAGATCTTATTCCTTCTGTGAAACGCGAGAGAGATGAAAGCATTTGAG	277
Db	1113	AAAAAGCTCAAAATGATGATTCGTGATCTTTATCTGAGAGAAAAAGACCTTTTAA	1172
Qy	278	ACCTGTCAAGGATATPACGTTTAAACAAGAGAGAAAAAGAAACAGCTTTGAA	334
Db	1173	TGAGATPACAGGTGATATGATGTAATCTTTATCTGAAAAAGAAAAAGACTTTTTTAA	1229

RESULT 14
US-09-864-761-7124/C
; Sequence 7124, Application US/09864761
; Patent No. US20020048765A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.

```

APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
CURRENT FILING DATE: US/09/864,761
PRIOR APPLICATION NUMBER: US 2001-05-23
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 7124
LENGTH: 544
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL157405.2
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.8
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.1
OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.2
US-09-864-761-7124

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Query Match      4.6%; Score 36; DB 10; Length 544;
Best Local Similarity 50.0%; Pred. No. 3.7;
Matches 90; Conservative 0; Mismatches 90; Indels 0; Gaps
Oy 129 TGTGATCTCATTAAGAGTTGCTATAGCTGACAAAGGAAGATAAACCCTCATGAAGATT 189
Db 416 TGTGTTATTAAGACAACTTTGTGCTGTCCTATAGCAATTTATTTACAAAATGCG 355
Oy 189 TGTATTCATTAATAAAGCTTAAGAGATGCAACAAGAGACAGATCTTATCTTCTGTAA 248
Db 356 TGAATATGAGAAACACCCAGAAAGACGAAAGAACTGAGAGGTAAAGGCTCTTAAGATTA 297

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QY 249 CTGTGAGAGATGAGAGCAATTGGAAGCCTTGTCAAGATATATACGTTAAACAAAGA 308
DB 296 GTGTGAAGAGGTTCAACAAAGTCATTAAGACTGTATTAGGATCAAGTGTCTCTAGA 237

RESULT 15

US-09-772-134B-31/c
; Sequence 31, Application US/09772134B
; Patent No. US20020144310A1
; GENERAL INFORMATION:
; APPLICANT: Southern Illinois University
; APPLICANT: Lightfoot, David
; APPLICANT: Meksem, Khalid
; TITLE OF INVENTION: ISOLATED POLYNUCLEOTIDES AND POLYPEPTIDES RELATING TO LOCI UNDER
; TITLE OF INVENTION: RESISTANCE TO SOYBEAN CYST NEMATODE AND SOYBEAN SUDDEN DEATH SYN
; FILE REFERENCE: 1268/4/2
; CURRENT APPLICATION NUMBER: US/09/772,134B
; PRIORITY FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: 60/178,811
; PRIORITY FILING DATE: 2000-01-28
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31
; LENGTH: 736
; TYPE: DNA
; ORGANISM: soybean
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(736)
; OTHER INFORMATION: n is an undetermined nucleotide (dATP, dCTP, dGTP, or dTTP)
US-09-772-134B-31

Query Match

Best Local Similarity 4.5%; Score 35.6; DB 10; Length 736;
Matches 86; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

QY 192 ATTCATTAATAAAGCTTAAGAGATGCAACAAAGAGAGATCTTATCCTTGCTGAACG 251
DB 184 ATTGAATAATAAATCAATGAAAAAATAATATCTTTTGTGTTTCTAGATTTCTA 125
QY 252 TGAGAGATGAGAGCAATTGGAAGCCTTGTCAAGATATATACGTTAAACAAAGAGA 311
DB 124 TTTACGATCTTAATATGATGAAATTATTTAGCAAGTTGAAATTTATGAAAAAATGA 65
QY 312 GAAAAAAGAAACAGCTTTGAAATGCAAGAGGTGATGAGATCTCAAT 362
DB 64 ATACAAAGACAAAAAATTAATAATGTTAAATTGAAATTCGATTCATAGT 14

Search completed: March 9, 2003, 09:46:53
Job time : 182.054 secs

7

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: March 8, 2003, 21:49:58 ; Search time 33.5164 Seconds
(without alignments)
7164.491 Million cell updates/sec

Title: US-08-982-272-5

Perfect score: 783

Sequence: 1 ATGATCGAACAATACACCA.....TTGCTTACTCAACTCTGTA 783

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:
1: /cgn2_6/prodata/2/ina/5A COMB.seq:*
2: /cgn2_6/prodata/2/ina/5B COMB.seq:*
3: /cgn2_6/prodata/2/ina/6A COMB.seq:*
4: /cgn2_6/prodata/2/ina/6B COMB.seq:*
5: /cgn2_6/prodata/2/ina/PCTUS COMB.seq:*
6: /cgn2_6/prodata/2/ina/backtile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	760.6	97.1	818	1 US-08-431-055-1	Sequence 1, Appl
2	760.6	97.1	818	4 US-08-858-197-1	Sequence 1, Appl
3	759	96.9	783	1 US-08-446-922-5	Sequence 5, Appl
4	759	96.9	783	2 US-08-249-189-1	Sequence 1, Appl
5	759	96.9	783	2 US-08-484-624A-1	Sequence 1, Appl
6	759	96.9	783	2 US-08-477-733B-1	Sequence 1, Appl
7	759	96.9	783	3 US-09-088-913A-1	Sequence 1, Appl
8	759	96.9	783	4 US-08-769-819-1	Sequence 1, Appl
9	759	96.9	783	4 US-08-770-974-1	Sequence 1, Appl
10	759	96.9	783	4 US-08-770-981-1	Sequence 1, Appl
11	759	96.9	783	4 US-09-399-106-1	Sequence 1, Appl
12	759	96.9	783	5 PCT-US93-10034-5	Sequence 5, Appl
13	631.4	80.6	878	2 US-08-249-189-22	Sequence 22, Appl
14	631.4	80.6	878	2 US-08-484-624A-22	Sequence 22, Appl
15	631.4	80.6	878	2 US-08-477-733B-22	Sequence 22, Appl
16	631.4	80.6	878	3 US-09-088-913A-22	Sequence 22, Appl
17	631.4	80.6	878	4 US-08-769-819-22	Sequence 22, Appl
18	631.4	80.6	878	4 US-08-770-974-22	Sequence 22, Appl
19	631.4	80.6	878	4 US-08-770-981-22	Sequence 22, Appl
20	631.4	80.6	878	4 US-09-399-106-22	Sequence 22, Appl
21	582.8	74.4	786	5 US-08-446-922-3	Sequence 3, Appl
22	582.8	74.4	786	5 PCT-US93-10034-3	Sequence 3, Appl
23	582.8	74.4	840	1 US-07-940-605A-1	Sequence 1, Appl
24	582.8	74.4	840	1 US-08-184-422-7	Sequence 7, Appl
25	582.8	74.4	840	1 US-08-360-923A-1	Sequence 1, Appl
26	582.8	74.4	840	1 US-08-431-055-3	Sequence 3, Appl
27	582.8	74.4	840	2 US-08-690-096-1	Sequence 1, Appl

28	582.8	74.4	840	2 US-08-249-189-11	Sequence 11, Appl
29	582.8	74.4	840	2 US-08-484-624A-11	Sequence 11, Appl
30	582.8	74.4	840	2 US-08-477-733B-11	Sequence 11, Appl
31	582.8	74.4	840	3 US-08-763-995-1	Sequence 1, Appl
32	582.8	74.4	840	3 US-09-088-913A-11	Sequence 11, Appl
33	582.8	74.4	840	3 US-08-589-771B-7	Sequence 7, Appl
34	582.8	74.4	840	4 US-08-769-819-11	Sequence 11, Appl
35	582.8	74.4	840	4 US-08-770-974-11	Sequence 11, Appl
36	582.8	74.4	840	4 US-08-858-197-3	Sequence 3, Appl
37	582.8	74.4	840	4 US-08-770-981-11	Sequence 11, Appl
38	582.8	74.4	840	4 US-09-399-106-11	Sequence 11, Appl
39	446.2	57.0	1425	2 US-08-484-624A-15	Sequence 15, Appl
40	446.2	57.0	1425	2 US-08-477-733B-15	Sequence 15, Appl
41	446.2	57.0	1425	2 US-08-477-733B-15	Sequence 15, Appl
42	446.2	57.0	1425	3 US-09-088-913A-15	Sequence 15, Appl
43	446.2	57.0	1425	3 US-08-769-819-15	Sequence 15, Appl
44	446.2	57.0	1425	4 US-08-770-974-15	Sequence 15, Appl
45	446.2	57.0	1425	4 US-08-770-981-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-08-431-055-1
Sequence 1, Application US/08431055
Patent No. 5817516
GENERAL INFORMATION:
APPLICANT: KERRY, MERILYN R
APPLICANT: CASTLE, BRIAN E
TITLE OF INVENTION: METHODS FOR PROLIFERATING AND
TITLE OF INVENTION: DIFFERENTIATING B CELLS, AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
STREET: 100 NEW YORK AVE. N.W. SUITE 600
CITY: WASHINGTON
STATE: D.C.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,055
FILING DATE: 28-Apr-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/234,580
FILING DATE: 28-Apr-1994
ATTORNEY/AGENT INFORMATION:
NAME: WILLMAN, ROBERT A
REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 1011,1030000/RAM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 818 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 13..795
US-08-431-055-1
Query Match 97.1%; Score 760.6; DB 1; Length 818;
Best Local Similarity 98.2%; Pred. No. 5.2e-216;
Matches 769; Conservative 0; Mismatches 14; Gaps 0;

QY	1	ATATCGAAACATCAACCAAACTTCTCCGAGCTGCGGGCACTGCACTGCCATCAGC	60
Db	13	ATGATGAACACATACAGCCAACTTCCCGAGATCGTGCACACTGCATTCACAGCAGC	72
QY	61	ATGAAAATTTTATGATATTACTTACTGTGTTTCCATATACCMAATGATTTGATCTG	120
Db	73	ATGAAATTTTATATATTTTACTACTGTGTTTCCATATACCMAATGATTTGATCTG	132
QY	121	CTTTTGTGCTGTATCTTCAATAGATTGGAATAGGTGGAAGAGAAATTAACCTTAT	180
Db	133	CTTTTGTGCTGTATCTTCAATAGATTGGAATAGGTGGAAGAGAAATTAACCTTAT	192
QY	181	GAAGATTTTGTATTCATATAAAAAAGCTAAAGATGCAACAAAGAGATCTTTATCC	240
Db	193	GAAGATTTTGTATTCATATAAAAAAGCTAAAGATGCAACAAAGAGATCTTTATCC	252
QY	241	TTGCTCACTGTGAGAGATGGAAGGCAATTGAAGACTTTGTCAAGATATAAGTTA	300
Db	253	TTGCTCACTGTGAGAGATGGAAGGCAATTGAAGACTTTGTCAAGATATAAGTTA	312
QY	301	AACAAAGAAAGAAAAAGAAAAAGCTTTGAAATSCAAAGAGTGATGAGATCTCTAA	360
Db	313	AACAAAGAAAGAAAAAGAAAAAGCTTTGAAATSCAAAGAGTGATGAGATCTCTAA	372
QY	361	ATTGCAGACACGTTGTAAACGAGCAACATATGACGATCCGTTCTACAGTGGGCC	420
Db	373	ATTGCAGACACGTTGTAAACGAGCAACATATGACGATCCGTTCTACAGTGGGCC	432
QY	421	AAGAAAGATATTATACATGAAAAGCACTTGGTATGCTTGAAAAATGGGAAACAAGCTG	480
Db	433	AAGAAAGATATTATACATGAAAAGCACTTGGTATGCTTGAAAAATGGGAAACAAGCTG	492
QY	481	ACGGTTAAAAAGAGAGACTATATATGCTACACACAGTACACTTGTCTGTAATGG	540
Db	493	ACGGTTAAAAAGAGAGACTATATATGCTACACACAGTACACTTGTCTGTAATGG	552
QY	541	GAGCTTGGATCAAGCCCATTCATGCTGGGCTCTGGCTGAAGCCACAGATTGGATCT	600
Db	553	GAGCTTGGATCAAGCCCATTCATGCTGGGCTCTGGCTGAAGCCACAGATTGGATCT	612
QY	601	GAGAGATCTTACTCAAGCGGCAATATCCACAGTTCCTCCACGCTTGGCGAGAGAG	660
Db	613	GAGAGATCTTACTCAAGCGGCAATATCCACAGTTCCTCCACGCTTGGCGAGAGAG	672
QY	661	TCTGTTCCTTGGCGGAGTGTTGTAATTAACAAGCTGTGCTCTGTGTTTGTACAAGTG	720
Db	673	TCTGTTCCTTGGCGGAGTGTTGTAATTAACAAGCTGTGCTCTGTGTTTGTACAAGTG	732
QY	721	ACTGAAGACACCAAGTGATTCACAGATTTGGCTTCTCATCTTTTGGCTTACCAATC	780
Db	733	ACTGAAGACACCAAGTGATTCACAGATTTGGCTTCTCATCTTTTGGCTTACCAATC	792
QY	781	TGA 783	
Db	793	TGA 795	

RESULT 2
US-08-858-197-1
Sequence 1, Application US/08858197
Patent No. 6297052
GENERAL INFORMATION:
APPLICANT: KEHRY, MERILYN R
APPLICANT: CASTLE, BRIN E
TITLE OF INVENTION: METHODS FOR PROLITERATING AND
TITLE OF INVENTION: DIFFERENTIATING B CELLS, AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESLER, GOLDSTEIN & FOX
STREET: 100 NEW YORK AVE. N.W. SUITE 600
CITY: WASHINGTON
STATE: D.C.

```

1      ZIP: 20005
2
3      COMPUTER READABLE FORM:
4
5      MEDIUM TYPE: Floppy disk
6
7      COMPUTER: IBM PC compatible
8
9      OPERATING SYSTEM: PC-DOS/MS-DOS
10     SOFTWARE: PatentIn Release #1.0, Version #1.25
11
12     CURRENT APPLICATION DATA:
13
14     APPLICATION NUMBER: US/08/858,197
15
16     FILING DATE:
17
18     CLASSIFICATION:
19
20     PRIOR APPLICATION DATA:
21
22     APPLICATION NUMBER: US/08/234,580
23
24     FILING DATE: 28-Apr-1994
25
26     ATTORNEY/AGENT INFORMATION:
27
28     NAME: MILLMAN, ROBERT A
29
30     REGISTRATION NUMBER: 36,217
31
32     REFERENCE/DOCKET NUMBER: 1011.1030000/RAM
33
34     TELECOMMUNICATION INFORMATION:
35
36     TELEPHONE: (202)371-2600
37
38     TELEFAX: (202) 371-2540
39
40     INFORMATION FOR SEQ ID NO: 1:
41
42     SEQUENCE CHARACTERISTICS:
43
44     LENGTH: 818 base pairs
45
46     TYPE: nucleic acid
47
48     STRANDEDNESS: both
49
50     TOPOLOGY: linear
51
52     MOLECULE TYPE: DNA
53
54     FEATURE:
55
56     NAME/KEY: CDS
57
58     LOCATION: 13...795
59
60     US-08-858-197-1

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	Query Match	97.1%;	Score 760.6;	DB 4;	Length 818;
	Best Local Similarity	98.2%;	Pred. No. 5.2e-216;		
	Matches 769;	Conservative 0;	Mismatches 14;	Indels 0;	Gaps 0;
Qy	1	ATGATCGAAACATCAACACCAACTTCTCCCGATCTGCGGCCCATCGACCTGCCCATCGC	60		
Db	13	ATGATATGAAACCATACGACCACTTCCCGCGATCGTGGCAACTGACCTTCCACGACGC	72		
Qy	61	ATGAAATTTTATGTATTTACTTACTTACTGTGTTTCCCTATACCCCAATGATGGATCTGTG	120		
Db	73	ATGAAAGATTTTATGTATTTACTTACTTACTGTGTTTCCCTATACCCCAATGATGGATCTGTG	132		
Qy	121	CTTTTTCGTGTATCTTCTCATATGAAATTTGGATTAAGTGTGAAGAGAAAGTAAACCTTCAT	180		
Db	133	CTTTTTCGTGTATCTTCTCATATGAAATTTGGATTAAGTGTGAAGAGAAAGTAAACCTTCAT	192		
Qy	181	GAAATTTTGTATTTTCATTAATAAAGCTTAAGAAGATGACCAAGAGAGAGATCTTTATCC	240		
Db	193	GAAATTTTGTATTTTCATTAATAAAGCTTAAGAAGATGACCAAGAGAGAGATCTTTATCC	252		
Qy	241	TTTGTGAACGTGAGAGAGATGGAAGAGCAATTTGAAGACTTTGTCAAGATTTAACTGTA	300		
Db	253	TTTGTGAACGTGAGAGAGATGGAAGAGCAATTTGAAGACTTTGTCAAGATTTAACTGTA	312		
Qy	301	AACAAAGAGAGAAAAAAGAAAACGCTTTGAAATGCAAAAGGTGATGAGATCTCTCA	360		
Db	313	AACAAAGAGAGAAAAAAGAAAACGCTTTGAAATGCAAAAGGTGATGAGATCTCTCA	372		
Qy	361	ATTGCGACACAGTTGTATACCGAACCAACGTAATGCAAGCATCCGTTCTACATGTGGCC	420		
Db	373	ATTGCGACACAGTTGTATACCGAACCAACGTAATGCAAGCATCCGTTCTACATGTGGCC	432		
Qy	421	AAGAAAGATATTATACATGAAAAAGCACTTGTATATGCTTGAATAATGGGAAACACCTG	480		
Db	433	AAGAAAGATATTATATCATGAAAAAGCACTTGTATATGCTTGAATAATGGGAAACACCTG	492		
Qy	481	ACGGTTAAAGAGAAAGACCTATTAATGTCTACACATCGCAAGCACTTTCGTCTTAATCG	540		
Db	493	ACGGTTAAAGAGAAAGACCTATTAATGTCTACACATCGCAAGCACTTTCGTCTTAATCG	552		
Qy	541	GAGCTCTTGAGTCAAGCCCATCATTCGTGCGCTCTGTGATGAAGCCACAGCATTTGATCT	600		

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Db 553 GAGCCCTCGAGTCAACGCCCATTCATCGTGGCTCTGGCTGAAGCCCGCATTTGATCT 612
Qy 601 GAGAGATCTTACTCAAGCGCGCAATACCCACAGTTCCTCCAGCTTTGGCAGCAGC 660
Db 613 GAGAGATCTTACTCAAGCGCGCAATACCCACAGTTCCTCCAGCTTTGGCAGCAGC 672
Qy 661 TCTGTTCACTTGGCGGAGTGTGTAATTAACAAGTGTGTTGTTGCAAGTG 720
Db 673 TCTGTTCACTTGGCGGAGTGTGTAATTAACAAGTGTGTTGTTGCAAGTG 732
Qy 721 ACTGAAGCAAGCAAGTATCAACAAGTGTGTTGTTGCTTCACTGAACTC 780
Db 733 ACTGAAGCAAGCAAGTATCAACAAGTGTGTTGTTGCTTCACTGAACTC 792
Qy 781 TGA 783
Db 793 TGA 795

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RESULT 3

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US-08-446-922-5
; Sequence 5, Application US/08446922
; Patent No. 5716805

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GENERAL INFORMATION:

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; APPLICANT: Spriggs, Melanie
; APPLICANT: Srinivasan, Subhashini
; TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.1
; SOFTWARE: Microsoft Word for Apple, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,922

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FILING DATE:

```

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/107,353
; FILING DATE: 08-13-93

```

CLASSIFICATION: 435

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 1003-A

```

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644

```

```

; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 783 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

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; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO

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; ANTI-SENSE: NO
; ORIGINAL SOURCE:

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; ORGANISM: Mouse
; STRAIN: CD40-L

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..780

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US-08-446-922-5

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Query Match 96.9%; Score 759; DB 1; Length 783;
Best Local Similarity 98.1%; Pred. No. 1,56-215;
Matches 768; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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Qy 1 ATGATCGAAACATACCAACCAACTTCTCCCGATCTGGGCACTGATCTGCCATCAGC 60
Db 1 ATGATGAAACATACCAACCAACTTCTCCCGATCTGGGCACTGATCTGCCATCAGC 60
Qy 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCACCAATGATTTGATCTGTG 120
Db 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCACCAATGATTTGATCTGTG 120
Qy 121 CTTTTCCTGTGATCTTCAATGAAGATTTGATGAGTGAAGAGAAAGTAACTTCAAT 180
Db 121 CTTTTCCTGTGATCTTCAATGAAGATTTGATGAGTGAAGAGAAAGTAACTTCAAT 180
Qy 181 GAAATTTTGTATTCATTAATAAAGCTAAAGATGCAACAAAGAGAGATCTTATCC 240
Db 181 GAAATTTTGTATTCATTAATAAAGCTAAAGATGCAACAAAGAGAGATCTTATCC 240
Qy 241 TTGCTGAATCTGTGAGATGAGAGGCAATTTGAAGACTTGTCAAGATTAAGCTTA 300
Db 241 TTGCTGAATCTGTGAGATGAGAGGCAATTTGAAGACTTGTCAAGATTAAGCTTA 300
Qy 301 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Db 301 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Qy 361 ATTGAGACACAGTTGTAAGCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 420
Db 361 ATTGAGACACAGTTGTAAGCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 420
Qy 421 AAGAAAGATTTATACATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Db 421 AAGAAAGATTTATACATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Qy 481 AAGTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Db 481 AAGTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Qy 541 GAGCCTTGAGTCAACGCCCATTCATCGTGGCTCTGGCTGAAGCCAGCAGATGATCT 600
Db 541 GAGCCTTGAGTCAACGCCCATTCATCGTGGCTCTGGCTGAAGCCAGCAGATGATCT 600
Qy 601 GAGAGATTTATCTCAAGGCGGCAATACCCACAGTTCCTCCAGCTTTGGCAGCAGC 660
Db 601 GAGAGATTTATCTCAAGGCGGCAATACCCACAGTTCCTCCAGCTTTGGCAGCAGC 660
Qy 661 TCTGTTCACTTGGCGGAGTGTGTAATTAACAAGTGTGTTGTTGCAAGTG 720
Db 661 TCTGTTCACTTGGCGGAGTGTGTAATTAACAAGTGTGTTGTTGCAAGTG 720
Qy 721 ACTGAAGCAAGCAAGTATCAACAAGTGTGTTGTTGCTTCACTGAACTC 780
Db 721 ACTGAAGCAAGCAAGTATCAACAAGTGTGTTGTTGCTTCACTGAACTC 780
Qy 781 TGA 783
Db 781 TGA 783

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RESULT 4

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US-08-249-189-1
; Sequence 1, Application US/08249189
; Patent No. 5961974

```

GENERAL INFORMATION:

```

; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: FANSLAW, WILLIAM
; APPLICANT: SPRIGGS, MELANIE
; APPLICANT: SRINIVASAN, SUBHASHINI
; APPLICANT: GIBSON, MARYLOU
; TITLE OF INVENTION: NOVEL CYTOKINE

```

QY	241	TCSTGACATGAGAGAGATGGAAGGCAATTTGAAGACCTTGACAGATATAACGTGA	3000
Db	241	TTGCTGTAAGTGTGAGAGATGAGAGGCAATTTGAAGACCTTGACAGATATAACGTGA	3000
QY	301	ACACAAAGAGAGAAAAAGAAAAACGCTTTGAATGCAAGAAGGTGATGAGATCTTCAA	3600
Db	301	ACACAAAGAGAGAAAAAGAAAAACGCTTTGAATGCAAGAAGGTGATGAGATCTTCAA	3600
QY	361	ATTGACAGACACGTTGTAAGCGAAGCCACAGTAATGACAGATCCGTTCTACAGTGGGCC	4200
Db	361	ATTGACAGACACGTTGTAAGCGAAGCCACAGTAATGACAGATCCGTTCTACAGTGGGCC	4200
QY	421	AAATAAGATTTTATACATGAAAAAGCACTTGTGTAATGCTTGAATAATGGAAAAACGCTG	4800
Db	421	AAATAAGATTTTATACATGAAAAAGCACTTGTGTAATGCTTGAATAATGGAAAAACGCTG	4800
QY	481	ACGGTTAAAAAGAGAGGACTCTATATATGTTCTACACTCAAGTCACTTGTGCTTAATCGG	5400
Db	481	ACGGTTAAAAAGAGAGGACTCTATATATGTTCTACACTCAAGTCACTTGTGCTTAATCGG	5400
QY	541	GACCGTTGAGATCAAGCCCAATCATGTGTGGCTCTGGTGAAGCCCAAGCATTTGATCT	6000
Db	541	GACCGTTGAGATCAAGCCCAATCATGTGTGGCTCTGGTGAAGCCCAAGCATTTGATCT	6000
QY	601	GAGAGAAATCTTACTCAAGGCGGCAATAATCCACAGTTCTCTCCAGCTTTGCAGACAGAG	6600
Db	601	GAGAGAAATCTTACTCAAGGCGGCAATAATCCACAGTTCTCTCCAGCTTTGCAGACAGAG	6600
QY	661	TCGTGTCACCTGGGCGAGTGTGTTGAATTAACAAGTGGTGCTCTGTGTTGTACAGTG	7200
Db	661	TCGTGTCACCTGGGCGAGTGTGTTGAATTAACAAGTGGTGCTCTGTGTTGTACAGTG	7200
QY	721	ACTGAGACAGCCCAATGATGCCACAGATTTGCGCTTCTATCTTTGGCTTAACTAACATC	7800
Db	721	ACTGAGACAGCCCAATGATGCCACAGATTTGCGCTTCTATCTTTGGCTTAACTAACATC	7800
QY	781	TGA 783	
Db	781	TGA 783	
RESULT 5			
US-08-484-624A-1			
Sequence 1, Application US/08484624A			
Patent No. 5962406			
GENERAL INFORMATION:			
APPLICANT: ARMITAGE, RICHARD			
APPLICANT: FANSLAW, WILLIAM			
APPLICANT: SPRIGGS, MELANIE			
APPLICANT: SRINIVASAN, SUBHASHINI			
APPLICANT: GIBSON, MARYLOU			
APPLICANT: MORRIS, ARVIA E.			
APPLICANT: MCGREW, JEFFERY			
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40			
NUMBER OF SEQUENCES: 26			
CORRESPONDENCE ADDRESSES:			
ADDRESSEE: IMMUNEX CORPORATION			
STREET: 51 UNIVERSITY STREET			
CITY: SEATTLE			
STATE: WASHINGTON			
COUNTRY: USA			
ZIP: 98101			
COMPUTER READABLE FORM:			
MEDIUM TYPE: floppy disk			
COMPUTER: Apple Macintosh			
OPERATING SYSTEM: Apple Operating System 7.5.5			
SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1			
CURRENT APPLICATION DATA:			
FILING DATE: US/08/484,624A			
CLASSIFICATION:			
PRIOR APPLICATION DATA:			

APPLICATION NUMBER: 08/477,733
 FILING DATE: June 07, 1995
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/969,703
 FILING DATE: October 23, 1992
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/805,723
 FILING DATE: December 5, 1991
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/783,707
 FILING DATE: October 25, 1991
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Perkins, Patricia A.
 REGISTRATION NUMBER: 34,693
 REFERENCE/DOCKET NUMBER: 2802-D
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 2065870430
 TELEFAX: 2065870606
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 783 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: MOUSE
 IMMEDIATE SOURCE:
 CLONE: CD40-L
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..783
 US-08-484-624A-1

Query Match 96.9%; Score 759; DB 2; Length 783;
 Best Local Similarity 98.1%; Pred. No. 1.5e-215;
 Matches 768; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 ATGATGAAACATACACCAACTTCTCCCGCATGCGGCACCTGAGTCCCATACG 60
 DB 1 ATGATGAAACATACACCAACTTCTCCCGCATGCGGCACCTGAGTCCCATACG 60
 QY 61 ATGAAATTTTATATTTACTTACTGTTTCTTATCAACCAATGATGATCTGTG 120
 DB 61 ATGAAATTTTATATTTACTTACTGTTTCTTATCAACCAATGATGATCTGTG 120
 QY 121 CTTTGGCTGTATCTTATGATGATGATGATGATGATGATGATGATGATGATG 180
 DB 121 CTTTGGCTGTATCTTATGATGATGATGATGATGATGATGATGATGATGATG 180
 QY 181 GAAGATTTTGTATCTTATGATGATGATGATGATGATGATGATGATGATGATG 240
 DB 181 GAAGATTTTGTATCTTATGATGATGATGATGATGATGATGATGATGATGATG 240
 QY 241 TTGCTGAACGTGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGAT 300
 DB 241 TTGCTGAACGTGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGAT 300
 QY 301 AACAAAG 360
 DB 301 AACAAAG 360
 QY 361 ATTGACACACGTTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
 DB 361 ATTGACACACGTTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
 QY 421 AAGAAAGATATTATACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480

DB 421 AAGAAAGATATTATACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
 QY 481 ACCTTAAAG 540
 DB 481 ACCTTAAAG 540
 QY 541 GAGCTTCGAGTCAG 600
 DB 541 GAGCTTCGAGTCAG 600
 QY 601 GAGAGATTTTATCTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
 DB 601 GAGAGATTTTATCTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
 QY 661 TCTGTTCACTTGGGCGAG 720
 DB 661 TCTGTTCACTTGGGCGAG 720
 QY 721 ACTGAG 780
 DB 721 ACTGAG 780
 QY 781 TGA 783
 DB 781 TGA 783

RESULT 6
 US-08-477-733B-1
 Sequence 1, Application US/08477733B
 Patent No. 5981724
 GENERAL INFORMATION:
 APPLICANT: ARMITAGE, RICHARD
 APPLICANT: FANSLAW, WILLIAM
 APPLICANT: SPRIGGS, MELANIE
 APPLICANT: SRINIVASAN, SUBHASHINI
 APPLICANT: GIBSON, MARYLOU
 APPLICANT: MORRIS, ARVITA B.
 APPLICANT: MCGREW, JEFFERY
 TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: IMMUNEX CORPORATION
 STREET: 51 UNIVERSITY STREET
 CITY: SEATTLE
 STATE: WASHINGTON
 COUNTRY: USA
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: Apple Operating System 7.5.5
 SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/477,733B
 FILING DATE: June 07, 1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/249,189
 FILING DATE: May 24, 1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/969,703
 FILING DATE: October 23, 1992
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/805,723
 FILING DATE: December 5, 1991
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/783,707
 FILING DATE: October 25, 1991

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 783 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: MOUSE
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 1..783
US-08-477-733B-1

Query Match

96.9% Score 759; DB 2; Length 783;

Best Local Similarity 98.1%; Pred. No. 1.5e-215;

Matches 768; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 ATGATCGAATTCATCAACCACTTCTCCGATCTGGCGCCACTGACCTGCCATCAGC 60
DB 1 ATGATGAAACATTCAGCCACCTTCCCGATCTGGCGCCACTGACCTGCCATCAGC 60
QY 61 ATGAAATTTTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 120
DB 61 ATGAAATTTTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 120
QY 121 CTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
DB 121 CTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
QY 181 GAAGATTTTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 240
DB 181 GAAGATTTTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 240
QY 241 TTGCTGAACCTGTGAGGATGGAAGCAATTTGAAGCACTTGTCAAGATTAATACCTTA 300
DB 241 TTGCTGAACCTGTGAGGATGGAAGCAATTTGAAGCACTTGTCAAGATTAATACCTTA 300
QY 301 AACAAAG 360
DB 301 AACAAAG 360
QY 361 ATTGAGAGACGCTGTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 420
DB 361 ATTGAGAGACGCTGTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 420
QY 421 AAGAAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 480
DB 421 AAGAAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 480
QY 481 ACGGTTAAAG 540
DB 481 ACGGTTAAAG 540
QY 541 GAGCCTTGAGTCAAGCCATTCATGCTGCGCTTGGCTGAAAGCCAGCAATGGATCT 600
DB 541 GAGCCTTGAGTCAAGCCATTCATGCTGCGCTTGGCTGAAAGCCAGCAATGGATCT 600
QY 601 GAGAGATTTACTCAAGGCGGCAATTAACCAAGTCTCTCCAGCTTTGCGAGAGAG 660
DB 601 GAGAGATTTACTCAAGGCGGCAATTAACCAAGTCTCTCCAGCTTTGCGAGAGAG 660

QY 661 TTGTTCACTTGGCGGAGGTGTTGAATTAACAAGCTGTGCTTCTGTGTTTCAACGTC 720
DB 661 TTGTTCACTTGGCGGAGGTGTTGAATTAACAAGCTGTGCTTCTGTGTTTCAACGTC 720
QY 721 ACTGAAGCAAGCCAAAGTATCAAGAGAGTGGCTTCTCATCTTTGGCTTACTCAAACTC 780
DB 721 ACTGAAGCAAGCCAAAGTATCAAGAGAGTGGCTTCTCATCTTTGGCTTACTCAAACTC 780
QY 781 TGA 783
DB 781 TGA 783

RESULT 7

US-09-088-913A-1

Sequence 1, Application US/09088913A

Patent No. 6087325

GENERAL INFORMATION:

APPLICANT: ARMITAGE, RICHARD

APPLICANT: FANSLAW, WILLIAM

APPLICANT: SPRIGGS, MELANIE

APPLICANT: SRINIVASAN, SUBHASHINI

APPLICANT: GIBSON, MARYLOU

APPLICANT: MORRIS, ARVIA E.

APPLICANT: MCGREW, JEFFERY

TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: IMMUNEX CORPORATION

STREET: 51 UNIVERSITY STREET

CITY: SEATTLE

STATE: WASHINGTON

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: Apple Macintosh

SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/088,913A

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/484,624

FILING DATE:

APPLICATION NUMBER: 08/477,733

FILING DATE: June 07, 1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/969,703

FILING DATE: October 23, 1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/805,723

FILING DATE: December 5, 1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/783,707

FILING DATE: October 25, 1991

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia A.

REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2802-D

TELECOMMUNICATION INFORMATION:

TELEPHONE: 2065870430

TELEFAX: 2065870606

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 783 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: MOUSE
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 1..783
US-09-088-913A-1

Query Match 96.9%; Score 759; DB 3; Length 783;
Best Local Similarity 98.1%; Pred. No. 1.5e-215;
Matches 768; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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QY 1 ATGATCGAAACATCAACCAACTCTCCCGATCTGCGGCGCACTGACCTGCCATCAGC 60
DB 1 ATGATGAAACATCAACCAACTCTCCCGATCTGCGGCGCACTGACCTGCCATCAGC 60
QY 61 ATGAAATTTTATGATTTTACTTACTCTGTTTCTTATCCCAATGATGATCTGTG 120
DB 61 ATGAAATTTTATGATTTTACTTACTCTGTTTCTTATCCCAATGATGATCTGTG 120
QY 121 CTTTGTGCTGATCTTCACTAGAGATGATGATGATGATGATGATGATGATGATGAT 180
DB 121 CTTTGTGCTGATCTTCACTAGAGATGATGATGATGATGATGATGATGATGATGAT 180
QY 181 GAAGATTTTGTATTCATTAATAAAGCTAAAGATGCAACAAAGAGATCTTTATCC 240
DB 181 GAAGATTTTGTATTCATTAATAAAGCTAAAGATGCAACAAAGAGATCTTTATCC 240
QY 241 TTGCTGACTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
DB 241 TTGCTGACTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
QY 301 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
DB 301 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
QY 361 ATTGACGACACGTTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 361 ATTGACGACACGTTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
QY 421 AAGAAAGATTTATTAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
DB 421 AAGAAAGATTTATTAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
QY 481 ACGGTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
DB 481 ACGGTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
QY 541 GAGCTTCAAGTCAACGCGGCTTCACTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 600
DB 541 GAGCTTCAAGTCAACGCGGCTTCACTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 600
QY 601 GAGGATCTTACTCAAGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
DB 601 GAGGATCTTACTCAAGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
QY 661 TCTGTTCACTGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
DB 661 TCTGTTCACTGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY 721 ACTGAAGCAAGCAAGTATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
DB 721 ACTGAAGCAAGCAAGTATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
QY 781 TGA 783
DB 781 TGA 783
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RESULT 8
US-08-769-819-1

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Sequence 1, Application US/08769819
Patent No. 6264951
GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: FANSLAW, WILLIAM
APPLICANT: SPRIGGS, MELANIE
APPLICANT: SRINIVASAN, SUBHASHINI
APPLICANT: GIBSON, MARYLOU
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESS: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.1
SOFTWARE: Microsoft Word for Apple, version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/769,819
FILING DATE: 19-DEC-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484,624
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: 08/249,189
FILING DATE: May 24, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,703
FILING DATE: October 23, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/805,723
FILING DATE: December 5, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/783,707
FILING DATE: October 25, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 783 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: MOUSE
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 1..783
US-08-769-819-1
Query Match 96.9%; Score 759; DB 4; Length 783;
Best Local Similarity 98.1%; Pred. No. 1.5e-215;
Matches 768; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 1 ATGATCGAAACATCAACCAACTCTCCCGATCTGCGGCGCACTGACCTGCCATCAGC 60
DB 1 ATGATGAAACATCAACCAACTCTCCCGATCTGCGGCGCACTGACCTGCCATCAGC 60
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/ MEDIUM TYPE: Floppy disk
/ COMPUTER: Apple Macintosh
/ OPERATING SYSTEM: Apple Operating System 7.1
/ SOFTWARE: Microsoft Word for Apple, version 5.1a
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/770,974
/ FILING DATE: 20-DEC-1996
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/477,733
/ FILING DATE: 02-AUG-1995
/ APPLICATION NUMBER: 08/249,189
/ FILING DATE: May 24, 1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/969,703
/ FILING DATE: October 23, 1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/805,723
/ FILING DATE: December 5, 1991
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/783,707
/ FILING DATE: October 25, 1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Perkins, Patricia A.
/ REGISTRATION NUMBER: 34,693
/ REFERENCE/DOCKET NUMBER: 2802-D
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 2065870606
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 783 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ HYPOTHEICAL: NO
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ ORGANISM: MOUSE
/ IMMEDIATE SOURCE:
/ CLONE: CD40-L
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1..783
/ US-08-770-974-1

Query Match          56.3%; Score 759; DB 4; Length 783;
Best Local Similarity 98.1%; Pred. No. 1.5e-215;
Matches 768; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

OY 1 ATGATCGAACAATACAAACCAACTTCTCCCGATCTGCGGCACTGGACCTGCCATACG 60
Db 1 AAGTAAAGAAACATACAGCGAACTTCTCCCGAATCGGTGGCACTGGACCTTCCACAGC 60

OY 61 AAGAAATTTTATGTATTTACTTACTGTGTTTCCCTTATACCCCAATGATGGATCTGTG 120
Db 61 ATGAAGATTTTATGTATTTACTTACTGTGTTTCCCTTATACCCCAATGATGGATCTGTG 120

OY 121 CTTTTCCTGTGTATCTTCATTAAGATTTGGATTAAGTGAAGAGGAAGTAACCTTCAT 180
Db 121 CTTTTCCTGTGTATCTTCATTAAGATTTGGATTAAGTGAAGAGGAAGTAACCTTCAT 180

OY 181 GAAAGTTTGATTCATTAAGAAAGCTAAAGATGCAACAAAGAGAAAGATCTTTATCC 240
Db 181 GAAAGTTTGATTCATTAAGAAAGCTAAAGATGCAACAAAGAGAAAGATCTTTATCC 240

OY 241 TTGCTGAACCTGAGAGATGAGAAGCAATTTGAAGCTTGTCAAGATATAACGTTA 300
Db 241 TTGCTGAACCTGAGAGATGAGAAGCAATTTGAAGCTTGTCAAGATATAACGTTA 300

OY 301 AACCAAGAGAAAGAAAGAAACACGCTTGAATGCAAGAGGTGATGAGATCTTCAC 360

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QY 541 GAGCTTCGAGTCAAGCCCATTCATGTCGGCTCTGCTGAAGCCGACAGTTGGATCT 600
 DB 541 GAGCTTCGAGTCAAGCCCATTCATGTCGGCTCTGCTGAAGCCGACAGTTGGATCT 600
 QY 601 GAGGAATCTTACTCAAGCGCGCAATATCCACAGTTCTCCAGCTTTGGCAGCAG 660
 DB 601 GAGGAATCTTACTCAAGCGCGCAATATCCACAGTTCTCCAGCTTTGGCAGCAG 660
 QY 661 TCTGTCACCTGGGCGAGTGTGTAATTACAAGTGTGCTCTGCTGTTGTCAGCTG 720
 DB 661 TCTGTCACCTGGGCGAGTGTGTAATTACAAGTGTGCTCTGCTGTTGTCAGCTG 720
 QY 721 ACTGAAGCAAGCCAGATGATCCAGAGTTGGCTTCTCATCTTTGGCTTACTCAATC 780
 DB 721 ACTGAAGCAAGCCAGATGATCCAGAGTTGGCTTCTCATCTTTGGCTTACTCAATC 780
 QY 781 TGA 783
 DB 781 TGA 783

RESULT 11

US-09-399-106-1

Sequence 1, Application US/09399106

Patent No. 6410711

GENERAL INFORMATION:

APPLICANT: ARMITAGE, RICHARD

APPLICANT: FANSLAW, WILLIAM

APPLICANT: SPRIGGS, MELANIE

APPLICANT: SRINIVASAN, SUBHASHINI

APPLICANT: GIBSON, MARYLOU

APPLICANT: MORRIS, ARVIA E.

TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: IMMUNEX CORPORATION

STREET: 51 UNIVERSITY STREET

CITY: SEATTLE

STATE: WASHINGTON

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Apple Operating System 7.5.5

SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09399,106

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/477,733

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/969,703

FILING DATE: October 23, 1992

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/805,723

FILING DATE: December 5, 1991

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/783,707

FILING DATE: October 25, 1991

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia A.

REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2802-D

TELECOMMUNICATION INFORMATION:

TELEPHONE: 2065870430

TELEFAX: 2065870606
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 783 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHEICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: MOUSE
 IMMEDIATE SOURCE:
 CLONE: CD40-L
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..783
 US-09-399-106-1

Query Match

96.9%; Score 759; DB 4; Length 783;

Best Local Similarity 98.1%; Pred. No. 1,5e-215;

Matches 768; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 ATGATCGAAATACATACCAACCTTCTCCCGATCTGCGGCACTGGACCTGCCATCAGC 60
 DB 1 ATGATCGAAATACATACCAACCTTCTCCCGATCTGCGGCACTGGACCTGCCATCAGC 60
 QY 61 ATGAAATTTTATATGATTTACTACTGTTTCTTATCACCAGATGATGATCTGTG 120
 DB 61 ATGAAATTTTATATGATTTACTACTGTTTCTTATCACCAGATGATGATCTGTG 120
 QY 121 CTTTGTGCTGTATCTTCATGAAAGATGATGATGATGATGATGATGATGATGAT 180
 DB 121 CTTTGTGCTGTATCTTCATGAAAGATGATGATGATGATGATGATGATGATGAT 180
 QY 181 GAAATTTTGTATTTCTATAAAAGCTTAAAGATGCAACAAGAGAGATCTTATCC 240
 DB 181 GAAATTTTGTATTTCTATAAAAGCTTAAAGATGCAACAAGAGAGATCTTATCC 240
 QY 241 TTGCTGAACCTGTAGAGATGAGAGCAATTTGAAAGCTTGTCAAGATTAACGTTA 300
 DB 241 TTGCTGAACCTGTAGAGATGAGAGCAATTTGAAAGCTTGTCAAGATTAACGTTA 300
 QY 301 AACCAAGAAAGAAAAAGAAAAAGAGCTTTGAATGCAAGAGGTATGAGATCTGCA 360
 DB 301 AACCAAGAAAGAAAAAGAAAAAGAGCTTTGAATGCAAGAGGTATGAGATCTGCA 360
 QY 361 ATTGACACACCTGTGTAAGCAAGCAACAGTAATGAGATCCGTTCTACAGTGGGCC 420
 DB 361 ATTGACACACCTGTGTAAGCAAGCAACAGTAATGAGATCCGTTCTACAGTGGGCC 420
 QY 421 AAGAAAGATATATATCATATGAAAGCACTTGTAATGCTTGAATATGGAAACAGCTG 480
 DB 421 AAGAAAGATATATATCATATGAAAGCACTTGTAATGCTTGAATATGGAAACAGCTG 480
 QY 481 ACGGTTAAAGAAAGCACTATATATGCTACACTCAAGTCACTTGTGCTTATCGG 540
 DB 481 ACGGTTAAAGAAAGCACTATATATGCTACACTCAAGTCACTTGTGCTTATCGG 540
 QY 541 GAGCTTCGAGTCAAGCCCATTCATGTCGGCTCTGCTGAAGCCGACAGTTGGATCT 600
 DB 541 GAGCTTCGAGTCAAGCCCATTCATGTCGGCTCTGCTGAAGCCGACAGTTGGATCT 600
 QY 601 GAGGAATCTTACTCAAGCGCGCAATATCCACAGTTCTCCAGCTTTGGCAGCAG 660
 DB 601 GAGGAATCTTACTCAAGCGCGCAATATCCACAGTTCTCCAGCTTTGGCAGCAG 660
 QY 661 TCTGTCACCTGGGCGAGTGTGTAATTACAAGTGTGCTCTGCTGTTGTCAGCTG 720
 DB 661 TCTGTCACCTGGGCGAGTGTGTAATTACAAGTGTGCTCTGCTGTTGTCAGCTG 720
 QY 721 ACTGAAGCAAGCCAGATGATCCAGAGTTGGCTTCTCATCTTTGGCTTACTCAATC 780

Db 721 ACTGAAGCAAGCAAGTATCCAGAGTTGGCTTCTATCTTTGGCTTACTGAACTC 780
 Qy 781 TGA 783
 Db 781 TGA 783

RESULT 12

PCT-US93-10034-5
 ; Sequence 5, Application PC/TUS9310034
 ; GENERAL INFORMATION:
 ; APPLICANT: Sprin99, Melanie
 ; APPLICANT: Srinivasan, Subhashini
 ; TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric
 ; TITLE OF INVENTION: Proteins
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Immunex Corporation
 ; STREET: 51 University Street
 ; CITY: Seattle
 ; STATE: WA
 ; COUNTRY: USA
 ; ZIP: 98101
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US93/10034
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Perkins, Patricia A
 ; REGISTRATION NUMBER: 34,693
 ; REFERENCE/DOCKET NUMBER: 1003
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206)587-0430
 ; TELEFAX: (206)233-0644
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 783 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA to mRNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Mouse
 ; STRAIN: CD40-L
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 1..780
 ; PCT-US93-10034-5

Query Match 96.9%; Score 759; DB 5; Length 783;
 Best local similarity 98.1%; Pred. No. 1.5e-215;
 Matches 768; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1 ATGATCAAAACATACACCAAACTTCTCCCGATCTGGCGCACTGAGTCCCATCAGC 60
 Db 1 ATGATCAAAACATACACCACTTCCCGATCTGGCGCACTGAGTCCCATCAGC 60
 Qy 61 ATGAAATTTTATGATTTCTACTGTTTCTTATCACCACCAATGATGATCTGTG 120
 Db 61 ATGAAATTTTATGATTTCTACTGTTTCTTATCACCACCAATGATGATCTGTG 120
 Qy 121 CTTTTCGTGTATCTTATGAAAGATGAGTAAAGTGAAGGAAAGAACTTAT 180
 Db 121 CTTTTCGTGTATCTTATGAAAGATGAGTAAAGTGAAGGAAAGAACTTAT 180
 Qy 181 GAAGATTTGTATTCATAAAAAAGCTAAAGATGCAACAAAGAGAGAGATCTTTATCC 240

Db 181 GAAGATTTGTATTCATAAAAAAGCTAAAGATGCAACAAAGAGAGAGATCTTTATCC 240
 Qy 241 TTGCTGAACCTGTGAGAGATGAGAGCAATTTGAAGACCTTGTCAAGATATAAGCTTA 300
 Db 241 TTGCTGAACCTGTGAGAGATGAGAGCAATTTGAAGACCTTGTCAAGATATAAGCTTA 300
 Qy 301 AACCAAG 360
 Db 301 AACCAAG 360
 Qy 361 ATTGACAGACCTGTTGAAGCAGACCAACAGATATGACGATCCCTTACAGTGGGCGC 420
 Db 361 ATTGACAGACCTGTTGAAGCAGACCAACAGATATGACGATCCCTTACAGTGGGCGC 420
 Qy 421 AAGAAAGATATTAATCAATGAAAGCAACTTGGTAATGCTTGAATAAGGAAACAGCTG 480
 Db 421 AAGAAAGATATTAATCAATGAAAGCAACTTGGTAATGCTTGAATAAGGAAACAGCTG 480
 Qy 481 AGGTTAAAG 540
 Db 481 AGGTTAAAG 540
 Qy 541 GAGCTTCAGTCAACGCCCATTCATCGTGGCTCTGCTGAAGCCAGCATTTGATCT 600
 Db 541 GAGCTTCAGTCAACGCCCATTCATCGTGGCTCTGCTGAAGCCAGCATTTGATCT 600
 Qy 601 GAGAAATCTTATCTCAAGCGGCAATCCCAAGTTCCTCCAGCTTTGGAGAGCAG 660
 Db 601 GAGAAATCTTATCTCAAGCGGCAATCCCAAGTTCCTCCAGCTTTGGAGAGCAG 660
 Qy 661 TCTGTTCACTTGGCGGAGAGTGTGTAATTAACAAGTGTGCTTGTGTGTTCAAGCTG 720
 Db 661 TCTGTTCACTTGGCGGAGAGTGTGTAATTAACAAGTGTGCTTGTGTGTTCAAGCTG 720
 Qy 721 ACTGAAGCAAGCAAGTATCCAGAGTTGGCTTCTATCTTTGGCTTACTGAACTC 780
 Db 721 ACTGAAGCAAGCAAGTATCCAGAGTTGGCTTCTATCTTTGGCTTACTGAACTC 780
 Qy 781 TGA 783
 Db 781 TGA 783

RESULT 13

US-08-249-189-22
 ; Sequence 22, Application US/08249189
 ; Patent No. 5961974
 ; GENERAL INFORMATION:
 ; APPLICANT: ARMITAGE, RICHARD
 ; APPLICANT: PANSLOW, WILLIAM
 ; APPLICANT: SPRIGGS, MELANIE
 ; APPLICANT: SRINIVASAN, SUBHASHINI
 ; APPLICANT: GIBSON, MARYLOU
 ; TITLE OF INVENTION: NOVEL CYTOKINE
 ; NUMBER OF SEQUENCES: 23
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: IMMUNEX CORPORATION
 ; STREET: 51 UNIVERSITY STREET
 ; CITY: SEATTLE
 ; STATE: WASHINGTON
 ; COUNTRY: USA
 ; ZIP: 98101
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Apple Macintosh
 ; OPERATING SYSTEM: Apple Operating System 7.1
 ; SOFTWARE: Microsoft Word for Apple, version 5.1a
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/249,189
 ; FILING DATE:
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:

Db 285 AGATGCAACAAGAGAGATCTTATCTTGGTGAACCTGTGAGAGATGAGAGCAA 344
Qy 271 TTTGAGACCTTTCACAGATATACGTAAACAAGAGAAAAAACAAGCTTT 330
Db 345 TTTGAGACCTTTCACAGATATACGTAAACAAGAGAAAAAACAAGCTTT 404
Qy 331 GAATGCAAGAAGGTGATGAGATCTCAAAATGACACACGTTGTAAAGCAAGCCAC 390
Db 405 GAATGCAAGAAGGTGATGAGATCTCAAAATGACACACGTTGTAAAGCAAGCCAC 464
Qy 391 AGTAATGACAGATCCGTTTACAGTGGGCAAGAAAGATATTAACATGAAGCAAC 450
Db 465 AGTAATGACAGATCCGTTTACAGTGGGCAAGAAAGATATTAACATGAAGCAAC 524
Qy 451 TTGTTAATGCTTGAATAATGGAAAAACGCTGACGGTTAAAGAGAAAGACTCTATTATGTC 510
Db 525 TTGTTAATGCTTGAATAATGGAAAAACGCTGACGGTTAAAGAGAAAGACTCTATTATGTC 584
Qy 511 TACACTCAAGTCACTTCTGCTTAATGGGAGGCTTCGAGTCAAGGCCATTGATGTC 570
Db 585 TACACTCAAGTCACTTCTGCTTAATGGGAGGCTTCGAGTCAAGGCCATTGATGTC 644
Qy 571 GGCCTTGGCTGAAGCCACAGATTGGATCTGAGAAATCTTAACAAGCGGCMAATACC 630
Db 645 GGCCTTGGCTGAAGCCACAGATTGGATCTGAGAAATCTTAACAAGCGGCMAATACC 704
Qy 631 CACAGTTCCTCCAGCTTTGCGAGCAGAGTCTGTCACTTGGGGGAGGTGAAATTA 690
Db 705 CACAGTTCCTCCAGCTTTGCGAGCAGAGTCTGTCACTTGGGGGAGGTGAAATTA 764
Qy 691 CAAGCTGGTCTTCTGTGTTTGTCAACGTGACTGAAAGCAAGCAAGTATCAACAGATT 750
Db 765 CAAGCTGGTCTTCTGTGTTTGTCAACGTGACTGAAAGCAAGCAAGTATCAACAGATT 824
Qy 751 GGCCTTCACTTTTGGCTTACTCAAACTCTGA 783
Db 825 GGCCTTCACTTTTGGCTTACTCAAACTCTGA 857

Search completed: March 9, 2003, 04:46:14
Job time : 35.5164 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: March 8, 2003, 18:35:23 ; Search time 2048.61 Seconds
(without alignments)

11166.008 Million cell updates/sec

Title: US-08-982-272-6

Perfect score: 1 ATGATGAAACATACAGCCA.....TTGGCTTACTCAACTCTGA 786

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

1: gb Da:*

2: gb Htg:*

3: gb In:*

4: gb On:*

5: gb Ov:*

6: gb Pat:*

7: gb Pl:*

8: gb Pr:*

9: gb Sts:*

10: gb Sts:*

11: gb Sts:*

12: gb Sts:*

13: gb Sts:*

14: gb Sts:*

15: gb Sts:*

16: gb Sts:*

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36: gb Sts:*

37: gb Sts:*

38: gb Sts:*

39: gb Sts:*

40: gb Sts:*

41: gb Sts:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	763.6	97.2	786	187864	187864 Sequence 3
2	763.6	97.2	840	AR044779	AR044779 Sequence
3	763.6	97.2	840	AR076926	AR076926 Sequence
4	763.6	97.2	840	AR078316	AR078316 Sequence
5	763.6	97.2	840	AR085419	AR085419 Sequence
6	763.6	97.2	840	AR103375	AR103375 Sequence
7	763.6	97.2	840	AR106246	AR106246 Sequence
8	763.6	97.2	840	AR169232	AR169232 Sequence
9	763.6	97.2	840	AR171647	AR171647 Sequence
10	763.6	97.2	840	123893	123893 Sequence 1
11	763.6	97.2	840	127345	127345 Sequence 7
12	763.6	97.2	840	167828	167828 Sequence 1
13	763.6	97.2	879	AX090039	AX090039 Sequence
14	763.6	97.2	879	HSCG39MR	Z15017 H. sapiens m
15	763.6	97.2	1803	HSCD40	X67878 H. sapiens m
16	763.6	97.2	1816	HUMCD40L	L07414 Human CD40-
17	762	96.9	1822	HSTRAPA	X68550 H. sapiens T
18	754	95.9	1058	AF344841	AF344841 Cercopithec
19	754	95.9	1058	AF344859	AF344859 Macaca mu
20	748.4	95.2	839	HACD40L	X96710 H. sapiens m
21	733.2	93.3	974	AF344860	AF344860 Actus tri
22	733.2	93.3	975	AF344844	AF344844 Callithrix
23	642	81.7	864	BTCD40LIG	Z48469 B. taurus mR
24	638.2	81.2	1425	AR076929	AR076929 Sequence
25	638.2	81.2	1425	AR078319	AR078319 Sequence
26	638.2	81.2	1425	AR085422	AR085422 Sequence
27	638.2	81.2	1425	AR103378	AR103378 Sequence
28	638.2	81.2	1425	AR169235	AR169235 Sequence
29	637.2	81.1	929	AR076932	AR076932 Sequence
30	637.2	81.1	929	AR078322	AR078322 Sequence
31	637.2	81.1	929	AR085425	AR085425 Sequence
32	637.2	81.1	929	AR103381	AR103381 Sequence
33	637.2	81.1	929	AR169238	AR169238 Sequence
34	637.2	81.1	929	AR169238	AR169238 Sequence
35	636	80.9	1566	AX455878	AX455878 Sequence
36	616.4	78.0	904	AF344853	AF344853 Macaca ne
37	613.2	77.6	788	AF079105	AF079105 Felis cat
38	610	77.6	786	AB040443	AB040443 Sus scrofa
39	589.2	75.0	783	AF013985	AF013985 Rattus no
40	584.4	74.4	783	AR076918	AR076918 Sequence
41	584.4	74.4	783	AR078308	AR078308 Sequence
42	584.4	74.4	783	AR085411	AR085411 Sequence
43	584.4	74.4	783	AR103367	AR103367 Sequence
44	584.4	74.4	783	AR169224	AR169224 Sequence
45	584.4	74.4	783	187865	187865 Sequence 5

ALIGNMENTS

RESULT 1

LOCUS 187864

DEFINITION Sequence 3 from patent US 5716805.

ACCESSION 187864

VERSION 187864.1 GI:3407804

KEYWORDS

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 786)

AUTHORS Srinivasan, S. and Spriggs, M. K.

TITLE Methods of preparing soluble, oligomeric proteins

JOURNAL Patent: US 5716805-A 3 10-FEB-1998;

FEATURES Location/Qualifiers

source 1..786
/organism="unknown"
BASE COUNT 250 a 168 c 168 g 200 t
ORIGIN

Query Match 97.2%; Score 763.6; DB 6; Length 786;
Best Local Similarity 98.2%; Pred. No. 9.8e-194;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGATAGAAACATACAGCCACCTTCCCGAGATCCGTGGCACTTGACCTTCCAGGAGC 60
DB 1 ATGATCGAAACATACAGCCACCTTCCCGAGATCCGTGGCACTTGACCTTCCAGGAGC 60
QY 61 ATGAAAGATTTTATGATATTTACTTACTCTGTTTTTCTTATACCCAGATGTTGGTCAGCA 120
DB 61 ATGAAAGATTTTATGATATTTACTTACTCTGTTTTTCTTATACCCAGATGTTGGTCAGCA 120
QY 121 CTTTTCGCTGTATCTTCACTAGAGGTGGCAAGATGAAAGATGAAAGGATCTTCAT 180
DB 121 CTTTTCGCTGTATCTTCACTAGAGGTGGCAAGATGAAAGATGAAAGGATCTTCAT 180
QY 181 GAAGATTTTGTATTCATGAAAAGATACAGATGCAACAGAGAAAGATCTTATCC 240
DB 181 GAAGATTTTGTATTCATGAAAAGATACAGATGCAACAGAGAAAGATCTTATCC 240
QY 241 TTAAGTGTGTAGAGATTAAGAGCCAGTTGAGAGCTTTGTAAGATATATGTTA 300
DB 241 TTAAGTGTGTAGAGATTAAGAGCCAGTTGAGAGCTTTGTAAGATATATGTTA 300
QY 301 AACAAAG 360
DB 301 AACAAAG 360
QY 361 CAATTTGGGCACTGATCATTAAGTGGCCAGAGTAAACAATCTGTGTACAGTGG 420
DB 361 CAATTTGGGCACTGATCATTAAGTGGCCAGAGTAAACAATCTGTGTACAGTGG 420
QY 421 GGTGAAAAAGATATCTACATGAGCAACATCTTGTAACCTTGAAAAATGGAAAAAG 480
DB 421 GGTGAAAAAGATATCTACATGAGCAACATCTTGTAACCTTGAAAAATGGAAAAAG 480
QY 481 CTGACCGTTAAAG 540
DB 481 CTGACCGTTAAAG 540
QY 541 CGGGAAGCTTCAGTCAAGCTCATTATATAGCCAGCTTGTCTAAAGTCCCGGATGA 600
DB 541 CGGGAAGCTTCAGTCAAGCTCATTATATAGCCAGCTTGTCTAAAGTCCCGGATGA 600
QY 601 TTGAGAGAAATCTTACTGAGAGCTGCAAAATACCAAGTTCGGCCAAACCTTGGGGCA 660
DB 601 TTGAGAGAAATCTTACTGAGAGCTGCAAAATACCAAGTTCGGCCAAACCTTGGGGCA 660
QY 661 CAATCCATTCATCTTGGAGAGAGATTTGATTTGCAACCAAGTTCGTTGGTTTGTCAAT 720
DB 661 CAATCCATTCATCTTGGAGAGAGATTTGATTTGCAACCAAGTTCGTTGGTTTGTCAAT 720
QY 721 GTGACTGATCAAGCCAGTGAAGCCATGAGCACTGCTTCAAGCTCTTGGCTTAACTCAA 780
DB 721 GTGACTGATCAAGCCAGTGAAGCCATGAGCACTGCTTCAAGCTCTTGGCTTAACTCAA 780
QY 781 CTCTGA 786
DB 781 CTCTGA 786

RESULT 2
AR044779 840 bp DNA linear PAT 29-SEP-1999
LOCUS AR044779
DEFINITION Sequence 3 from patent US 5817516.
ACCESSION AR044779
VERSION AR044779.1 GI:5966244
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 840)
AUTHORS Kehry, M. and Castle, B.
TITLE Methods for proliferating and differentiating B cells with high density membrane CD40 ligand
JOURNAL Patent: US 5817516-A 3 06-OCT-1998;
FEATURES
source location/Qualifiers
1..840
BASE COUNT 263 a 182 c 181 g 214 t
ORIGIN

Query Match 97.2%; Score 763.6; DB 6; Length 840;
Best Local Similarity 98.2%; Pred. No. 9.8e-194;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGATAGAAACATACAGCCACCTTCCCGAGATCCGTGGCACTTGACCTTCCAGGAGC 60
DB 22 ATGATCGAAACATACAGCCACCTTCCCGAGATCCGTGGCACTTGACCTTCCAGGAGC 81
QY 61 ATGAAAGATTTTATGATATTTACTTACTCTGTTTTTCTTATACCCAGATGTTGGTCAGCA 120
DB 82 ATGAAAGATTTTATGATATTTACTTACTCTGTTTTTCTTATACCCAGATGTTGGTCAGCA 141
QY 121 CTTTTCGCTGTATCTTCACTAGAGGTGGCAAGATGAAAGATGAAAGGATCTTCAT 180
DB 142 CTTTTCGCTGTATCTTCACTAGAGGTGGCAAGATGAAAGATGAAAGGATCTTCAT 201
QY 181 GAAGATTTTGTATTCATGAAAAGATACAGATGCAACAGAGAAAGATCTTATCC 240
DB 202 GAAGATTTTGTATTCATGAAAAGATACAGATGCAACAGAGAAAGATCTTATCC 261
QY 241 TTAAGTGTGTAGAGATTAAGAGCCAGTTGAGAGCTTTGTAAGATATATGTTA 300
DB 262 TTAAGTGTGTAGAGATTAAGAGCCAGTTGAGAGCTTTGTAAGATATATGTTA 321
QY 301 AACAAAG 360
DB 322 AACAAAG 381
QY 361 CAATTTGGGCACTGATCATTAAGTGGCCAGAGTAAACAATCTGTGTACAGTGG 420
DB 382 CAATTTGGGCACTGATCATTAAGTGGCCAGAGTAAACAATCTGTGTACAGTGG 441
QY 421 GGTGAAAAAGATATCTACATGAGCAACATCTTGTAACCTTGAAAAATGGAAAAAG 480
DB 442 GGTGAAAAAGATATCTACATGAGCAACATCTTGTAACCTTGAAAAATGGAAAAAG 501
QY 481 CTGACCGTTAAAG 540
DB 502 CTGACCGTTAAAG 561
QY 541 CGGGAAGCTTCAGTCAAGCTCATTATATAGCCAGCTTGTCTAAAGTCCCGGATGA 600
DB 562 CGGGAAGCTTCAGTCAAGCTCATTATATAGCCAGCTTGTCTAAAGTCCCGGATGA 621
QY 601 TTGAGAGAAATCTTACTGAGAGCTGCAAAATACCAAGTTCGGCCAAACCTTGGGGCA 660
DB 622 TTGAGAGAAATCTTACTGAGAGCTGCAAAATACCAAGTTCGGCCAAACCTTGGGGCA 681
QY 661 CAATCCATTCATCTTGGAGAGAGATTTGATTTGCAACCAAGTTCGTTGGTTTGTCAAT 720
DB 682 CAATCCATTCATCTTGGAGAGAGATTTGATTTGCAACCAAGTTCGTTGGTTTGTCAAT 741
QY 721 GTGACTGATCAAGCCAGTGAAGCCATGAGCACTGCTTCAAGCTCTTGGCTTAACTCAA 780
DB 742 GTGACTGATCAAGCCAGTGAAGCCATGAGCACTGCTTCAAGCTCTTGGCTTAACTCAA 801
QY 781 CTCTGA 786
DB 802 CTCTGA 807

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RESULT 3
LOCUS AR076926 840 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 11 from patent US 5961974.
ACCESSION AR076926
VERSION AR076926.1 GI:10003672
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 840)
AUTHORS Armitage, R.J., Fanslow, W.C. and Spriggs, M.K.
TITLE Monoclonal antibodies to CD40 ligand, pharmaceutical composition comprising the same and hybridomas producing the same
JOURNAL Patent: US 5961974-A 11 05-OCT-1999;
FEATURES
source 1..840
location/Qualifiers
BASE COUNT 266 a 185 c 175 g 214 t
ORIGIN
Query Match 97.2%; Score 763.6; DB 6; Length 840;
Best Local Similarity 98.2%; Pred. No. 9.8e-194;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1 ATGATGAAACATACACCACTTCCCGAGTCGTGGCACTGGACTCCAGGAGC 60
Db 46 ATGATCGAAACATACCAAACTTCTCCGATCTGGCGCACTGGACTCCATCAGC 105
Qy 61 ATGAGATTTTATGATTTACTTACTCTGTTTCTTATCACCAGATGTTGGTGACA 120
Db 106 ATGAAATTTTATGATTTACTTACTCTGTTTCTTATCACCAGATGTTGGTGACA 165
Qy 121 CTTTTCGTGCTATCTTCTTGAAGTTGACAAAGTAGAAGTAGAAGATCTTCAAT 180
Db 166 CTTTTCGTGCTATCTTCTTGAAGTTGACAAAGTAGAAGTAGAAGATCTTCAAT 225
Qy 181 GAAGATTTTATTCATGAAAAGATAGAGATGCAACAGAGAAAGATCTTATCC 240
Db 226 GAAGATTTTATTCATGAAAAGATAGAGATGCAACAGAGAAAGATCTTATCC 285
Qy 241 TTAAGTCTGTGAGAGATTAAGCCAGTTGAAGCTTTGTAAGATTAATGTTA 300
Db 286 TTAAGTCTGTGAGAGATTAAGCCAGTTGAAGCTTTGTAAGATTAATGTTA 345
Qy 301 AACAAAGAGAGAGAGAAAGAAACAGCTTTGAATGCAAAAGTGATCAGAAATCCT 360
Db 346 AACAAAGAGAGAGAGAAAGAAACAGCTTTGAATGCAAAAGTGATCAGAAATCCT 405
Qy 361 CAAATTTGGGCAATGTCATTAAGTGGCGCAGCATTAACCAATCTGTGTTACGTGG 420
Db 406 CAAATTTGGGCAATGTCATTAAGTGGCGCAGCATTAACCAATCTGTGTTACGTGG 465
Qy 421 GCTGAAAAAGATCTACACCATGAGCAAACTTGTGTAACCTGGAAGATGGAAAACAG 480
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Qy 481 CTGACCGTTTAAAGACAGAGACTCTATTATATCTATGCCCCAAGTCACTTGTGTCAT 540
Db 526 CTGACCGTTTAAAGACAGAGACTCTATTATATCTATGCCCCAAGTCACTTGTGTCAT 585
Qy 541 CCGGAGCTTTCAGTCAAGCTCATTATTAAGCCAGCTTGTGCTTAAAGTCCCCCGGTAGA 600
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Qy 601 TTGAGAGATCTTACTCAGAGCTGAATACCAAGTTTCGCGCAAACTGTGGGGCAA 660
Db 646 TTGAGAGATCTTACTCAGAGCTGAATACCAAGTTTCGCGCAAACTGTGGGGCAA 705
Qy 661 CAATCATTCACCTGGAGAGATTTGAATGCAACAGGTGCTTGGGTGTTGTCAT 720

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Db 706 CAATCATTCACCTGGAGAGATTTGAATGCAACAGGTGCTTGGGTGTTGTCAT 765
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Db 766 GTGACTGATCCAAAGCCAAAGTGAAGCCATGAGCATCTTCAAGTCTTGGCTTACTCAA 825
Qy 781 CTCTGA 786
Db 826 CTCTGA 831

RESULT 4
LOCUS AR078316 840 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 11 from patent US 5962406.
ACCESSION AR078316
VERSION AR078316.1 GI:10005062
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 840)
AUTHORS Armitage, R.J., Fanslow, W.C., Spriggs, M.K., Srinivasan, S.,
TITLE Recombinant soluble CD40 ligand polypeptide and pharmaceutical composition containing the same
JOURNAL Patent: US 5962406-A 11 05-OCT-1999;
FEATURES
source 1..840
location/Qualifiers
BASE COUNT 266 a 185 c 175 g 214 t
ORIGIN
Query Match 97.2%; Score 763.6; DB 6; Length 840;
Best Local Similarity 98.2%; Pred. No. 9.8e-194;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1 ATGATGAAACATACACCACTTCCCGAGTCGTGGCACTGGACTCCAGGAGC 60
Db 46 ATGATCGAAACATACCAAACTTCTCCGATCTGGCGCACTGGACTCCATCAGC 105
Qy 61 ATGAGATTTTATGATTTACTTACTCTGTTTCTTATCACCAGATGTTGGTGACA 120
Db 106 ATGAAATTTTATGATTTACTTACTCTGTTTCTTATCACCAGATGTTGGTGACA 165
Qy 121 CTTTTCGTGCTATCTTCTTGAAGTTGACAAAGTAGAAGTAGAAGATCTTCAAT 180
Db 166 CTTTTCGTGCTATCTTCTTGAAGTTGACAAAGTAGAAGTAGAAGATCTTCAAT 225
Qy 181 GAAGATTTTATTCATGAAAAGATAGAGATGCAACAGAGAAAGATCTTATCC 240
Db 226 GAAGATTTTATTCATGAAAAGATAGAGATGCAACAGAGAAAGATCTTATCC 285
Qy 241 TTAAGTCTGTGAGAGATTAAGCCAGTTGAAGCTTTGTAAGATTAATGTTA 300
Db 286 TTAAGTCTGTGAGAGATTAAGCCAGTTGAAGCTTTGTAAGATTAATGTTA 345
Qy 301 AACAAAGAGAGAGAGAAAGAAACAGCTTTGAATGCAAAAGTGATCAGAAATCCT 360
Db 346 AACAAAGAGAGAGAGAAAGAAACAGCTTTGAATGCAAAAGTGATCAGAAATCCT 405
Qy 361 CAAATTTGGGCAATGTCATTAAGTGGCGCAGCATTAACCAATCTGTGTTACGTGG 420
Db 406 CAAATTTGGGCAATGTCATTAAGTGGCGCAGCATTAACCAATCTGTGTTACGTGG 465
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Db 466 GCTGAAAAAGATCTACACCATGAGCAAACTTGTGTAACCTGGAAGATGGAAAACAG 525
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QY 541 CGGAGAGCTTCGAGTCAAGCTTCATTTATAGCCAGCTTCGCTAAAGTCCCGGGTGA 600
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DB 646 TTGAGAGAACTTCTACTGAGCTGCAAAATACCAAGTTCGCGCAAACTTGGCGGCA 705
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DB 706 CAATCCATTCCTTGGGAGAGTATTTGAATTCGCAACCGAGGCTTCGCGTGTTCAT 765
QY 721 GTGACTGATCCAAAGCCAAAGTGAAGCCATGCGCACTGCTTCAGTCTTGGCTTAA 780
DB 766 GTGACTGATCCAAAGCCAAAGTGAAGCCATGCGCACTGCTTCAGTCTTGGCTTAA 825
QY 781 CTCCTGA 786
DB 826 CTCCTGA 831

RESULT 5
AR085419 840 bp DNA linear PAT 01-SEP-2000
LOCUS AR085419
DEFINITION Sequence 11 from patent US 5981724.
ACCESSION AR085419
VERSION AR085419.1 GI:10012188
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 840)
AUTHORS Armitage,R.J., Fanslow,W.C., Spriggs,M.K., Srinivasan,S.,
Gibson,M.G., Morris,A.E. and McGrew,J.T.
TITLE DNA encoding CD40 ligand, a cytokine that binds CD40
JOURNAL Patent: US 5981724-A 11 09-NOV-1999;
FEATURES
Location/Qualifiers
source 1..840
BASE COUNT 266 a 185 c 175 g 214 t
ORIGIN

Query Match 97.2%; Score 763.6; DB 6; Length 840;
Best Local Similarity 98.2%; Pred. No. 9.8e-194;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGATGAAACATACAGCCACCTTCCCGAATCCGCGCACTGCACTTCCAGCAGC 60
DB 46 ATGATGAAACATACAGCCACCTTCCCGAATCCGCGCACTGCACTGCGCCATCAGC 105
QY 61 ATGAAAGATTTTATGATTTACTTACTGTTTCTTATCACCAGATGATGGGTACAGA 120
DB 106 ATGAAAGATTTTATGATTTACTTACTGTTTCTTATCACCAGATGATGGGTACAGA 165
QY 121 CTTTTCGTGTATCTTATGAAAGTTGACAGATGAAAGTGAAGAACTTCTAT 180
DB 166 CTTTTCGTGTATCTTATGAAAGTTGACAGATGAAAGTGAAGAACTTCTAT 225
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DB 286 TTACTGAACTGTGAGAGATTTAAAGCAAGTTTGAAGGCTTGGAAAGATTAATGTTA 345
QY 301 AACAAAGAGAGAGAGAAAGAAAGCAAGTTTGAAGGCTTGGAAAGATTAATGTTA 360
DB 346 AACAAAGAGAGAGAGAAAGAAAGCAAGTTTGAAGGCTTGGAAAGATTAATGTTA 405
QY 361 CAATTCGCGCACTGCTTAAGTGAAGCCAGAGTAAAGCAATCTTGTGTTACAGTGG 420
DB 406 CAATTCGCGCACTGCTTAAGTGAAGCCAGAGTAAAGCAATCTTGTGTTACAGTGG 465

QY 421 GCTGAAAGAGATCTACATACCATGAGCAACACTTGGTAAACCTGGAAAAATGGGAAACAG 480
DB 466 GCTGAAAGAGATCTACATACCATGAGCAACACTTGGTAAACCTGGAAAAATGGGAAACAG 525
QY 481 CTGACCGTTTAAAGCAAGAGCTCTATATATCTATGCCCCAGTCACTTCTGTTCCAT 540
DB 526 CTGACCGTTTAAAGCAAGAGCTCTATATATCTATGCCCCAGTCACTTCTGTTCCAT 585
QY 541 CGGAGAGCTTCGAGTCAAGCTTCATTTATAGCCAGCTTCGCTAAAGTCCCGGGTGA 600
DB 586 CGGAGAGCTTCGAGTCAAGCTTCATTTATAGCCAGCTTCGCTAAAGTCCCGGGTGA 645
QY 601 TTGAGAGAACTTCTACTGAGCTGCAAAATACCAAGTTCGCGCAAACTTGGCGGCA 660
DB 646 TTGAGAGAACTTCTACTGAGCTGCAAAATACCAAGTTCGCGCAAACTTGGCGGCA 705
QY 661 CAATCCATTCCTTGGGAGAGTATTTGAATTCGCAACCGAGGCTTCGCGTGTTCAT 720
DB 706 CAATCCATTCCTTGGGAGAGTATTTGAATTCGCAACCGAGGCTTCGCGTGTTCAT 765
QY 721 GTGACTGATCCAAAGCCAAAGTGAAGCCATGCGCACTGCTTCAGTCTTGGCTTAA 780
DB 766 GTGACTGATCCAAAGCCAAAGTGAAGCCATGCGCACTGCTTCAGTCTTGGCTTAA 825
QY 781 CTCCTGA 786
DB 826 CTCCTGA 831

RESULT 6
AR103375 840 bp DNA linear PAT 14-FEB-2001
LOCUS AR103375
DEFINITION Sequence 11 from patent US 6087329.
ACCESSION AR103375
VERSION AR103375.1 GI:12814963
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 840)
AUTHORS Armitage,R.J., Fanslow,W.C. and Spriggs,M.K.
TITLE CD40 ligand polypeptide
JOURNAL Patent: US 6087329-A 11 11-JUL-2000;
FEATURES
Location/Qualifiers
source 1..840
BASE COUNT 266 a 185 c 175 g 214 t
ORIGIN

Query Match 97.2%; Score 763.6; DB 6; Length 840;
Best Local Similarity 98.2%; Pred. No. 9.8e-194;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGATGAAACATACAGCCACCTTCCCGAATCCGCGCACTGCACTTCCAGCAGC 60
DB 46 ATGATGAAACATACAGCCACCTTCCCGAATCCGCGCACTGCACTGCGCCATCAGC 105
QY 61 ATGAAAGATTTTATGATTTACTTACTGTTTCTTATCACCAGATGATGGGTACAGA 120
DB 106 ATGAAAGATTTTATGATTTACTTACTGTTTCTTATCACCAGATGATGGGTACAGA 165
QY 121 CTTTTCGTGTATCTTATGAAAGTTGACAGATGAAAGTGAAGAACTTCTAT 180
DB 166 CTTTTCGTGTATCTTATGAAAGTTGACAGATGAAAGTGAAGAACTTCTAT 225
QY 181 GAAGATTTTATGATTTACTTACTGTTTCTTATCACCAGATGATGGGTACAGA 240
DB 226 GAAGATTTTATGATTTACTTACTGTTTCTTATCACCAGATGATGGGTACAGA 285
QY 241 TTACTGAACTGTGAGAGATTTAAAGCAAGTTTGAAGGCTTGGAAAGATTAATGTTA 300
DB 286 TTACTGAACTGTGAGAGATTTAAAGCAAGTTTGAAGGCTTGGAAAGATTAATGTTA 345

QY	301	AACAAAGAGAAACGAAAGAAAAGAAAACACCTTGGAAATGCAAAAAAGTATCAAGATCCT	360
Db	346	AACAAAGAGAAACGAAAGAAAAGAAAACACTTTGAAATGCAAAAAAGTATCAAGATCCT	405
QY	361	CAAAATGGGGGCATGTCATTAAGTAGGGCGACGAGTAAACCATCTGTGTTCACTGG	420
Db	406	CAAAATGGGGGCATGTCATTAAGTAGGGCGACGAGTAAACCATCTGTGTTCACTGG	465
QY	421	GCTGAAAAAGATCTACACATGACGACAACTTGGTAAACCTGGAAAAATGGAAAAAG	480
Db	466	GCTGAAAAAGATCTACACATGACGACAACTTGGTAAACCTGGAAAAATGGAAAAAG	525
QY	481	CTGACCGTTAAAGACAAGAGACTCTTATTAATCTATGAGCCAGTCACTTCTGTTCCAT	540
Db	526	CTGACCGTTAAAGACAAGAGACTCTTATTAATCTATGAGCCAGTCACTTCTGTTCCAT	585
QY	541	CGGGAAGCTTGAGTCAAGCTCCACTTATTAAGCAAGCTCTGCTTAAAGTCCCGGATGA	600
Db	586	CGGGAAGCTTGAGTCAAGCTCCACTTATTAAGCAAGCTCTGCTTAAAGTCCCGGATGA	645
QY	601	TTGAGAGATTTTACTCAGAGCTGCAAAATCCCAAGTTCCGCAACCTTGGCGGGCAA	660
Db	646	TTGAGAGATTTTACTCAGAGCTGCAAAATCCCAAGTTCCGCAACCTTGGCGGGCAA	705
QY	661	CAATTCATTCACCTTGGAGAGATTTTGAATTTGCAACCAAGGCTCTCGGTGTTGTCAAT	720
Db	706	CAATTCATTCACCTTGGAGAGATTTTGAATTTGCAACCAAGGCTCTCGGTGTTGTCAAT	765
QY	721	GTAGCTGATTCGAAGCAAGTAGCAATGGCACTGGCTTCAAGTCCCTTTGGCTTACTCAAA	780
Db	766	GTAGCTGATTCGAAGCAAGTAGCAATGGCACTGGCTTCAAGTCCCTTTGGCTTACTCAAA	825
QY	781	CTCTGA	786
Db	826	CTCTGA	831

[illegible]

Qy	181	GAAGATTTTGTTATCATGAAAAAGATACAGAGATGCAACACAGAGAAAAGATCTTTATCC	240
Db	226	GAAGATTTTGTTATCATGAAAAAGATACAGAGATGCAACACAGAGAAAAGATCTTTATCC	285
Qy	241	TTATCTGAACCTGTGAGAGATTTAAAAAGCCAGTTTGAAAGCTTTGTGAAAGATTAATGTGA	300
Db	286	TTATCTGAACCTGTGAGAGATTTAAAAAGCCAGTTTGAAAGCTTTGTGAAAGATTAATGTGA	345
Qy	301	AACAAAGAGAGACGAGAAAAAGAAAACGCTTTTGAAATGCAAAAAGGTGATCAGATCTCT	360
Db	346	AACAAAGAGAGACGAGAAAAAGAAAACGCTTTTGAAATGCAAAAAGGTGATCAGATCTCT	405
Qy	361	CAAAATTCGGGCACATGTCATTAATGTAGGCGCAGCATTAATAACAATCTGTGTTACAGTGG	420
Db	406	CAAAATTCGGGCACATGTCATTAATGTAGGCGCAGCATTAATAACAATCTGTGTTACAGTGG	465
Qy	421	GCTGAAAAAGATTACTAACCATGAGCAAACTTGGTAAACCTTGAAAAATGGGAAAACAG	480
Db	466	GCTGAAAAAGATTACTAACCATGAGCAAACTTGGTAAACCTTGAAAAATGGGAAAACAG	525
Qy	481	CTGACGCTTTAAAGAACAAGACCTTAATTAATCTAATGCCCAAGTCACTTCTGTTCCAAAT	540
Db	526	CTGACGCTTTAAAGAACAAGACCTTAATTAATCTAATGCCCAAGTCACTTCTGTTCCAAAT	585
Qy	541	CGGGAAGCTTCAAGTCAAGGCTCCATTTATTAAGCCAGGCTTCTGCTAAAGTCCCGGGTAGA	600
Db	586	CGGGAAGCTTCAAGTCAAGGCTCCATTTATTAAGCCAGGCTTCTGCTAAAGTCCCGGGTAGA	645
Qy	601	TTTCGAGAGATCTTACTCAGAGGTGCAAAATCCCAAGTTCCGGGCCAAACCTTTGCGGGCAA	660
Db	646	TTTCGAGAGATCTTACTCAGAGGTGCAAAATCCCAAGTTCCGGGCCAAACCTTTGCGGGCAA	705
Qy	661	CAATTCATTTCACTTGGAGAGAGATTTGAATTGCAACCAAGGTCTTGGTGTGTCAAT	720
Db	706	CAATTCATTTCACTTGGAGAGAGATTTGAATTGCAACCAAGGTCTTGGTGTGTCAAT	765
Qy	721	GTGACTGATCCAAAGCAAGTGAAGCCATGGACCTGAGCTTCAAGTCTTTGGCTTAACTCAAA	780
Db	766	GTGACTGATCCAAAGCAAGTGAAGCCATGGACCTGAGCTTCAAGTCTTTGGCTTAACTCAAA	825
Qy	781	CTCTGGA	786
Db	826	CTCTGGA	831

RESULT	8
LOCUS	ARI69232
DEFINITION	ARI69232
ACCESSION	Sequence 11 from patent US 6290972.
VERSION	ARI69232
KEYWORDS	ARI69232.1 GI:17907047
SOURCE	.
ORGANISM	Unknown.
REFERENCE	Unknown.
AUTHORS	Unclassified.
TITLE	1 (bases 1 to 840)
JOURNAL	Amitage,R.J., Fanslow,W.C., Spriggs,M.K., Srinivasan,S. and Gibson,M.G.
FEATURES	Method of augmenting a vaccine response by administering CD40 ligand
source	Patent: US 6290972-A 11 18-SEP-2001; Location/Qualifiers
BASE COUNT	1..840 /organism="unknown"
ORIGIN	266 a 185 c 214 t
Query Match	97.2%; Score 763.5; DB 6;
Best Local Similarity	96.2%; Pred.No. 9.8e-194; Length 840;
Matches 772; Conservative	0; Mismatches 14; Indels 0; Gaps 0;
by	1 ATGATGAAGCACTACAGCCAACTTCCCCCAGATTGGTGCGCAACTGAGACTTCAGCAGGC 60

Db 46 ATGATGAAAACATACAAACCAACTTCTCCCATCTGGGGCCATCGAGATGCCATCAGC 105
 Qy 61 ATGAAGATTTTATGATTTACTTACTGTTTTCTTATCACCATGATGATGGGTACCA 120
 Db 106 ATGAAAATTTTATGATTTACTTACTGTTTTCTTATCACCATGATGATGGGTACCA 165
 Qy 121 CTTTTCCTGATCTTCAATAGAGGTTGACAGATAGAGATGAGAGATCTTCAT 180
 Db 166 CTTTTCCTGATCTTCAATAGAGGTTGACAGATAGAGATGAGAGATCTTCAT 225
 Qy 181 GAAGATTTTATGATTTACTTACTGTTTTCTTATCACCATGATGATGGGTACCA 240
 Db 226 GAAGATTTTATGATTTACTTACTGTTTTCTTATCACCATGATGATGGGTACCA 285
 Qy 241 TTACTGAATCTGAGAGATTTAAAGCCAGTTTGAAGCTTTGTGAAGATTAATGTTA 300
 Db 286 TTACTGAATCTGAGAGATTTAAAGCCAGTTTGAAGCTTTGTGAAGATTAATGTTA 345
 Qy 301 AACAAAGAGAGACAAAGAAAACAGCTTTGAATGCAAAAAGGTGATCAGATCTT 360
 Db 346 AACAAAGAGAGACAAAGAAAACAGCTTTGAATGCAAAAAGGTGATCAGATCTT 405
 Qy 361 CAAATTCGCGCACATGTCATAGTGAGCCAGCAATTAACAATCTGTGTACAGTGG 420
 Db 406 CAAATTCGCGCACATGTCATAGTGAGCCAGCAATTAACAATCTGTGTACAGTGG 465
 Qy 421 GCTGAAAAAGATCTACACCATGAGCAACATTTGTTACCTGGAAAAATGGAAAAAG 480
 Db 466 GCTGAAAAAGATCTACACCATGAGCAACATTTGTTACCTGGAAAAATGGAAAAAG 525
 Qy 481 CTGACCGTTAAAGACAAAGACTCTATTAATATCTATGCCCAGTCACTTCTGTTCAT 540
 Db 526 CTGACCGTTAAAGACAAAGACTCTATTAATATCTATGCCCAGTCACTTCTGTTCAT 585
 Qy 541 CGGAACTTCGAGTCAAGCTCCATTTATAGCCAGCTTCCTTAAGTCCCCCGGTGA 600
 Db 586 CGGAACTTCGAGTCAAGCTCCATTTATAGCCAGCTTCCTTAAGTCCCCCGGTGA 645
 Qy 601 TTGAGAGAACTTACTCAGAGCTGCAAAATCCACAGTTCGCGCAAACTTGGCGGCA 660
 Db 646 TTGAGAGAACTTACTCAGAGCTGCAAAATCCACAGTTCGCGCAAACTTGGCGGCA 705
 Qy 661 CAATCCATTCATCTGGAGAGATTTGAATTGCAACAGAGTGTGGGTGTTCAT 720
 Db 706 CAATCCATTCATCTGGAGAGATTTGAATTGCAACAGAGTGTGGGTGTTCAT 765
 Qy 721 GTGACTGATCAAGCCAAAGTGAAGCCATGAGCACTGGCTTCAAGTCTTTGCTTACTCAA 780
 Db 766 GTGACTGATCAAGCCAAAGTGAAGCCATGAGCACTGGCTTCAAGTCTTTGCTTACTCAA 825
 Qy 781 CTCTGA 786
 Db 826 CTCTGA 831
 RESULT 9
 ARI71647 840 bp DNA linear PAT 17-DEC-2001
 LOCUS Sequence 3 from patent US 6297052.
 DEFINITION ARI71647
 ACCESSION ARI71647
 VERSION ARI71647.1 GI:17910597
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 UNCLASSIFIED.
 REFERENCE 1 (bases 1 to 840)
 AUTHORS Kehry, M. and Castle, B.
 TITLE B cell culture system comprising high density membrane bound CD40 ligand
 JOURNAL Patent: US 6297052-A 3 02-OCT-2001;
 FEATURES Location/Qualifiers
 source I. 840

BASE COUNT 263 a 182 c 181 g 214 t
 ORIGIN
 Query Match 97.2%; Score 763.6; DB 6; Length 840;
 Best Local Similarity 98.2%; Pred. No. 9,8e-194;
 Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
 Qy 1 ATGATGAAAACATACAGCAACCTTCCCATGATGAGTGAAGATGAGATCTTCAT 60
 Db 22 ATGATGAAAACATACAGCAACCTTCCCATGATGAGTGAAGATGAGATCTTCAT 81
 Qy 61 ATGAGATTTTATGATTTACTTACTGTTTTCTTATCACCATGATGATGGGTACCA 120
 Db 82 ATGAAAATTTTATGATTTACTTACTGTTTTCTTATCACCATGATGATGGGTACCA 141
 Qy 121 CTTTTCCTGATCTTCAATAGAGGTTGACAGATAGAGATGAGAGATCTTCAT 180
 Db 142 CTTTTCCTGATCTTCAATAGAGGTTGACAGATAGAGATGAGAGATCTTCAT 201
 Qy 181 GAAGATTTTATGATTTACTTACTGTTTTCTTATCACCATGATGATGGGTACCA 240
 Db 202 GAAGATTTTATGATTTACTTACTGTTTTCTTATCACCATGATGATGGGTACCA 261
 Qy 241 TTACTGAATCTGAGAGATTTAAAGCCAGTTTGAAGCTTTGTGAAGATTAATGTTA 300
 Db 262 TTACTGAATCTGAGAGATTTAAAGCCAGTTTGAAGCTTTGTGAAGATTAATGTTA 321
 Qy 301 AACAAAGAGAGACAAAGAAAACAGCTTTGAATGCAAAAAGGTGATCAGATCTT 360
 Db 322 AACAAAGAGAGACAAAGAAAACAGCTTTGAATGCAAAAAGGTGATCAGATCTT 381
 Qy 361 CAAATTCGCGCACATGTCATAGTGAGCCAGCAATTAACAATCTGTGTACAGTGG 420
 Db 382 CAAATTCGCGCACATGTCATAGTGAGCCAGCAATTAACAATCTGTGTACAGTGG 441
 Qy 421 GCTGAAAAAGATCTACACCATGAGCAACATTTGTTACCTGGAAAAATGGAAAAAG 480
 Db 442 GCTGAAAAAGATCTACACCATGAGCAACATTTGTTACCTGGAAAAATGGAAAAAG 501
 Qy 481 CTGACCGTTAAAGACAAAGACTCTATTAATATCTATGCCCAGTCACTTCTGTTCAT 540
 Db 502 CTGACCGTTAAAGACAAAGACTCTATTAATATCTATGCCCAGTCACTTCTGTTCAT 561
 Qy 541 CGGAACTTCGAGTCAAGCTCCATTTATAGCCAGCTTCCTTAAGTCCCCCGGTGA 600
 Db 562 CGGAACTTCGAGTCAAGCTCCATTTATAGCCAGCTTCCTTAAGTCCCCCGGTGA 621
 Qy 601 TTGAGAGAACTTACTCAGAGCTGCAAAATCCACAGTTCGCGCAAACTTGGCGGCA 660
 Db 622 TTGAGAGAACTTACTCAGAGCTGCAAAATCCACAGTTCGCGCAAACTTGGCGGCA 681
 Qy 661 CAATCCATTCATCTGGAGAGATTTGAATTGCAACAGAGTGTGGGTGTTCAT 720
 Db 682 CAATCCATTCATCTGGAGAGATTTGAATTGCAACAGAGTGTGGGTGTTCAT 741
 Qy 721 GTGACTGATCAAGCCAAAGTGAAGCCATGAGCACTGGCTTCAAGTCTTTGCTTACTCAA 780
 Db 742 GTGACTGATCAAGCCAAAGTGAAGCCATGAGCACTGGCTTCAAGTCTTTGCTTACTCAA 801
 Qy 781 CTCTGA 786
 Db 802 CTCTGA 807
 RESULT 10
 123893 840 bp DNA linear PAT 07-OCT-1996
 LOCUS Sequence 1 from patent US 5540926.
 DEFINITION 123893
 ACCESSION 123893
 VERSION 123893.1 GI:1603763
 KEYWORDS
 SOURCE Unknown.

ORGANISM

Unknown.

REFERENCE 1 (bases 1 to 840)

AUTHORS Aruffo, A., Hollenbaugh, D. and Ledbetter, J. A.

TITLE Soluble and its use in B cell stimulation

JOURNAL Patent: US 5540926-A 1 30-JUL-1996;

FEATURES Location/Qualifiers

source 1..840

BASE COUNT 263 a 182 c 181 g 214 t

ORIGIN

Query Match

Best Local Similarity 97.2%; Score 763.6; DB 6; Length 840;

Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGATAGAAACATACAGCCACCTTCCCGGAGATCCGAGCACTGACCTTCCAGGAC 60
 DB 22 ATGATCGAAACATACACCAACTTCTCCCGATCTGCGGCACTGACCTGCCATCAGC 81
 QY 61 ATGAAATTTTATGATATTTACTTACTGTTTCTTATCAACCAAGATGATGGGTACGA 120
 DB 82 ATGAAATTTTATGATATTTACTTACTGTTTCTTATCAACCAAGATGATGGGTACGA 141
 QY 121 CTTTTCCTGATCTTCAATAGAGTTGACCAAGATGATGAAAGAAATCTTCAAT 180
 DB 142 CTTTTCCTGATCTTCAATAGAGTTGACCAAGATGATGAAAGAAATCTTCAAT 201
 QY 181 GAAGATTTTGTATCATGAAACGATACAGATGCAACAGGAAAGATCTTATCC 240
 DB 202 GAAGATTTTGTATCATGAAACGATACAGATGCAACAGGAAAGATCTTATCC 261
 QY 241 TTAAGTCTGATCTTCAATAGAGTTGAAAGGCTTTGTAAGATATATATGTTA 300
 DB 262 TTAAGTCTGATCTTCAATAGAGTTGAAAGGCTTTGTAAGATATATATGTTA 321
 QY 301 AACAAAG 360
 DB 322 AACAAAG 381
 QY 361 CAAATTTGGGCACTGATCTAATAGAGGCGAGAGTAAACAACTGTGTACAGTGG 420
 DB 382 CAAATTTGGGCACTGATCTAATAGAGGCGAGAGTAAACAACTGTGTACAGTGG 441
 QY 421 GCTGAAAAAGATCTACACATGACCAACTTGGTAACTGTGTACAGTGG 480
 DB 442 GCTGAAAAAGATCTACACATGACCAACTTGGTAACTGTGTACAGTGG 501
 QY 481 CTGACCGTTAAAGACAAAGAGCTTATATATCTATAGCCCAAGTCACTTGTGCAAT 540
 DB 502 CTGACCGTTAAAGACAAAGAGCTTATATATCTATAGCCCAAGTCACTTGTGCAAT 561
 QY 541 CGGAAAGCTTGAAGTCAAGTCACTTATATAGCCGCTTGTAAAGTCCCCGTAGA 600
 DB 562 CGGAAAGCTTGAAGTCAAGTCACTTATATAGCCGCTTGTAAAGTCCCCGTAGA 621
 QY 601 TTGAGAGAACTTACTAGAGCTCAATATCCCAAGTTCCGCAAACTTCCGGGCA 660
 DB 622 TTGAGAGAACTTACTAGAGCTCAATATCCCAAGTTCCGCAAACTTCCGGGCA 681
 QY 661 CAATCATTTCACTTGGAGAGAGATTTGAATTGCAACAGGTGCTTGGTGTTCAT 720
 DB 682 CAATCATTTCACTTGGAGAGAGATTTGAATTGCAACAGGTGCTTGGTGTTCAT 741
 QY 721 GTGACTGATCCAAAGCAAGTGAAGCACTGGCTTCACTGCTTGGCTTACTCAA 780
 DB 742 GTGACTGATCCAAAGCAAGTGAAGCACTGGCTTCACTGCTTGGCTTACTCAA 801
 QY 781 CTCTGA 786
 DB 802 CTCTGA 807

RESULT 11

127345

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Unknown.

REFERENCE 1 (bases 1 to 840)

AUTHORS Spriggs, M. K., Armitage, R. J. and Fanlow, W. C. III.

TITLE Detection of mutations in a CD40 ligand gene

JOURNAL Patent: US 5565321-A 7 15-OCT-1996;

FEATURES Location/Qualifiers

source 1..840

BASE COUNT 266 a 185 c 175 g 214 t

ORIGIN

Query Match

Best Local Similarity 97.2%; Score 763.6; DB 6; Length 840;

Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGATAGAAACATACAGCCACCTTCCCGGAGATCCGAGCACTGACCTTCCAGGAC 60
 DB 46 ATGATCGAAACATACACCAACTTCTCCCGATCTGCGGCACTGACCTGCCATCAGC 105
 QY 61 ATGAAATTTTATGATATTTACTTACTGTTTCTTATCAACCAAGATGATGGGTACGA 120
 DB 106 ATGAAATTTTATGATATTTACTTACTGTTTCTTATCAACCAAGATGATGGGTACGA 165
 QY 121 CTTTTCCTGATCTTCAATAGAGTTGAAAGGCTTTGTAAGATATATATGTTA 180
 DB 166 CTTTTCCTGATCTTCAATAGAGTTGAAAGGCTTTGTAAGATATATATGTTA 225
 QY 181 GAAGATTTTGTATCATGAAACGATACAGATGCAACAGGAAAGATCTTATCC 240
 DB 226 GAAGATTTTGTATCATGAAACGATACAGATGCAACAGGAAAGATCTTATCC 285
 QY 241 TTAAGTCTGATCTTCAATAGAGTTGAAAGGCTTTGTAAGATATATATGTTA 300
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 QY 301 AACAAAG 360
 DB 346 AACAAAG 405
 QY 361 CAAATTTGGGCACTGATCTAATAGAGGCGAGAGTAAACAACTGTGTACAGTGG 420
 DB 406 CAAATTTGGGCACTGATCTAATAGAGGCGAGAGTAAACAACTGTGTACAGTGG 465
 QY 421 GCTGAAAAAGATCTACACATGACCAACTTGGTAACTGTGTACAGTGG 480
 DB 466 GCTGAAAAAGATCTACACATGACCAACTTGGTAACTGTGTACAGTGG 525
 QY 481 CTGACCGTTAAAGACAAAGAGCTTATATATCTATAGCCCAAGTCACTTGTGCAAT 540
 DB 526 CTGACCGTTAAAGACAAAGAGCTTATATATCTATAGCCCAAGTCACTTGTGCAAT 585
 QY 541 CGGAAAGCTTGAAGTCAAGTCACTTATATAGCCGCTTGTAAAGTCCCCGTAGA 600
 DB 586 CGGAAAGCTTGAAGTCAAGTCACTTATATAGCCGCTTGTAAAGTCCCCGTAGA 645
 QY 601 TTGAGAGAACTTACTAGAGCTCAATATCCCAAGTTCCGCAAACTTCCGGGCA 660
 DB 646 TTGAGAGAACTTACTAGAGCTCAATATCCCAAGTTCCGCAAACTTCCGGGCA 705
 QY 661 CAATCATTTCACTTGGAGAGAGATTTGAATTGCAACAGGTGCTTGGTGTTCAT 720
 DB 706 CAATCATTTCACTTGGAGAGAGATTTGAATTGCAACAGGTGCTTGGTGTTCAT 765
 QY 721 GTGACTGATCCAAAGCAAGTGAAGCACTGGCTTCACTGCTTGGCTTACTCAA 780

Db 766 GTGACTGATCCAGGCAAGTACGACCTGCTTCACTTCTTGGCTTACTCAAA 825

Qy 781 CTCCTGA 786
Db 826 CTCCTGA 831

RESULT 12

167828 LOCUS 167828
DEFINITION Sequence 1 from patent US 5674492.
ACCESSION 167828
VERSION 167828.1 GI:2829950
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE

1 (bases 1 to 840)
Armitage, R.J., Fanslow, W.C. III, Longo, D.L. and Murphy, W.J.
TITLE Method of preventing or treating disease characterized by
neoplastic cells expressing CD40
JOURNAL Patent: US 5674492-A 1 07-OCT-1997;
FEATURES Location/Qualifiers
source 1..840
/organism="unknown"

BASE COUNT 266 a 185 c 175 g 214 t
ORIGIN

Query Match 97.2%; Score 763.6; DB 6; Length 840;
Best Local Similarity 98.2%; Pred. No. 9,8e-194;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1 ATGATAGAAACATACACGCACTTCCCGATCCGCGGCACTGAGCTTCGAGGAGC 60
Db 46 ATGATCGAACAATACCAACCACTTCCCGATCCGCGGCACTGAGCTTCGAGGAGC 105
Qy 61 ATGAGATTTTATGATTTTACTTCTGTTTCTTATCACCAGATGATGGGTACGA 120
Db 106 ATGAAAATTTTATGATTTTACTTCTGTTTCTTATCACCAGATGATGGGTACGA 165
Qy 121 CTTTTCCTGATCTTCATATGAGGTTGACAGATGAGATGAGATGATCTTAT 180
Db 166 CTTTTCCTGATCTTCATATGAGGTTGACAGATGAGATGAGATGATCTTAT 225
Qy 181 GAGATTTTGTATTCATGAAAACATACAGAGATGCAACAGAGAAAGATCTTATCC 240
Db 226 GAGATTTTGTATTCATGAAAACATACAGAGATGCAACAGAGAAAGATCTTATCC 285
Qy 241 TTAAGTAACTGTAGAGATTTAAAGCAGTTGAAAGCTTTGTGAAGATTAATGTTA 300
Db 286 TTAAGTAACTGTAGAGATTTAAAGCAGTTGAAAGCTTTGTGAAGATTAATGTTA 345
Qy 301 AACAAAGAGAGACGAAAGAAAGAAAGCTTTGAAATGCAAAAAGGTATCAAGATCT 360
Db 346 AACAAAGAGAGACGAAAGAAAGAAAGCTTTGAAATGCAAAAAGGTATCAAGATCT 405
Qy 361 CAAATTCGCGCACTGTCAATAGTGAAGGCGAGAGTAAACATCTGTGTTACAGTGG 420
Db 406 CAAATTCGCGCACTGTCAATAGTGAAGGCGAGAGTAAACATCTGTGTTACAGTGG 465
Qy 421 GCTGAAAAAGATATCAACATAGAGCAACATCTGTGTTACAGTGG 480
Db 466 GCTGAAAAAGATATCAACATAGAGCAACATCTGTGTTACAGTGG 525
Qy 481 CTGACCGTTAAAGACAGAGACTCTATTATATCTATGCGCAAGTCACTTGTGTTCAAT 540
Db 526 CTGACCGTTAAAGACAGAGACTCTATTATATCTATGCGCAAGTCACTTGTGTTCAAT 585
Qy 541 CGGAGAGCTTCAGTCAAGCTTCATTTATAGCCAGCTTCCTTAAAGTCCCCGGTAGA 600
Db 586 CGGAGAGCTTCAGTCAAGCTTCATTTATAGCCAGCTTCCTTAAAGTCCCCGGTAGA 645

Qy 601 TTGAGAGATCTTACTCAGAGCTGCAAAATCCAGAGTTCCGCCAAAACCTTGGGGGCA 660
Db 646 TTGAGAGATCTTACTCAGAGCTGCAAAATCCAGAGTTCCGCCAAAACCTTGGGGGCA 705

Qy 661 CAATTCATCTTGGGAGAGATTTGAAATTTGCAACAGAGTCTTGGTGTTCAT 720
Db 706 CAATTCATCTTGGGAGAGATTTGAAATTTGCAACAGAGTCTTGGTGTTCAT 765

RESULT 13

AX090039 LOCUS AX090039 879 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 1 from Patent WO0116180.
ACCESSION AX090039
VERSION AX090039.1 GI:13444004
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 879)
Ahuja, S.U. and Bonewald, L.U.
TITLE Cd40 agonist compositions and methods of use
JOURNAL Patent: WO 0116180-A 1 08-MAR-2001;
FEATURES Location/Qualifiers
source 1..879
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 274 a 193 c 190 g 222 t
ORIGIN

Query Match 97.2%; Score 763.6; DB 6; Length 879;
Best Local Similarity 98.2%; Pred. No. 9,8e-194;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1 ATGATGAAACATACAGCACTTCCCGATCCGCGGCACTGAGCTTCGAGGAGC 60
Db 22 ATGATGAAACATACAGCACTTCCCGATCCGCGGCACTGAGCTTCGAGGAGC 81
Qy 61 ATGAGATTTTATGATTTTACTTCTGTTTCTTATCACCAGATGATGGGTACGA 120
Db 82 ATGAAAATTTTATGATTTTACTTCTGTTTCTTATCACCAGATGATGGGTACGA 141
Qy 121 CTTTTCCTGATCTTCATATGAGGTTGACAGATGAGATGAGATGATCTTAT 180
Db 142 CTTTTCCTGATCTTCATATGAGGTTGACAGATGAGATGAGATGATCTTAT 201
Qy 181 GAAGATTTTGTATCATGAAAACATACAGAGATGCAACAGAGAAAGATCTTATCC 240
Db 202 GAAGATTTTGTATCATGAAAACATACAGAGATGCAACAGAGAAAGATCTTATCC 261
Qy 241 TTAAGTAACTGTAGAGATTTAAAGCAGTTGAAAGCTTTGTGAAGATTAATGTTA 300
Db 262 TTAAGTAACTGTAGAGATTTAAAGCAGTTGAAAGCTTTGTGAAGATTAATGTTA 321
Qy 301 AACAAAGAGAGACGAAAGAAAGAAAGCTTTGAAATGCAAAAAGGTATCAAGATCT 360
Db 322 AACAAAGAGAGACGAAAGAAAGAAAGCTTTGAAATGCAAAAAGGTATCAAGATCT 381
Qy 361 CAAATTCGCGCACTGTCAATAGTGAAGGCGAGAGTAAACATCTGTGTTACAGTGG 420
Db 382 CAAATTCGCGCACTGTCAATAGTGAAGGCGAGAGTAAACATCTGTGTTACAGTGG 441
Qy 421 GCTGAAAAAGATATCAACATAGAGCAACATTTGTAACTCTGAAATGGGAAACAG 480

```

Db      |||||
442 GCTGAAAAAGATCTACACCATGAGCAACACTGGTATACCTGGAAGAAAGGAAAGG 501
Qy      |||||
481 CTGACCGTTAAAGACAGAGCTCTTATATCTATGAGCCAGTACCTTCTGTTCCAT 540
Db      |||||
502 CTGACCGTTAAAGACAGAGCTCTTATATCTATGAGCCAGTACCTTCTGTTCCAT 561
Qy      |||||
541 CGGGAAGCTTCGAGTCAGCTCATTATATAGCCAGCTGCTTAAAGTCCCCGGTAGA 600
Db      |||||
562 CGGGAAGCTTCGAGTCAGCTCATTATATAGCCAGCTGCTTAAAGTCCCCGGTAGA 621
Qy      |||||
601 TTGAGAGAACTTCTACAGAGTCGAAATCCACAGTTCGCCAAACCTTGGCGGCA 660
Db      |||||
622 TTGAGAGAACTTCTACAGAGTCGAAATCCACAGTTCGCCAAACCTTGGCGGCA 681
Qy      |||||
661 CAATCATTCACTTGGAGAGATTTGAAATTCAGCAAGTGTCTGGTGTTCAT 720
Db      |||||
682 CAATCATTCACTTGGAGAGATTTGAAATTCAGCAAGTGTCTGGTGTTCAT 741
Qy      |||||
721 GTGACTGATCCAGCCAGAGGACATGGCACTGGCTTCAAGCTTGGCTTACTCAA 780
Db      |||||
742 GTGACTGATCCAGCCAGAGGACATGGCACTGGCTTCAAGCTTGGCTTACTCAA 801
Qy      |||||
781 CTCTGA 786
Db      |||||
802 CTCTGA 807

RESULT 14
HSGP39MR      879 bp      mRNA      linear      PRI 01-SEP-1996
LOCUS      HSGP39MR
DEFINITION      H. sapiens mRNA for glycoprotein 39 (gp39).
ACCESSION      Z15017.1 S49392
VERSION      Z15017.1 GI:38483
KEYWORDS      glycoprotein 39.
SOURCE      Homo sapiens.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 879)
AUTHORS      Hollenbaugh,D., Grosmaire,L.S., Kullas,C.D., Chalupny,N.J.,
      Braesch-Andersen,S., Noelle,R.J., Stamenkovic,I., Ledbetter,J.A.
      and Aruffo,A.
      The human T cell antigen gp39, a member of the TNF gene family, is
      a ligand for the CD40 receptor: expression of a soluble form of
      gp39 with B cell co-stimulatory activity
      EMBO J. 11 (12), 4313-4321 (1992)

TITLE      The human T cell antigen gp39, a member of the TNF gene family, is
      a ligand for the CD40 receptor: expression of a soluble form of
      gp39 with B cell co-stimulatory activity

JOURNAL      EMBO J. 11 (12), 4313-4321 (1992)
MEDLINE      93049181
PUBMED      1385114
REFERENCE      2 (bases 1 to 879)
AUTHORS      Hollenbaugh,D.L.
TITLE      Direct Submission
JOURNAL      Submitted (21-SEP-1992) Diane L Hollenbaugh, Bristol-Myers Squibb
      PRI, Seattle, WA, 98121
COMMENT      The original submission [1] reported 934bp.
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DEFINITION      H. sapiens mRNA for CD40 ligand.
ACCESSION      X67878.1 S50586
VERSION      X67878.1 GI:38411

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KEYWORDS

glycoprotein.

Homo sapiens.

ORGANISM

Homo sapiens.

Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE

1 (bases 1 to 1803)

Spriggs, M.

Direct Submision

Submitted (28-JUL-1992) M. Spriggs, Immunex Res & Development

Corporation, 51 University Street, Seattle WA 98101, USA

2 (bases 1 to 1803)

Spriggs, M.K., Armitage, R.J., Strockbine, L., Clifford, K.N.,

Macduff, B.M., Sato, T.A., Maliszewski, C.R., and Fanslow, W.C.

Recombinant human CD40 ligand stimulates B cell proliferation and

immunoglobulin E secretion

J. Exp. Med. 176 (6), 1543-1550 (1992)

JOURNAL

MEDLINE

93094757

PUBMED

1281209

FEATURES

source

location/Qualifiers

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ORIGIN

Query Match

97.2%; Score 763.6; DB 9; Length 1803;

Best Local Similarity 98.2%; Pred. No. 9,6e-194;

Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY

1 ATGATGAAACATACACGCACTTCCCGAGTCGCGCACTGCACTTCCACGCGC 60

DB

46 ATGATCGAACAATACCAACCACTTCTCCCGATCGCGCACTGCACTGCGCAAT 105

QY

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QY

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DB

826 CTCTGA 831

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Job time: 2051.61 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 8, 2003, 21:32:03 ; Search time 1291.53 Seconds
(without alignments)
9856.249 Million cell updates/sec

Title: US-08-982-272-6

Perfect score: 786

Sequence: 1 ATGATGAAACATACAGCA.....TTGGCTTACTCAAACTCTGA 786

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	69.6	8.9	638	9	AI982044 pac.pk007
4	50.2	6.4	1027	17	AZ166561 SP.008B_B
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ALIGNMENTS

RESULT 1
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DEFINITION 263218 MARC 3BOV Bos taurus CDNA 5', mRNA sequence.
ACCESSION BF599437
VERSION BF599437.1 GI:11695919
KEYWORDS
SOURCE
ORGANISM

Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.

REFERENCE
AUTHORS Smith,T.P.L., Grose,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Casas,E., Wray,J.E., White,J., Cho,J., Fahrmeier,S.C., Bennett,
G.L., Heathon,M.F., Laegreid,W.W., Rohrer,G.A., Chitko-Mckown,C.G.,
Petee,G., Holt,A., Karayancheva,S., Liang,F., Quackenbush,J. and
Keefe,J.W.

TITLE
JOURNAL Sequence evaluation of four pooled-tissue normalized bovine cDNA
MEDLINE libraries and construction of a gene index for cattle
21180013 Genome Res. 11 (4), 626-630 (2001)

COMMENT
Contact: Smith TP
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred

v0.980904.e. Vector identified by cross_match with the -minscore 18 and -mismatch 12 options.

PCR Primers
FORWARD: AGGAACAGCTATGACAT
BACKWARD: GTTTCCTCAGTCAGCAG
Plate: 33 row: N column: 5
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FEATURES

source

Location/Qualifiers

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macrophage, ovary, fetal semitendinosus muscle, and fetal
longissimus muscle."

BASE COUNT 163 a 103 c 104 g 122 t
ORIGIN

Query Match

Best Local Similarity 45.7%; Score 359; DB 12; Length 492;
Matches 392; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 1 ATGATGAAACATACAGCAACCTTCCCGAGATCCGTCGACCTGCGAGC 60
DB 46 ATGATGAAACATACAGCAACCTTCCCGAGATCCGTCGACCTGCGAGC 105
QY 61 ATGAAAGATTTTATGATTTTACTTACTGTTTCTTATCACCAGATGTTGGTCAGCA 120
DB 106 ATGAAAGATTTTATGATTTTACTTACTGTTTCTTATCACCAGATGTTGGTCAGCG 165
QY 121 CTTTTCGTGTATCTTATGAGGTTGAGACAGATGAGATGAAAGATCTTATC 180
DB 166 CTTTTCGTGTATCTTATGAGGTTGAGACAGATGAGATGAAAGATCTTATC 225
QY 181 GAAGATTTTGTATCTTATGAGGTTGAGACAGATGAGATGAAAGATCTTATC 240
DB 226 GAAGATTTTGTATCTTATGAGGTTGAGACAGATGAGATGAAAGATCTTATC 285
QY 241 TTAAGTAACTGTGAGAGATTTAAAGCAGTTTGAAGCTTTGAAAGATATATGTTA 300
DB 286 TTAAGTAACTGTGAGAGATTTAAAGCAGTTTGAAGCTTTGAAAGATATATGTTA 345
QY 301 AACAAAG 360
DB 346 AACAAAG 405
QY 361 CAAATTTGGCCACATGTCATTAAGTGGCCAGACAGTAAACAGATCTGTGTTACAGTGG 420
DB 406 CAGATAGCGCCACATGTCATGAGTGGCCAGTAAAGCACTCTGTTCAGAGTGG 465
QY 421 GCTGAAAAGGATCTACACCATGAGC 447
DB 466 GCCCCCAAGAGATCTACACCATGAGC 492

RESULT 2

AM486605

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

COW.

Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

Bovidae; Bovinae; Bos.

REFERENCE

AUTHORS

Smith, T.P.L., Groves, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,

Czern, E., Wray, D.E., White, J., Cho, D., Fahrenkrug, S.C., Bennett

TITLE

JOURNAL

MEDLINE

COMMENT

G.L., Heaton, M.P., Laegreid, W.M., Rohrer, G.A., Chitko-McKown, C.G.,
Peters, G., Holt, I., Karanycheva, S., Liang, F., Quackenbush, J. and
Keele, J.W.
Sequence evaluation of four pooled-tissue normalized bovine CDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
21180013
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4356
Fax: 402 762 4350
Email: smtlhe@mail.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 20
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACAT
BACKWARD: GTTTCCTCAGTCAGCAG
Plate: 34 row: F column: 23
Seq primer: ATTAGGTGACACTATAG.
Location/Qualifiers

FEATURES

source

1..398
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 180Y"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: PCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from lymph node, ovary,
fat, hypothalamus, and pituitary."

BASE COUNT

134 a 82 g 105 t

ORIGIN

Query Match

Best Local Similarity 36.1%; Score 283.6; DB 10; Length 398;
Matches 307; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 1 ATGATGAAACATACAGCAACCTTCCCGAGATCCGTCGACCTGCGAGC 60
DB 53 ATGATGAAACATACAGCAACCTTCCCGAGATCCGTCGACCTGCGAGC 112
QY 61 ATGAAAGATTTTATGATTTTACTTACTGTTTCTTATCACCAGATGTTGGTCAGCA 120
DB 113 ATGAAAGATTTTATGATTTTACTTACTGTTTCTTATCACCAGATGTTGGTCAGCG 172
QY 121 CTTTTCGTGTATCTTATGAGGTTGAGACAGATGAGATGAAAGATCTTATC 180
DB 173 CTTTTCGTGTATCTTATGAGGTTGAGACAGATGAGATGAAAGATCTTATC 232
QY 181 GAAGATTTTGTATCTTATGAGGTTGAGACAGATGAGATGAAAGATCTTATC 240
DB 226 GAAGATTTTGTATCTTATGAGGTTGAGACAGATGAGATGAAAGATCTTATC 282
QY 241 TTAAGTAACTGTGAGAGATTTAAAGCAGTTTGAAGCTTTGAAAGATATATGTTA 300
DB 293 TTAAGTAACTGTGAGAGATTTAAAGCAGTTTGAAGCTTTGAAAGATATATGTTA 352
QY 301 AACAAAG 346
DB 353 AACAAAG 398

RESULT 3

A1982044

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

chicken.

Gallus gallus

A1982044 638 bp mRNA linear EST 07-MAY-2001
pat.pK0072.c9.f chicken activated T cell cDNA Gallus gallus CDNA
clone pat.pK0072.c9.f 5' similar to CD40 ligand, mRNA sequence.

REFERENCE 1. (bases 1 to 638)
 TITLE Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 JOURNAL Irtinagaru, V.G., Sofer, L., Cui, J. and Burnside, J.
 MEDLINE An expressed sequence tag database of T-cell-enriched activated
 COMMENT chicken splenocytes: sequence analysis of 5251 clones
 20318616
 Contact: Joan Burnside
 Molecular Endocrinology
 University of Delaware
 40 Townsend Hall, Newark, DE 19717, USA
 Tel: 302 831-1345
 Fax: 302-831-3411
 Email: joan@udel.edu, www.chickest.udel.edu

FEATURES

source

Location/Qualifiers

1. .638
 /organism="Gallus gallus"
 /db_xref="taxon:9031"
 /clone_1b="pat.p0072.c9.f"
 /clone_1b="chicken activated T cell cDNA"
 /sex="male"
 /cell_type="Con A-activated splenic T cell"
 /lab_host="E.coli TOP10 P"
 /note="Vector: pCDNA3"

BASE COUNT 132 a 171 c 151 g 180 t 4 others
 ORIGIN

Query Match

Best Local Similarity 57.6%; Score 69.6; DB 9; Length 638;
 Matches 167; Conservative 0; Mismatches 114; Indels 9; Gaps 2;

QY 498 AGGACTCTATTATCTCAGCCAGTCACTTGTTCATTCGGAGAGTTGAGTCA 557
 DB 2 AGGGCTTACTACTACTCAAGTCACTTGTTCAGCAGCGCGCTTCG----- 56
 QY 558 AGCTCATTTATAGCCAGCTCTGCTTAAGTCCCGGAGATTGAGAGAACTTACT 617
 DB 57 -GGCCATTACCTCTATATTTATTTATTTGATCTCCAGTGAAGAGAGCGGCTCGAT 115
 QY 618 CAGAGTGCAGAAATCCAGAGTTCCGCGCAACTCT--TGGGGGCAACATTCATCTT 674
 DB 116 GAAAGACTGACAGCAGACGACCTCCAGCGCTCTGTGAGCTCCAGTCCGGA 175
 QY 675 GGGAGAGTATTTGAAATGCAACAGTGTCTCGTGTTCATATGATGATCCAG 734
 DB 176 GGGCGGTGCTTTCAGCTGCGGAGGAGAGATGCTTTGTCAATGAGAGCTCAAC 235
 QY 735 CCAATGAGCCATGCGCTGCTTCACTCTTTGGTTCATCAACTCT 784
 DB 236 AGCAGTGAACGTCAACCTCGGCAACCTACTTGGAGATGTTCAAGCTGT 285

RESULT 4

AZ166561/c

LOCUS

SP_0088_B1_C02_T7A Strongylocentrotus purpuratus, purple sea urchin
 DEFINITION , sperm genomic BAC library Strongylocentrotus purpuratus genomic
 clone Plate=88 Col=3 Row=F, DNA sequence.

ACCESSION

AZ166561

VERSION

KEYWORDS

SOURCE

ORGANISM

Strongylocentrotus purpuratus.
 Strongylocentrotus purpuratus.
 Echinoidae; Echinozoa; Echinodermata; Eleutherozoa; Echinozoa;
 Echinoidae; Echinozoa; Echinodermata; Echinodermata; Echinodermata;
 Strongylocentrotidae; Strongylocentrotidae;
 1 (bases 1 to 1027)
 Cameron, R.A., Mahaffey, G., Rast, J.P., Martinez, P., Biondi, T.R.,
 Swartzell, S., Wallace, J.C., Poulet, A.J., Livingston, B.T., Wray,
 G.A., Ettensohn, C.A., Lehnach, H., Bitten, R.J., Davidson, E.H. and

TITLE

A sea urchin genome project: Sequence scan, virtual map, and
 additional resources

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)
 MEDLINE 20402566

COMMENT

Contact: Cameron, RA, Davidson, EH, Hood, L
 Division of Biology 156-29
 Pasadena California 91125, USA
 Tel: (626) 395-8421
 Fax: (626) 793-3047
 Email: acameron@caltech.edu
 Plate: 88 row: F column: 3
 Seq primer: 17
 Class: BAC ends
 High quality sequence stop: 1027.

FEATURES

source

Location/Qualifiers

1. 1027
 /organism="Strongylocentrotus purpuratus"
 /db_xref="taxon:7668"
 /clone_1b="Plate=88 Col=3 Row=F"
 /clone_1b="Strongylocentrotus purpuratus, purple sea
 urchin, sperm genomic BAC library"
 /note="Organ: sperm; Vector: BAC3.6; BAC clones in E-Coli
 DH10B"

BASE COUNT 159 a 162 c 147 g 559 t
 ORIGIN

Query Match

Best Local Similarity 48.1%; Score 50.2; DB 17; Length 1027;
 Matches 142; Conservative 0; Mismatches 153; Indels 0; Gaps 0;

QY 141 TAGAAGTGGACAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 200
 DB 1027 TAGAAT 968
 QY 201 AAGCATACAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 260
 DB 967 AAGGAAAAAAG 908
 QY 261 TAAAGGCACTTGAAGGCTTGGAGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 320
 DB 907 AAAAAAGTTGGAT 848
 QY 321 AGAAAAAGCTTTGAAATGCAAAAAAGTGAATCCTCAATTTGCGGACATGTCAT 380
 DB 847 AAAAAAGAAAAAAG 788
 QY 381 AAGTGAAGGAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 435
 DB 787 AAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAGAC 733

RESULT 5

BM854912

LOCUS

K-EST0137615 S21SN520 Homo sapiens cDNA clone S21SN520-58-D01 5',
 mRNA sequence.

ACCESSION

BM854912

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 1 (bases 1 to 412)
 Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
 Oh, K.J., Cheong, J.B., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
 Kim, Y.S.
 21C Frontier Korean EST Project 2001
 Unpublished (2002)
 Contact: Kim YS
 Genome Research Center

Korea Research Institute of Bioscience & Biotechnology
52 Eoem-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr
Plate: 58 row: D column: 01
High quality sequence stop: 412.
Location/Qualifiers

FEATURES

source

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S21SNUS20-58-D01"
/clone_lib="S21SNUS20"
/sex="F"
/tissue_type="Stomach"
/cell_type="Floating aggregates"
/cell_line="SNU-520"
/lab_host="Top10F"
/note="Organ: Stomach; Vector: pTZ18P1; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then deapped with tabacco acid pyrophosphatase (TAP). The deapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

BASE COUNT

147 a 72 c 119 g 74 t

ORIGIN

Query Match 6.2%; Score 48.8; DB 14; Length 412;
Best Local Similarity 50.4%; Pred. No. 0.13;
Matches 119; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

238 TCCTTACTGACAGTGTGAGAGATTAAAGCATTGAAAGCTTTGTGAAGATTAATG 297
171 TTCATACATTACAGTGTGTTGATTAATAATGATGATGTTCCGAGAGCAGACTA 230
298 TTTAAACAAGAGACGCAAGAAAGAAAGCTTTGAATGCAAAAGGTGATCAGAT 357
231 CTCAAATACGTGACACCAATTTGCAGAAACAGCAAGAACTTCAAAAAGCAATCAGAG 290
358 CCTCAAAATTCGGCAGATGTCATAGTGAAGCCAGAGCAATTAACAATCTGTGTAAG 417
291 CAGTATGCATGAGGGAAGATGAGGGGCTGCCAAGAAAGAAAGATCTGTGTGCA 350
418 TGGGCTGAAAAAGATATCAACCATGACAGCAAGACTTGTGTAACCTCGAAAAATGG 473
351 CAGAAAAATGTGAGTGAAGCAAAACAAACAAACAGAAAAACACCTGGAATGG 406

RESULT 6

CNS005TE/c

LOCUS

DEFINITION

CNS005TE 997 bp DNA linear GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR12K22 of RPL1-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION

AL060767

VERSION

AL060767.1

GI:4943573

GSS

SOURCE

ORGANISM

Drosophila melanogaster.

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

REFERENCE

1. (bases 1 to 997)

AUTHORS

Direct Submission

JOURNAL

BP 191 91006 EVRY cedex - FRANCE [E-mail : seget@genoscope.cns.fr

COMMENT

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org>. The BDGP Drosophila melanogaster BAC library was prepared by Kazuo Ogoe and Aaron Mammoser in Peter de Jong's laboratory in the department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPL1-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's p1 and Est libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
Location/Qualifiers

FEATURES

source

/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="BACR12K22"
/clone_lib="RPL1-98"
/note="end : TET3"

BASE COUNT

89 a 99 c 13 g 258 t 538 others

ORIGIN

Query Match 6.2%; Score 48.8; DB 17; Length 997;
Best Local Similarity 16.3%; Pred. No. 0.13;
Matches 59; Conservative 143; Mismatches 160; Indels 0; Gaps 0;
140 ATGAAGTTGACAGATGAGATGAAGATCTTCATGAGATTTGTATTCTACG 199
850 AGRRRARGAGRGRRGRRGRRRABARARARARARARARARARAR 791
200 AAACGATACAGATGACACACAGAAAGATCTTATCTTACGACCTGTGAGAG 259
790 RARGARRRRGRRRRGRRRRRABARARARARARARARARARAR 731
260 TTAAGCCAGTTGAAGCTTGTGAAGATATATGTTAAACAAGAGAGACGAG 319
730 RRRRRRRRGAGARARARARARARARARARARRRRGAGARRRRGRRRGA 671
320 AAGAAACAGCTTTGAATGCAAAAGTATCTCAATCTCAAAATTCGGCACATGTA 379
670 GARRRRGRMRTRARRRRRARGAARRRARGARRRRGRRRRARRAG 611
380 TAAGTAGGCGACAGTAAACAACATCTGTGTAACAGTGGCTGAAAAAGATATCA 439
610 RRRRRRRRGARRRRRRRABARARARARARRRRRGRRRRRABARAR 551
440 CCATGACAACTTGTGTAACCTGGAAGAAATGGAAAAAGCTGACCTTAAAAAGAC 499
550 RRRRRRABRGAAGARARARARARARARARARRRRRRRGRRRRRAGAR 491
500 GA 501
490 RR 489

RESULT 7

B0935454

LOCUS

DEFINITION

B0935454 999 bp mRNA linear EST 21-AUG-2002
AGENCOURT 877337 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:6372460
5', mRNA sequence.

ACCESSION

B0935454

VERSION

B0935454.1

GI:22350837

EST

human.

SOURCE

ORGANISM

Homo sapiens

REFERENCE 1 (bases 1 to 999)
 AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs@mail.nih.gov
 Tissue Procurement: DCTD/DRP/Gazdar
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LMC2548 row: e column: 05
 High quality sequence start: 309
 High quality sequence stop: 663.
 Location/Qualifiers

FEATURES

source

1. 999
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:6372460"
 /clone_1b="NIH MGC 18"
 /tissue_type="large cell carcinoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the Laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC library."

BASE COUNT 328 a 190 c 254 g 227 t
 ORIGIN

Query Match 6.2%; Score 48.8; DB 14; Length 999;
 Best Local Similarity 50.4%; Pred. No. 0.13;

Matches 119; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

QY 238 TCCTTACGACCTGTGAGAGATTAAGCCAGTTGAAGGCTTTGTGAAGATTAATG 297
 Db 223 TTCAATACATTCAGTGTGATTAAGATTAAGGATTAAGGATTAAGGATTAAG 282
 QY 298 TTAAACAAAGAT 357
 Db 283 CTCAATACGTCGACCAATTTGCAAGATTAATTAAGAACTTCAAAAGCCATCAGAG 342
 QY 358 CCTCAATTTGGCGACATGTCATTAAGAGGCGACAGTAAGAAAGCAATCTGTGTTACAG 417
 Db 343 CAGTATGCAAGAGGAGAGATGAGAGGCTGCCCGAGAAAGAGACATCTGCTGCAA 402
 QY 418 TGGGCTGAAAAAGATACACCAATGAGCAACCTTGTAACTTGGAAATGG 473
 Db 403 CAGAAAAATGTTGAAAGTGAAGAAAGAAAGCAACAGAAACACCTGGAATGG 458

RESULT 8

BF820152 396 bp mRNA linear EST 13-JAN-2001
 LOCUS MRL-R70025-171100-003-C06 RT0025 Homo sapiens cDNA, mRNA sequence.
 DEFINITION BF820152
 VERSION BF820152.1 GI:12158440
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 396)
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Negai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bata, G.S., Simpson, D.H.,

TITLE Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, U.F., de Souza, S.J. and Simpson, A.J.
 JOURNAL Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 MEDLINE Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3492-3496 (2000)
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the PAPSP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?cl=MR1et2=MRL-RT0025-171100-003-c06&t3=2000-11-17&t4=1>)
 Seq primer: puc 18 forward
 High quality sequence start: 8
 High quality sequence stop: 396.
 Location/Qualifiers

FEATURES

source

1. 396
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_1b="RT0025"
 /dev_stage="Adult"
 /note="Organ: kidney tumor; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from OES2ES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 138 a 73 c 112 g 73 t
 ORIGIN

Query Match 6.0%; Score 47.2; DB 12; Length 396;
 Best Local Similarity 50.0%; Pred. No. 0.32;

Matches 118; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

QY 238 TCCTTACGACCTGTGAGAGATTAAGCCAGTTGAAGGCTTTGTGAAGATTAATG 297
 Db 86 TTCAATACATTCAGTGTGATTAAGATTAAGGATTAAGGATTAAGGATTAAG 145
 QY 298 TTAAACAAAGAT 357
 Db 146 CTCAATACGTCGACCAATTTGCAAGATTAATTAAGAACTTCAAAAGCCATCAGAG 205
 QY 358 CCTCAATTTGGCGACATGTCATTAAGAGGCGACAGTAAGAAAGCAATCTGTGTTACAG 417
 Db 206 CAGTATGCAAGAGGAGAGATGAGAGGCTGCCCGAGAAAGAGACATCTGCTGCAA 265
 QY 418 TGGGCTGAAAAAGATACACCAATGAGCAACCTTGTAACTTGGAAATGG 473
 Db 266 CAGAAAAATGTTGAAAGTGAAGAAAGAAAGCAACAGAAACACCTGGAATGG 321

RESULT 9

AV714252 486 bp mRNA linear EST 11-OCT-2000
 LOCUS AV714252 DCB Homo sapiens cDNA clone DCBADP07 5', mRNA sequence.
 DEFINITION AV714252
 VERSION AV714252.1 GI:10795769
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 486)
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 Xu, X., Gu, J., Liu, F., Qu, J., Zhao, M., Li, Y., Huang, Q., Zhou, J., Song, H., Gu, Y., Yang, Y., Gao, G., Xiao, H., Li, N., Qian, B., Gao, X.,

Cheng Z., Xu S., Gu W., Tu Y., Jia J., Fu G., Ren S., Zhong M., Lu G., Cheng Z. and Han Z.
Homo sapiens cDNA DCB clones
Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES

source
1..486
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DCBADF07"
/cell_type="endritic cells"
/dev_stage="mature"
/lab_host="BM25.8"
/note="Vector: pTriblEX2; Site_1: sfilA; Site_2: sfilB"

BASE COUNT 182 a 87 c 124 g 93 t
ORIGIN

Query Match 6.0%; Score 47.2; DB 10; Length 486;
Best Local Similarity 50.0%; Pred. No. 0.32; Indels 0; Gaps 0;
Matches 118; Conservative 0; Mismatches 118;

QY 238 TCCTTACTGAAGCTGTGAGAGATTAAAGCAGTTGAAAGCTTTGTAAGATTAATG 297
DB 139 TTCAATACATTACAGTGTGAGATTAATAATGTGATGATGGTTCGCGAGCAAAATTA 198
QY 228 TTAACAAGAT 357
DB 139 CTCATATACGTGACACCAATTTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGATGAG 258
QY 358 CCTCAATTGCGGACATGCTATTAAGAGCGAGAGAGAGAGAGAGAGAGAGAGAGATG 417
DB 259 CAGTATGCAAGATG 318
QY 418 TGGGCTGAAAAAGATACACACCATGAGCAACATTTGATGCTGTAAGAAATG 473
DB 319 CAGAAAAATGTTGAACTGAAACCAAAAAAGACAAACAAAAACCTGAAATG 374

RESULT 10

AV724813 578 bp mRNA linear EST 16-OCT-2000
LOCUS AV724813 HTB Homo sapiens cDNA clone HTBAK04 5', mRNA sequence.
DEFINITION AV724813
ACCESSION AV724813
VERSION AV724813.1 GI:10829575
KEYWORDS EST.

SOURCE

human.
ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 578)
Gu, Y., Peng, Y., Song, H., Huang, Q., Yang, Y., Gao, G., Xiao, H., Xu, X.,
Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu
S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R.,
Chen, J., Chen, Z. and Han, Z.
Homo sapiens cDNA HTB clones
Unpublished (2000)

TITLE
JOURNAL
COMMENT

Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES

Location/Qualifiers

source

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/db_xref="taxon:9606"
/clone="HTBAK04"
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XhoI"

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Best Local Similarity 50.0%; Pred. No. 0.32;
Matches 118; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

QY 238 TCCTTACTGAAGCTGTGAGAGATTAAAGCAGTTGAAAGCTTTGTAAGATTAATG 297
DB 28 TTCAATACATTACAGTGTGAGATTAATAATGTGATGATGGTTCGCGAGCAAAATTA 87
QY 298 TTAACAAGAT 357
DB 88 CTCATATACGTGACACCAATTTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGATGAG 147
QY 358 CCTCAATTGCGGACATGCTATTAAGAGCGAGAGAGAGAGAGAGAGAGAGAGAGATG 417
DB 148 CAGTATGCAAGATG 207
QY 418 TGGGCTGAAAAAGATACACACCATGAGCAACATTTGATGCTGTAAGAAATG 473
DB 208 CAGAAAAATGTTGAACTGAAACCAAAAAAGACAAACAAAAACCTGAAATG 263

RESULT 11

BI713130 583 bp mRNA linear EST 11-MAR-2002
LOCUS BI713130
DEFINITION BI713130
ACCESSION BI713130
VERSION BI713130.1 GI:15688825
KEYWORDS EST.

SOURCE

human.
ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 583)
Melton, D., Brown, J., Kenty, G., Permut, A., Lee, C., Kaestner, K.,
Lemishka, I., Pearce, M., Breastelli, J., Gradwohl, G., Clifton, S.,
Hillier, L., Marra, M., Page, D., Wylie, T., Martin, D., Blaisstein, A.,
Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas
M., Gibbons, M., McCan, R., Cole, R., Tsagarelis, R., Williams, T.,
Jackson, Y. and Bowers, Y.
Endocrine Pancreas Consortium
Unpublished (2000)

TITLE
JOURNAL
COMMENT

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biochem.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center for information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Seq primer: -40bp from Gibco
High quality sequence stop: 471.
Location/Qualifiers

FEATURES
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/db_xref="taxon:9606"
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 /clone_1ib="HR85 1s1et"
 /tissue type="Purified pancreatic islet"
 /lab host="DH108"
 /note="Organ: Pancreas; Vector: plasmidscript SK(-); Site_1
 Notti, Site_2: XhoI; cDNA made by oligo-dT priming.
 Size-selected on agarose gel. Average insert size ~1kb. 5'
 XhoI site was destroyed after directional cloning.
 Amplified once. Contact information: Hiroshi Inoue, MD,
 Metabolism Div. (Alan Pernutt lab), Washington University
 School of Medicine, Box 8127, 660 South Euclid Ave., St.
 Louis, MO 63110, E-mail: hinoue@ingate.wustl.edu, Tel:
 314-362-1916, Fax: 314-747-2692."

Query Match	6.0%;	Score 47.2;	DB 13;	Length 583;
Best Local Similarity	50.0%;	Pred. No. 0.32;		
Matches 118;	Conservative 0;	Mismatches 118;	Indels 0;	Gaps 0;

Qy 238 TCCTTACGACCTGTAGAGATTAAAGCCAGTTTGAAAGCGTTGTGAAGCATATAATG 297
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Db 104 TTCATACATTACACTGTGGTAATAAAATTGGATGAATGGCTTCGGAGACAGACAGTA 1633

QY 298 TTTAACAAGAGGAGACCGAAGAAAAGAAACAGCTTTGAATGC AAAAGGTGTCAGAT 357
| | | | | | | | | | | | | | | | | | | | |
Db 164 CTCCAATACGTGACACCAATTGGCAGAAACAGCGAGAATTCAAAAAGCCAAATCAGGAG 223

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QY      358  CCTCAATTGCGGACATCTCATAGTAGGCCGACGACGTAACCAACATCTGTCTACG  417
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QY 418 TGGGCTGAAAAAGATACTACCATGAGCAACAATTGTAACCTGGAAAAATGG 473

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RESULT 12
BF791160
TODD
DE701160
EAC has
-DUA
JANUARY
EOM 12 JAN 2001

DEFINITION	602251255F1 NIH_MGC_81 Homo sapiens CDNA clone IMAGE:4338656 5', mRNA sequence.
ACCESSION	BF791160
VERSION	BF791160.1
DATE	07-12-2006

KEYWORDS	EST.	.
SOURCE	human.	
ORGANISM	Homo sapiens	

REFERENCE
Mammalia; Euteria; Primates; Carnivora; Homini; Homo.
1 (bases 1 to 586)
NIH-MGC <http://mgc.ncbi.nlm.nih.gov/>.
National Institutes of Health. Mammalian Gene Collection (MGC)

JOURNAL COMMENT
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov

CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCBI clone distribution information can be

found through the I.M.A.G.E. Consortium/LINTL at:
<http://image.llnl.gov>
 Plate: LUCM1214 row: n column: 13
 web_email: cormier@llnl.gov

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FEATURES
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/ab_xref="Hlxon.9505"
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/note="Organ: muscle (skeletal) ; Vector: pDNR-LIB

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Best Local Similarity	50.0%; Pred. No. 0.32;			
Matches 118; Conservative	0; Mismatches 118; Indels 0; Gaps 0;			

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Dy 298 TTAACAAAGAGGAGCAGAAAGAATAACGCTTTGAATTCAGAAAAGGTGATCAGAAAT 357
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Oy 358 CCTCAATTGCCGACATCTCATTAAGTAGGCGACAGTAACAACATCTGTTCAG 417
 Db 264 CAGTATGCAGAGGGGAGATGAGAGGGGCTGCCAGAAAGMAGACATCTGTCTGCAA 323

QY 418 TGGGCTGAAAAGGATACTACACCATGAGCAACAACCTTGTAACCTGAAAAATGG 473

Db 324 CAGAAAAATGTTGAGTGAAAAAGAAAAAGAACAAACAGAAAAACCTGGAAATGG 379

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MDNA
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EST 13-FEB-2001

DEFINITION	AL534443 LTI FL013_FBrn1 Homo sapiens cDNA clone CSDF004YD24 5 prime, mRNA sequence.
ACCESSION	AL534443
VERSION	AL534443.1
VERSION	CT_13707016
VERSION	AF534443.1

KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
<i>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;</i>	

REFERENCE
1 (bases 1 to 797)
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
Li W.B., Gruber, C., Jesse, J. and Polayes, D.
Full-length cDNA libraries and normalization

JOURNAL
COMMENT
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Séquençage
RD 101 91006 Evry cedex - France

Email: segrif@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
 source
 Location/Qualifiers
 1..797
 /deviation where confidence

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week_24 week and 26 week"
/lab_host="DH10B"
/notice="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand
cDNA was primed with a NotI-3' (ccg/gm) primer. Blue prime
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end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact: Peng Liang, Life Technologies, a

, Maryland 20850, USA Fax : (1) 301 610 8371 Email :
flang@lifetech.com URL :
<http://fulllength.invitrogen.com>"

Bluescript KS+; Site 1: BamHI; Site 2: SalI-XhoI (GTCGAG
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3',
size-selected for average insert size 2.3 kb and
normalized to ROT 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIMH/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."

BASE COUNT 279 a 145 c 243 g 178 t

ORIGIN

Query Match

Best Local Similarity 6.0%; Score 47.2; DB 13; Length 845;

Matches 118; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

QY 238 TCCTTACTGAACTGTGAGAGATTAAAGCCATTGTAAGCTTTGTGAGATATATG 297
Db 209 TTCATACATTACAGTGGTTGGATTAATAATGGGTTCCGAGGCGAGAGTA 268
QY 298 TTAAACAAG 357
Db 269 CTCAAATAGTGAACCAATTTGCAAGAACGAGAACTTCAAAAAGCCATCAGAG 328
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Search completed: March 9, 2003, 04:42:23
Job time : 1295.53 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 8, 2003, 18:30:53 ; Search time 164.215 Seconds
(without alignments)
10778.963 Million cell updates/sec

Title: US-08-982-272-6

Perfect score: 786
Sequence: 1 ATGATGAAACATACAGCCA.....TTGCTTACTCAAACTCTGA 786

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2185239 segs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N.Geneseq.101002:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	763.6	97.2	786	15	AAO63959
4	763.6	97.2	786	19	AAV38997
5	763.6	97.2	786	19	AAV12852
6	763.6	97.2	840	14	AAO41506
7	763.6	97.2	840	15	AAO67123
8	763.6	97.2	840	16	AAO5763
9	763.6	97.2	840	18	AAV3782

10	763.6	97.2	840	19	AAV61063	Human CD40 ligand
11	763.6	97.2	840	20	AAZ27525	Human CD40-L codin
12	763.6	97.2	879	22	AAZ55339	Nucleotide sequenc
13	763.6	97.2	1816	21	AAZ51745	Human CD40 ligand
14	763.6	97.2	1816	23	AAZ86571	DNA encoding novel
15	762	96.9	840	15	AAO57984	Genomic sequence o
16	760.6	96.8	840	18	AAZ8122	Human CD40L muteln
17	758.8	96.5	840	16	AAO94091	Human CD40-L cDNA.
18	754	95.9	786	19	AAV39000	Exemplary CD40 lig
19	704.4	89.6	783	19	AAV42184	Exemplary CD40 lig
20	642.2	82.5	1552	22	AAZ55525	Nucleotide sequenc
21	642.8	81.8	865	22	AAZ82935	HIV-1 gp120 V3 100
22	642.8	81.8	906	22	AAZ82932	HIV-1 gp120 V3 100
23	642.8	81.8	2209	22	AAZ82929	HIV-1 gp120-human
24	642.8	81.8	2252	22	AAZ82928	HIV-1 gp120-human
25	642	81.7	864	19	AAV39004	CD40 ligand gene u
26	638.2	81.2	1425	14	AAO41516	Human CD40-L/Rc fu
27	638.2	81.2	1425	20	AAZ27534	Human CD40-L/Rc fu
28	637.2	81.1	929	18	AAZ58123	CDNA encoding yeas
29	637.2	81.1	929	20	AAZ27537	Human trimeric CD4
30	636	80.9	1566	24	ABK12874	Chimeric SA-CD40L
31	608.4	77.4	885	21	AAZ55540	Feline CD154 CDNA.
32	608.4	77.4	885	21	AAZ55541	Feline CD154 CDNA.
33	605.4	77.0	780	21	AAZ55542	Feline CD154 CDNA
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36	584.4	74.4	783	19	AAV12853	CD40 ligand codin
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38	582.8	74.1	783	19	AAV38998	CD40 ligand gene u
39	582.8	74.1	818	19	AAV61062	Human CD40 ligand
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42	580.2	73.6	782	14	AAO41507	Canine CD40-L DNA.
43	580.2	73.6	780	21	AAZ55536	Canine CD154 CDNA
44	576.2	73.6	780	21	AAZ55537	Canine CD154 CDNA
45	570	72.5	783	19	AAV38999	Exemplary CD40 lig

ALIGNMENTS

AAV39002	AAV39002 standard; DNA; 786 BP.
AAV39002;	
23-SEP-1998 (first entry)	
Exemplary CD40 ligand gene used in the course of the invention.	
CD40 ligand; alteration; immunoreactivity; human cell;	
accessory molecule ligand; AMU; gene therapy; treatment; neoplasia;	
autoimmune disorder; rheumatoid arthritis; vaccine; chimera; se.	
Chimeric - Mus sp.	
Chimeric - Homo sapiens.	
WO9826061-A2.	
18-JUN-1998.	
08-DEC-1997; 97WO-US22740.	
01-DEC-1997; 97US-0982272.	
09-DEC-1996; 96US-0032145.	
(REGC) UNIV CALIFORNIA.	
Cantwell M, Kipps TJ, Sharma S;	
WPI, 1998-348521/30.	

PT Vectors containing accessory molecule ligand genes - used for
PT altering immunoreactivity of cells, particularly for treatment of
PT neoplasia or autoimmune disorders, e.g. rheumatoid arthritis
PS Disclosure; Page 106; 167pp; English.

XX The present sequence represents an exemplary CD40 ligand gene,
CC comprising nucleotides encoding the extracellular domains (Domains III
CC and IV) and transmembrane domain (Domain II) of human CD40 ligand gene
CC (AAV38998) operatively linked to nucleotides encoding the cytoplasmic
CC domain (Domain I) of the murine CD40 ligand gene (AAV38997). The sequence
CC is used to exemplify the method of the invention. The specification
CC describes a method for altering the immunoreactivity of human cells which
CC comprises introducing a gene encoding an accessory molecule ligand (AML)
CC into the cells so that the AML is expressed on the surface of the cells.
CC Vectors containing the AML genes can be used in gene therapy for
CC treating neoplasia or autoimmune disorders such as rheumatoid arthritis.
CC They can also be used for vaccination to produce immunity against a virus
CC cell, bacteria, protein, fungus or neoplasia.

XX Sequence 786 BP; 250 A; 166 C; 171 G; 199 T; 0 other;

Query Match 100.0%; Score 786; DB 19; Length 786;
Best Local Similarity 100.0%; Pred. No. 3.2e-219;
Matches 786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATAGAAACATACAGCACTCCCGAGATCCGGGCACTGGACCTCCAGCGAGC 60
DB 1 ATGATAGAAACATACAGCACTCCCGAGATCCGGGCACTGGACCTCCAGCGAGC 60
QY 61 ATGAGATTTTATGATTTTCTTACTGTTTCTTATCACCAGATGGGTGACGA 120
DB 61 ATGAGATTTTATGATTTTCTTACTGTTTCTTATCACCAGATGGGTGACGA 120
QY 121 CTTTTCCTGCTGATCTTCATAGAGGTTGACAGATAGAGATGAAAGATCTTAT 180
DB 121 CTTTTCCTGCTGATCTTCATAGAGGTTGACAGATAGAGATGAAAGATCTTAT 180
QY 181 GAGATTTTGTATTCATGAAACGATACAGATGCAACAGAGAAAGATCTTATCC 240
DB 181 GAGATTTTGTATTCATGAAACGATACAGATGCAACAGAGAAAGATCTTATCC 240
QY 241 TTACTGAACTGTAGAGATTTAAAGCAGTTTGAAGCTTTGAGAGATTAATGTTA 300
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QY 361 CAAATTCGCGCATGTCATAGAGGCGAGCAATTAACATATGTTGATCAGTGG 420
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QY 661 CAATTCATCTTGGAGAGATTTGATTTGCAACCAAGTCTTGGTGTGTTGTAAT 720
DB 661 CAATTCATCTTGGAGAGATTTGATTTGCAACCAAGTCTTGGTGTGTTGTAAT 720

QY 721 GTGACTGATTCAGCAAGGCAAGTGCATGTCAGTTCACGCTTTGGTACTGCAAA 780
DB 721 GTGACTGATTCAGCAAGGCAAGTGCATGTCAGTTCACGCTTTGGTACTGCAAA 780
QY 781 CTCCTGA 786
DB 781 CTCCTGA 786
RESULT 2
ID AAV39003 standard; DNA; 786 BP.
XX AAV39003;
AC AAV39003;
XX 23-SEP-1998 (first entry)
DT 23-SEP-1998 (first entry)
XX Exemplary CD40 ligand gene used in the course of the invention.
DE Exemplary CD40 ligand gene used in the course of the invention.
XX CD40 ligand; alteration; immunoreactivity; human cell;
KW accessory molecule ligand; AML; gene therapy; treatment; neoplasia;
XX autoimmune disorder; rheumatoid arthritis; vaccine; chimera; ss.
OS Chimeric - Mus sp.
OS Chimeric - Homo sapiens.
PN MO9826061-A2.
PD 18-JUN-1998.
XX 08-DEC-1997; 97MO-US22740.
PF 01-DEC-1997; 97US-0982272.
PR 09-DEC-1996; 96US-0032145.
XX (REGC) UNIV CALIFORNIA.
PA Cantwell M, Kipps TJ, Sharma S;
PI WPI; 1998-348521/30.
DR Vectors containing accessory molecule ligand genes - used for
PT altering immunoreactivity of cells, particularly for treatment of
PT neoplasia or autoimmune disorders, e.g. rheumatoid arthritis
XX Disclosure; Page 107; 167pp; English.
XX The present sequence represents an exemplary CD40 ligand gene,
CC comprising nucleotides encoding the extracellular domains (Domains III
CC and IV) of the human CD40 ligand gene (AAV38998) operatively linked to
CC nucleotides encoding the cytoplasmic domain (Domain I) and transmembrane
CC domain (Domain II) of the murine CD40 ligand gene (AAV38997). The
CC sequence is used to exemplify the method of the invention. The
CC specification describes a method for altering the immunoreactivity of
CC human cells which comprises introducing a gene encoding an accessory
CC molecule ligand (AML) into the cells so that the AML is expressed on the
CC surface of the cells. Vectors containing the AML genes can be used in
CC gene therapy for treating neoplasia or autoimmune disorders such as
CC rheumatoid arthritis. They can also be used for vaccination to produce
CC immunity against a virus cell, bacteria, protein, fungus or neoplasia.
XX Sequence 786 BP; 250 A; 166 C; 170 G; 200 T; 0 other;

Query Match 98.8%; Score 776.4; DB 19; Length 786;
Best Local Similarity 99.2%; Pred. No. 2e-216;
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGATAGAAACATACAGCACTCCCGAGATCCGGGCACTGGACCTCCAGCGAGC 60
DB 1 ATGATAGAAACATACAGCACTCCCGAGATCCGGGCACTGGACCTCCAGCGAGC 60
QY 61 ATGAGATTTTATGATTTTCTTACTGTTTCTTATCACCAGATGGGTGACGA 120

Db 61 ATGAAGATTTTATGATTTTACTTACTGTTTCTTATCAACCAATATGATCTG 120
 Qy 121 CTTTTCCTGCTGATCTTCAATGAAAGTTGACAAAGTAAAGATGAAATCTTCA 180
 Db 121 CTTTTCCTGCTGATCTTCAATGAAAGTTGACAAAGTAAAGATGAAATCTTCA 180
 Qy 181 GAAGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATG 240
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 Db 241 TTAAGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATG 300
 Qy 301 AACAAAG 360
 Db 301 AACAAAG 360
 Qy 361 CAATTTGGGCACTGTCATAGTGGCCAGAGTAAACAACTGTTGTTACAGTGG 420
 Db 361 CAATTTGGGCACTGTCATAGTGGCCAGAGTAAACAACTGTTGTTACAGTGG 420
 Qy 421 GCTGAAAAAGATCTACACATGAGCAACAACTTGTAAACCTGGAAGATGGAAGAG 480
 Db 421 GCTGAAAAAGATCTACACATGAGCAACAACTTGTAAACCTGGAAGATGGAAGAG 480
 Qy 481 CTGACCGTTAAAG 540
 Db 481 CTGACCGTTAAAG 540
 Qy 541 CGGAAAGCTTGAAGTCAAGTCCATTTATGAGCAAGCTTGTCTAAAGTCCCGGAG 600
 Db 541 CGGAAAGCTTGAAGTCAAGTCCATTTATGAGCAAGCTTGTCTAAAGTCCCGGAG 600
 Qy 601 TTGAGAGATCTTATCTGAGAGTGGCAATACCAAGTTCGCGCAACCTTGGGGGCA 660
 Db 601 TTGAGAGATCTTATCTGAGAGTGGCAATACCAAGTTCGCGCAACCTTGGGGGCA 660
 Qy 661 CAATCATTTCACTTGGAGAGAGATTTGAAATGCAACAGTGTCTGCTTTGTTCAAT 720
 Db 661 CAATCATTTCACTTGGAGAGAGATTTGAAATGCAACAGTGTCTGCTTTGTTCAAT 720
 Qy 721 GTGACGTATCCAGAGCAAGTGGAGCCAGTGGCTTCACTGCTTTGCTTATCAAA 780
 Db 721 GTGACGTATCCAGAGCAAGTGGAGCCAGTGGCTTCACTGCTTTGCTTATCAAA 780
 Qy 781 CTCTGA 786
 Db 781 CTCTGA 786
 RESULT 3
 ID AA063959 standard; cDNA to mRNA; 786 BP.
 AC AA063959;
 XX 11-JUN-1995 (first entry)
 DE Human CD40-L type II transmembrane protein coding sequence.
 XX Leucine zipper; trimerisation; trimeric CD40-L; fusion protein;
 KW hetero-oligomer; homo-oligomer; type II transmembrane protein;
 KM soluble CD40-L; tumour necrosis factor family; ss.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT 1..786
 FT CDS /*tag= a
 FT /product= human CD40-L
 FT /note= "nucleotides 148-783 code for the

FT extracellular region (amino acids 50-261)"
 PN MO9410308-A.
 XX 11-MAY-1994.
 PD 20-OCT-1993; 93WO-US10034.
 PF 23-OCT-1992; 92US-0969703.
 PR 13-AUG-1993; 93US-0107353.
 XX (IMMUNEX CORP.
 PA Spriggs MK, Srinivasan S;
 PI WPI: 1994-167465/20.
 DR P-PSDB; AARS3969.
 XX
 XX Prepn. of soluble oligomeric mammalian proteins - using host
 PT cells to express a fusion protein comprising a leucine zipper
 PT domain and a heterologous mammalian protein
 XX
 PS Example 1; Page 22-23; 35pp; English.
 CC A DNA fragment encoding the extracellular (soluble) region of human
 CC CD40-L was ligated to a synthetic oligonucleotide sequence coding
 CC for a leader peptide, a 33 amino acid leucine zipper sequence
 CC (AARS3968) and the flag (KRW) linker sequence. Cells expressing the
 CC fusion construct are grown to accumulate oligomeric, soluble CD40-L
 CC in the supernatant. The leucine zipper sequence spontaneously
 CC trimerises in solution and fusion proteins comprising
 CC the sequence fused to a heterologous mammalian protein also form
 CC oligomers.
 CC
 SQ Sequence 786 BP; 250 A; 168 C; 168 G; 200 T; 0 other;
 Query Match 97.2%; Score 763.6; DB 15; Length 786;
 Best Local Similarity 98.2%; Pred. No. 1,1e-212;
 Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
 Qy 1 ATGATAGAAACATACAGCAAGCTTCCCGAGTCCGAGCACTGAGCTTCAGAGAGC 60
 Db 1 ATGATAGAAACATACAGCAAGCTTCCCGAGTCCGAGCACTGAGCTTCAGAGAGC 60
 Qy 61 ATGAAAGTTTATGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATG 120
 Db 61 ATGAAAGTTTATGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATG 120
 Qy 121 CTTTTCCTGCTGATCTTCAATGAAAGTTGACAAAGTAAAGATGAAATCTTCA 180
 Db 121 CTTTTCCTGCTGATCTTCAATGAAAGTTGACAAAGTAAAGATGAAATCTTCA 180
 Qy 181 GAAGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATG 240
 Db 181 GAAGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATG 240
 Qy 241 TTAAGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATG 300
 Db 241 TTAAGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATG 300
 Qy 301 AACAAAG 360
 Db 301 AACAAAG 360
 Qy 361 CAATTTGGGCACTGTCATAGTGGCCAGAGTAAACAACTGTTGTTACAGTGG 420
 Db 361 CAATTTGGGCACTGTCATAGTGGCCAGAGTAAACAACTGTTGTTACAGTGG 420
 Qy 421 GCTGAAAAAGATCTACACATGAGCAACAACTTGTAAACCTGGAAGATGGAAGAG 480
 Db 421 GCTGAAAAAGATCTACACATGAGCAACAACTTGTAAACCTGGAAGATGGAAGAG 480
 Qy 481 CTGACCGTTAAAG 540

KW heterologous mammalian type I transmembrane protein; antibody production;
 KM CD40-L; B-cell proliferation; CD27-L; lymphocyte antigen; ss.

OS Homo sapiens.

PH Key Location/Qualifiers

FT CDS 1..786

FT /*tag= a

US5716805-A.

PD 10-FEB-1998.

PF 18-MAY-1995; 95US-0446922.

PR 18-MAY-1995; 95US-0446922.

PR 25-OCT-1991; 91US-0783707.

PR 05-DEC-1991; 91US-0805723.

PR 23-OCT-1993; 92US-0969703.

PR 13-AUG-1993; 93US-0107353.

PA (IMMV) IMMUNEX CORP.

PI Spriggs MK, Srinivasan S;

DR WPI: 1998-144799/13.

DR P-PSDB; AAM41178.

XX Example 1; column 19-20; 21bp; English.

XX This sequence is the coding sequence for the human CD40 ligand (CD40-L).
 CC The encoded protein can be used in a fusion protein produced using the
 CC method of the invention. The method is for preparing soluble oligomeric
 CC protein by culturing a host cell transfected with a vector for the
 CC fusion protein. The soluble oligomeric proteins comprise a leucine zipper
 CC fused to the N terminus of the extracellular region of a heterologous
 CC mammalian type II transmembrane protein or to the C terminus of the
 CC extracellular region of a heterologous mammalian type I transmembrane
 CC protein, where the leucine zipper is a peptide comprising at least part
 CC of AAM41171 or AAM41172, optionally with conservative amino acid
 CC substitutions, provided that the peptide trimerizes in solution. A
 CC soluble fusion protein comprising the leucine zipper of AAM41171 linked
 CC to the extracellular region of CD40-L (a type II transmembrane protein
 CC that is found on activated T cells and acts as a ligand for the B-cell
 CC antigen CD40) stimulates B-cell proliferation and antibody production in
 CC a similar manner to membrane-bound CD40-L. A soluble fusion protein
 CC comprising the leucine zipper of AAM41172 linked to the extracellular
 CC region of CD27-L (a type II transmembrane protein that binds to the
 CC lymphocyte antigen CD27) inhibits binding of CD27c (a fusion protein
 CC comprising the extracellular region of CD27 and a human IgG1 Fc region)
 CC to BSV-transformed B cells expressing CD27-L.

XX Sequence 786 BP; 250 A; 168 C; 168 G; 200 T; 0 other;

Query Match 97.2%; Score 763.6; DB 19; Length 786;

Best Local Similarity 98.2%; Pred. No. 1,1e-212; Mismatches 14; Indels 0; Gaps 0;

DB 1 ATGATGAAACATGACGACCACTTCCCGACATCGGTGCACTGACCTTCAGCAGC 60
 ATGATGAAACATGACGACCACTTCCCGACATCGGTGCACTGACCTTCAGCAGC 60
 61 ATGAAATTTTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 120
 ATGAAATTTTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 120
 61 ATGAAATTTTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 120
 ATGAAATTTTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 120
 121 CTTTGGCTGTGATCTTCAATAGAGGTTGACAAAGTGAAGATGAAGAAATCTTCA 180
 CTTTGGCTGTGATCTTCAATAGAGGTTGACAAAGTGAAGATGAAGAAATCTTCA 180

QY 181 GAAGTTTGTATTCATGAAAACGATACAGAGTGCACACGAGAAAGATCTTATCC 240
 DB 181 GAAGTTTGTATTCATGAAAACGATACAGAGTGCACACGAGAAAGATCTTATCC 240
 QY 241 TTACTGAATCTGTGAGAGATTAATAAGCAGTTTGAAGCTTTGAGAGATTAATGTTA 300
 DB 241 TTACTGAATCTGTGAGAGATTAATAAGCAGTTTGAAGCTTTGAGAGATTAATGTTA 300
 QY 301 AACAAAGAGAGACGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 360
 DB 301 AACAAAGAGAGACGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 360
 QY 361 CAATTTGGGACATGTCTATAGTGAAGCCAGCAATTAATTAATTAATTAATTAATTA 420
 DB 361 CAATTTGGGACATGTCTATAGTGAAGCCAGCAATTAATTAATTAATTAATTAATTA 420
 QY 421 GCTGAAAAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 480
 DB 421 GCTGAAAAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 480
 QY 481 CTGACCGTTAAAGACAGAGACTTATTAATTAATTAATTAATTAATTAATTAATTA 540
 DB 481 CTGACCGTTAAAGACAGAGACTTATTAATTAATTAATTAATTAATTAATTAATTA 540
 QY 541 GGGAGAGCTTGAAGTCAAGCTTCAATTAATTAATTAATTAATTAATTAATTAATTA 600
 DB 541 GGGAGAGCTTGAAGTCAAGCTTCAATTAATTAATTAATTAATTAATTAATTAATTA 600
 QY 601 TTGAGAGAAATCTTACTGAGAGCTGCAATTAATTAATTAATTAATTAATTAATTA 660
 DB 601 TTGAGAGAAATCTTACTGAGAGCTGCAATTAATTAATTAATTAATTAATTAATTA 660
 QY 661 CAATTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 720
 DB 661 CAATTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 720
 QY 721 GTGACTGATCAAGCCAGAGAGGATGAGGATGAGGATGAGGATGAGGATGAGGAT 780
 DB 721 GTGACTGATCAAGCCAGAGAGGATGAGGATGAGGATGAGGATGAGGATGAGGAT 780
 QY 781 CTCTGA 786
 DB 781 CTCTGA 786

RESULT 6
 AAQ41506
 AAQ41506 standard; DNA; 840 BP.
 AC AAQ41506;
 XX
 XX 12-AUG-1993 (first entry)
 DT
 XX
 XX CD40-L DNA.
 DE
 XX
 XX Human; CD40-L; CD40; type II; membrane; polypeptide; extracellular;
 KM transmembrane; region; intracellular; soluble; activity; B cell;
 KM proliferation; induction; antibody; secretion; IgE; agonist;
 KM antagonist; binding assay; ss.
 OS Homo sapiens.
 XX
 XX
 PH Key Location/Qualifiers
 FT CDS 46..831
 FT /*tag= a
 PN W09308207-A.
 PD 29-APR-1993.
 XX
 PF 23-OCT-1992; 92WO-US08990.
 XX
 PR 25-OCT-1991; 91US-0783707.

PR 05-DEC-1991; 91US-0805723.

XX (IMMUNEX CORP.

XX Armitage RJ, Fanslow WC, Spriggs MK;

XX WPI, 1993-152417/18.

DR P-PSDB; AAR36701.

XX New cytokine CD40-L as CD40 agonist and antagonist - is used for
PT treating allergies, lupus, rheumatoid arthritis, diabetes mellitus
PT graft-versus-host disease and insulin-dependent diabetes mellitus
XX
XX Claim 1; Fig 2; 80pp; English.

XX This sequence encodes a human CD40-L polypeptide which binds to CD40.
CC CD40-L is a type II membrane polypeptide which has an extracellular
CC region at its C-terminus, a transmembrane region and an
CC intracellular region at its N-terminus. A soluble form of CD40-L
CC lacks the transmembrane domain. CD40-L activity is mediated by
CC binding with CD40 an induces B cell proliferation and induction of
CC antibody secretion, including IgE. Membrane bound CD40-L acts as a
CC CD40 agonist and soluble CD40-L acts as a CD40 antagonist. CD40-L
CC can be used in a binding assay to detect cells expressing CD40.

XX Sequence 840 BP; 266 A; 185 C; 175 G; 214 T; 0 other;

Query Match 97.2%; Score 763.6; DB 14; Length 840;

Best Local Similarity 98.2%; Pred. No. 1.1e-212;

Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGATAGAAAATACATACAGCACTCCCGAGATCCGTGGCACTGACCTTCAGCGAGC 60
DB 46 ATGATCGAAACATACAACTTCCTCCCGATCGCGGCACTGGACCTGCCATCAAGC 105
QY 61 ATGAAGATTTTATGATTTACTTACTCTGTTTCTTATCACCAGATGGGTCACGA 120
DB 106 ATGAAATTTTATGATTTACTTACTCTGTTTCTTATCACCAGATGGGTCACGA 165
QY 121 CTTTTCCTGATCTTCTATGAGGTTGACAGATGAGATGAGATCTTCAT 180
DB 166 CTTTTCCTGATCTTCTATGAGGTTGACAGATGAGATGAGATCTTCAT 225
QY 181 GAGATTTTGTATTCATGAAACGATACAGATGACACAGAGAAATCTTATCC 240
DB 226 GAGATTTTGTATTCATGAAACGATACAGATGACACAGAGAAATCTTATCC 285
QY 241 TTACTGAACCTGTGAGAGATTAAAGCCAGTTGAAAGCTTTGTGAAGATATATGTTA 300
DB 286 TTACTGAACCTGTGAGAGATTAAAGCCAGTTGAAAGCTTTGTGAAGATATATGTTA 345
QY 301 AACCAAGAGAGAGCAAGAAAGAAACGCTTTGAAATGCCAAAGGTATGAGATCCT 360
DB 346 AACCAAGAGAGAGCAAGAAAGAAACGCTTTGAAATGCCAAAGGTATGAGATCCT 405
QY 361 CAAATGGGCGACATGTCATTAAGTGAGGCCAGAGTAAGAAACAATCTGTGTTACATGG 420
DB 406 CAAATGGGCGACATGTCATTAAGTGAGGCCAGAGTAAGAAACAATCTGTGTTACATGG 465
QY 421 GGTGAAAAGGATATACACATGAGCAACATCTGTGTAACCTGGAAAATGGGAAAAG 480
DB 466 GGTGAAAAGGATATACACATGAGCAACATCTGTGTAACCTGGAAAATGGGAAAAG 525
QY 481 CTGACCGTTAAAGACAGAGACTCTATTATATCTATGATCCCAAGTACCTTGTTCAT 540
DB 526 CTGACCGTTAAAGACAGAGACTCTATTATATCTATGATCCCAAGTACCTTGTTCAT 585
QY 541 GGGGAGCTTCGAGTCAAGCTCCATTATATGACAGCTCTGCTTAAAGTCCCGGGTGA 600
DB 586 GGGGAGCTTCGAGTCAAGCTCCATTATATGACAGCTCTGCTTAAAGTCCCGGGTGA 645
QY 601 TTGAGAGAAATCTTACTGAGCTGCAATATCCCAAGTTCGCGCAAACTTTCGGGCA 660

DB 646 TTGAGAGAAATCTTACTGAGCTGCAATATCCCAAGTTCGCGCAAACTTTCGGGCA 705

QY 661 CAATCATTCCTGAGAGAGATTTGAAATGGCAACGAGGCTTCGTGTTGCAAT 720

DB 706 CAATCATTCCTGAGAGAGATTTGAAATGGCAACGAGGCTTCGTGTTGCAAT 765

QY 721 GTGACTGATCCAAAGCAAGTGAAGCCATGAGCACTGCTTCCTTTGGCTTACTCA 780

DB 766 GTGACTGATCCAAAGCAAGTGAAGCCATGAGCACTGCTTCCTTTGGCTTACTCA 825

QY 781 CTCTGA 786

DB 826 CTCTGA 831

RESULT 7

ID AA067123 standard; DNA; 840 BP.

XX AA067123;

AC 23-MAR-1995 (first entry)

XX CD40 ligand gene.

XX Probe; primer; PCR; amplify; polymerase chain reaction; detection;
KW mutation; CD40 ligand gene; IgM; ss.

XX Synthetic.

XX Key Location/Qualifiers

FT CDS 46..831

FT /tag= a

FT /product= CD40 ligand

XX MO9411796-A.

PD 04-AUG-1994.

XX 21-JAN-1994; 94WO-US00786.

XX 22-JAN-1993; 93US-0009258.

PR 20-JAN-1994; 94US-0184422.

XX (IMMUNEX CORP.

XX Armitage RJ, Fanslow WC, Renshaw BR;

PI Spriggs MK, Wilder MB;

DR WPI; 1994-264109/32.

DR P-PSDB; AAR57469.

XX Method for detecting mutation in CD 40 ligand gene - comprises

PT amplification of nucleic acid, and mutational analysis

XX Disclosure; Page 22-24; 38pp; English.

XX This sequence represents the CD40 ligand gene. Mutations within

CC this gene were identified by the method of the invention. The

CC method comprises isolating DNA from an individual and selectively

CC amplifying the isolated DNA derived from the CD40 ligand gene. The

CC amplification product is then analyzed to determine if there is a

CC mutation present and determining if a protein expressed from the

CC ligand gene will bind CD40. The detection of mutations in the CD40

CC ligand gene allows subsequent treatment of a syndrome resulting in

CC elevated levels of serum IgM and diminished levels of other Ig

CC isotypes, due to mutation in the CD40 ligand gene. ie. X-linked

CC hyperigm syndrome.

XX Sequence 840 BP; 266 A; 185 C; 175 G; 214 T; 0 other;

QY Query Match 97.2%; Score 763.6; DB 15; Length 840;

Best Local Similarity 98.2%; Pred. No. 1.1e-212;

Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGATGAAACATACAGCAACCTTCCCGAGTCCGTGCAACTGCACTTCCAGCAGC 60
 DB 46 ATGATGAAACATACAGCAACCTTCCCGAGTCCGTGCAACTGCACTTCCAGCAGC 105
 QY 61 ATGAAATTTTATGATTTTACTTACTGTTTCTTATACCCAGATGATGGTCCAGCA 120
 DB 106 ATGAAATTTTATGATTTTACTTACTGTTTCTTATACCCAGATGATGGTCCAGCA 165
 QY 121 CTTTGGCTGTGATCTTCAATAGAGTTGACAAAGTAAAGATGAAGAACTTCTCAT 180
 DB 166 CTTTGGCTGTGATCTTCAATAGAGTTGACAAAGTAAAGATGAAGAACTTCTCAT 225
 QY 181 GAAATTTTGTATTCATGAAACGATACAGATGCAACACAGAGAAATCTTATCC 240
 DB 226 GAAATTTTGTATTCATGAAACGATACAGATGCAACACAGAGAAATCTTATCC 285
 QY 241 TTACTGAACCTGTGAGAGATTTAAAGCCGTTTGAAGCTTGTGAGAGATATATGTTA 300
 DB 286 TTACTGAACCTGTGAGAGATTTAAAGCCGTTTGAAGCTTGTGAGAGATATATGTTA 345
 QY 301 AACAAAGAGAGACGAAAGAAAGAAACAGCTTGAATGCAAAAAGTGATCAGAACTCT 360
 DB 346 AACAAAGAGAGACGAAAGAAAGAAACAGCTTGAATGCAAAAAGTGATCAGAACTCT 405
 QY 361 CAAATTTGGGCACTGTCAATAGAGGCGAGCTAAACAAACATCTGTGTTACAGTGG 420
 DB 406 CAAATTTGGGCACTGTCAATAGAGGCGAGCTAAACAAACATCTGTGTTACAGTGG 465
 QY 421 GCTGAAAAAGATCTACACCATGACCAACCTTGTAAACCTGTAATGAGAAACAG 480
 DB 466 GCTGAAAAAGATCTACACCATGACCAACCTTGTAAACCTGTAATGAGAAACAG 525
 QY 481 CTGACCGTTTAAAGACAAAGACTCTATATATCTATGCCCCAAGTCACTTGTCTCAAT 540
 DB 526 CTGACCGTTTAAAGACAAAGACTCTATATATCTATGCCCCAAGTCACTTGTCTCAAT 585
 QY 541 CGGAAAGCTTCAAGTCAAGCTTCATTTATAGCCAGCTTGTGCTTAAGTCCCCCGTAGA 600
 DB 586 CGGAAAGCTTCAAGTCAAGCTTCATTTATAGCCAGCTTGTGCTTAAGTCCCCCGTAGA 645
 QY 601 TTGAGAGATCTTACTCAGAGCTGCAATACCAAGTTCCGCAAACTTGGGGGCA 660
 DB 646 TTGAGAGATCTTACTCAGAGCTGCAATACCAAGTTCCGCAAACTTGGGGGCA 705
 QY 661 CAATTCATTCATCTGGAGAGATTTGAAATTTGCAACAGAGTCTTGGTGTTCAT 720
 DB 706 CAATTCATTCATCTGGAGAGATTTGAAATTTGCAACAGAGTCTTGGTGTTCAT 765
 QY 721 GTGACTGATCCAAAGCAAGTGAAGGCACTGGCTTCACTGCTTGGCTTGAATCTCAA 780
 DB 766 GTGACTGATCCAAAGCAAGTGAAGGCACTGGCTTCACTGCTTGGCTTGAATCTCAA 825
 QY 781 CTCTGA 786
 DB 826 CTCTGA 831

RESULT 8

AA105763
 ID AA105763 standard; DNA; 840 BP.

XX AC AA105763;

XX D7 18-MAR-1996 (first entry)

XX DB Human CD40 ligand DNA.

XX KW High density membrane-bound CD40 ligand; B-lymphocyte; B-cell;
 KW differentiation; proliferation; baculovirus; Spodoptera frugiperda;
 KW Sf9; insect cell culture; tumour necrosis factor receptor; ss.

OS Homo sapiens.

PH Key Location/Qualifiers

FT CDS 22..807

FT /*tag= a

XX W09529935-A1.

XX 28-APR-1995; 95WO-US05448.

XX 28-APR-1994; 94US-0234580.

XX (BOEH) BOEHRINGER INGELHEIM PHARM INC.

XX Castle BE, Kenly M;

XX WPI: 1995-393038/50.

XX P-PSDB; AAR85486.

XX High density membrane bound CD40 ligand - for stimulating the

XX proliferation of B cells in vitro or in vivo, partic. for producing

XX differentiated cells

XX Disclosure; Fig 1; 74pp; English.

XX The nucleotide sequence given in AA105763 encodes a human high-density,

XX membrane-bound (hmb) CD40 ligand (AAR85486) that induces long-term

XX proliferation of B-cells in culture. These proliferating B-cells

XX can be induced to differentiate into antibody-prod. cells. The

XX nucleotide sequence is incorporated into a baculovirus vector that

XX is used to transfect Sf9 insect cells for prodn. of recombinant

XX hmbCD40.

XX Sequence 840 BP; 263 A; 182 C; 181 G; 214 T; 0 other;

XX Query Match 97.2%; Score 763.6; DB 16; Length 840;

XX Best Local Similarity 98.2%; Pred. No. 1..le-212;

XX Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGATGAAACATACAGCAACCTTCCCGAGTCCGTGCAACTGCACTTCCAGCAGC 60

DB 22 ATGATGAAACATACAGCAACCTTCCCGAGTCCGTGCAACTGCACTTCCAGCAGC 81

QY 61 ATGAAATTTTATGATTTTACTTACTGTTTCTTATACCCAGATGATGGTCCAGCA 120

DB 82 ATGAAATTTTATGATTTTACTTACTGTTTCTTATACCCAGATGATGGTCCAGCA 141

QY 121 CTTTGGCTGTGATCTTCAATAGAGTTGACAAAGTAAAGATGAAGAACTTCTCAT 180

DB 142 CTTTGGCTGTGATCTTCAATAGAGTTGACAAAGTAAAGATGAAGAACTTCTCAT 201

QY 181 GAAATTTTGTATTCATGAAACGATACAGAGTGCACACAGAGAAAGATCTTATCC 240

DB 202 GAAATTTTGTATTCATGAAACGATACAGAGTGCACACAGAGAAAGATCTTATCC 261

QY 241 TTACTGAACCTGTGAGAGATTTAAAGCCGTTTGAAGCTTGTGAGAGATATATGTTA 300

DB 262 TTACTGAACCTGTGAGAGATTTAAAGCCGTTTGAAGCTTGTGAGAGATATATGTTA 321

QY 301 AACAAAGAGAGACGAAAGAAAGAAACAGCTTGAATGCAAAAAGTGATCAGAACTCT 360

DB 322 AACAAAGAGAGACGAAAGAAAGAAACAGCTTGAATGCAAAAAGTGATCAGAACTCT 381

QY 361 CAAATTTGGGCACTGTCAATAGAGGCGAGCTAAACAAACATCTGTGTTACAGTGG 420

DB 382 CAAATTTGGGCACTGTCAATAGAGGCGAGCTAAACAAACATCTGTGTTACAGTGG 441

QY 421 GCTGAAAAAGATCTACACCATGACCAACCTTGTAAACCTGTAATGAGAAACAG 480

DB 442 GCTGAAAAAGATCTACACCATGACCAACCTTGTAAACCTGTAATGAGAAACAG 501

AAV61063,
 ID AAV61063 standard; DNA; 840 BP.
 AC AAV61063;
 XX
 XX
 XX 08-DEC-1998 (first entry)
 DE Human CD40 ligand encoding DNA sequence.
 XX
 KM Human; CD40 ligand; TNF receptor family; activated T cell;
 KM type 2 membrane glycoprotein; cell proliferation; differentiation;
 KM B cell; ds.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT 22..807
 FT CDS /tag= a
 XX /product= "CD40 ligand"
 XX
 PN US5817516-A.
 PD 06-OCT-1998.
 XX
 XX 28-APR-1995; 95US-0431055.
 PF
 XX 28-APR-1995; 95US-0431055.
 PR 28-APR-1994; 94US-0234580.
 XX
 PA (BOEH) BOEHRINGER INGELHEIM PHARM INC.
 PI Castle B, Kehy M;
 DR MPI; 1998-556393/47.
 DR P-PSDB; AAW71751.
 XX
 PT Increased proliferation of B cells in culture - by incubating them
 PT in the presence of membrane-bound CD40 ligand
 XX
 PS Example 1; Fig 1; 37pp; English.
 XX
 CC The present sequence encodes human CD40 ligand which is used in the
 CC method of the invention. The method has been developed for proliferating
 CC B cells to increase their number at least 100-fold. The method
 CC comprises: (a) providing high density, membrane bound CD40 ligand; and
 CC (b) culturing one or more B cells in the presence of this ligand. The
 CC culture results in a proliferation in the number of B cells of at least
 CC 100 fold. Also described is a method as above where the B cells are
 CC induced to differentiate into antibody-producing cells in the presence
 CC of one or more cytokines. The method can be used for stimulating B-cell
 CC proliferation in vitro or in vivo, e.g. for treating conditions in which
 CC B-cell proliferation and activation is suppressed. Eight rounds of
 CC division over six days can be achieved, corresponding to a 256-fold
 CC increase in cell numbers, which is a vast increase compared to previous
 CC culturing methods.
 CC
 XX
 SQ Sequence 840 BP; 263 A; 182 C; 181 G; 214 T; 0 other;
 XX
 Query Match 97.2%; Score 763.6; DB 19; Length 840;
 Best Local Similarity 98.2%; Pred. No. 1.1e-212;
 Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
 XX
 QY 1 ATGATGAAACATACAGCCACCTTCCCGCATCCGATCCGATGCACTTCAGCGAGC 60
 DB 22 ATGATCGAAACATACAGCCACCTTCCCGCATCCGATCGCGGCACTGAGCCCATCAGC 81
 QY 61 ATGAGATTTTATGATTTACTTACCTGTTTCTTATACCCAGATGATGGTCAAGA 120
 DB 82 ATGAAATTTTATGATTTACTTACCTGTTTCTTATACCCAGATGATGGTCAAGA 141
 QY 121 CTTTGTGCTGTATCTTATGAAAGTTGAGCAAGATGAAAGATGAAATCTTCAT 180
 DB 142 CTTTGTGCTGTATCTTATGAAAGTTGAGCAAGATGAAAGATGAAATCTTCAT 201

QY 181 GAAAGTTTGTATTTCTGAAAAAGCATACAGAGTGCACACAGAGAAAGATCTTATCC 240
 DB 202 GAAAGTTTGTATTTCTGAAAAAGCATACAGAGTGCACACAGAGAAAGATCTTATCC 261
 QY 241 TTACTGAACTGTGAGAGATTTAAAGCCAGTTTGAAGCTTTGGAAGTAAATGTTA 300
 DB 262 TTACTGAACTGTGAGAGATTTAAAGCCAGTTTGAAGCTTTGGAAGTAAATGTTA 321
 QY 301 AACCAAGAGAGACCAAGAAAGAAAGAAAGCTTTGAAATGCAAAAGGTGATCAATCT 360
 DB 322 AACCAAGAGAGACCAAGAAAGAAAGAAAGCTTTGAAATGCAAAAGGTGATCAATCT 381
 QY 361 CAAATTCGCGCATGTCTAATGAGGCGAGAGCAAGTAAACAAATCTGTGTTACATG 420
 DB 382 CAAATTCGCGCATGTCTAATGAGGCGAGAGCAAGTAAACAAATCTGTGTTACATG 441
 QY 421 GCTGAAAAAGATATCTACACCAATGAGCAACACTTGTAACTTGGAAAAATGGAAAC 480
 DB 442 GCTGAAAAAGATATCTACACCAATGAGCAACACTTGTAACTTGGAAAAATGGAAAC 501
 QY 481 CTGACCGTTAAAGACAAAGAGCTTATATCTATGCCCAAGTCACTTGTTCAT 540
 DB 502 CTGACCGTTAAAGACAAAGAGCTTATATCTATGCCCAAGTCACTTGTTCAT 561
 QY 541 CGGAGACCTTCAGATCAAGCTTCATTTATGCGAGCTTCTGCTAAAGTCCCGGTAGA 600
 DB 562 CGGAGACCTTCAGATCAAGCTTCATTTATGCGAGCTTCTGCTAAAGTCCCGGTAGA 621
 QY 601 TTGAGAGAAATCTTACTGAGAGTGCAGTAAATCCACAGTTCGCGCAACCTTGGCGG 660
 DB 622 TTGAGAGAAATCTTACTGAGAGTGCAGTAAATCCACAGTTCGCGCAACCTTGGCGG 681
 QY 661 CAATTCATTCATCTGGAGAGATTTTGAATTCGCAACAGGTGCTTGGTGTTCAT 720
 DB 682 CAATTCATTCATCTGGAGAGATTTTGAATTCGCAACAGGTGCTTGGTGTTCAT 741
 QY 721 GTGACTGATCAAGCAAGTGCATGAGCTTCAAGTCTTGGCTTAACTCAAA 780
 DB 742 GTGACTGATCAAGCAAGTGCATGAGCTTCAAGTCTTGGCTTAACTCAAA 801
 QY 781 CTCGGA 786
 DB 802 CTCGGA 807
 XX
 RESULT 11
 AA227525
 ID AA227525 standard; CDNA; 840 BP.
 XX
 XX AA227525;
 AC
 XX 13-DEC-1999 (first entry)
 DT
 XX
 DE Human CD40-L coding sequence.
 XX
 KM CD40-L; CD40 receptor ligand; anti-human CD40-L monoclonal antibody;
 KM binding inhibitor; trimelic CD40-L; anti-immunoglobulin M;
 KM peripheral blood B cell; proliferation inhibitor; ss.
 XX
 OS Homo sapiens.
 XX
 XX US5961974-A.
 XX
 PD 05-OCT-1999.
 XX
 XX
 PF 24-MAY-1994; 94US-0249189.
 XX
 XX 25-OCT-1991; 91US-0783707.
 PR 05-DEC-1991; 91US-0805723.
 PR 23-OCT-1992; 92US-0969703.
 XX
 PA (IMMUNEX CORP.

XX Spriggs MK, Fanslow WC, Armitage RJ;
 XX WPI; 1999-579604/49.
 DR P-PSDB; AAY39938.
 XX
 XX Anti-human CD40-Ligand monoclonal antibodies -
 PS
 XX Disclosure; Fig 2; 59pp; English.
 XX
 CC This sequence encodes the human CD40 receptor ligand (CD40-L). The
 CC invention relates to anti-human CD40-L monoclonal antibodies M90 secreted
 CC by hybridoma hCD40L-M90 (ATCC HB-12053) and M91 secreted by hybridoma
 CC hCD40L-M91 (ATCC HB-12056). M90 and M91 inhibit CD40-L binding to CD40
 CC and the ability of trimeric CD40-L and anti-Immunoglobulin M to induce
 CC proliferation of peripheral blood B cells.
 XX
 SQ Sequence 840 BP; 266 A; 185 C; 175 G; 214 T; 0 other;

Query Match 97.2%; Score 763.6; DB 20; Length 840;
 Best Local Similarity 98.2%; Pred. No. 1.1e-212;
 Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGATAGAAACATACACGCACTTCCCGAGATCCGTGGCACTGGACTTCACGAGC 60
 DB 46 ATGATCGAAACATACACCAACTTCCCGAGATCCGTGGCACTGGACTTCACGAGC 105
 QY 61 ATGAAGATTTTATGATTTTATCTTCTTATCCACCGAGATGGTCCAGCA 120
 DB 106 ATGAAATTTTATGATTTTATCTTCTTATCCACCGAGATGGTCCAGCA 165
 QY 121 CTTTTCGTGTGATCTTATGAGAGTTGACAGATGAGATGAGAGATCTTCAT 180
 DB 166 CTTTTCGTGTGATCTTATGAGAGTTGACAGATGAGATGAGAGATCTTCAT 225
 QY 181 GAAGATTTGATTTATGAGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 240
 DB 226 GAAGATTTGATTTATGAGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 285
 QY 241 TTTACTGAACTGTGAGAGATTTAAAGCAGTTTGAAGCTTTGTGAAGATTAATGTTA 300
 DB 286 TTTACTGAACTGTGAGAGATTTAAAGCAGTTTGAAGCTTTGTGAAGATTAATGTTA 345
 QY 301 AACAAAG 360
 DB 346 AACAAAG 405
 QY 361 CAAATTCGGCAGATGTCATTAAGTGAAGCCAGCACTAAACACATCTGTGTACAGTGG 420
 DB 406 CAAATTCGGCAGATGTCATTAAGTGAAGCCAGCACTAAACACATCTGTGTACAGTGG 465
 QY 421 GCTGAAAAAGATACATACCACTGAGCAACAATGTTGATCCCTGGAAAAATGGGAAACG 480
 DB 466 GCTGAAAAAGATACATACCACTGAGCAACAATGTTGATCCCTGGAAAAATGGGAAACG 525
 QY 481 CTGACCGTTAAAAAGACAGAGACTTATTAATATGATCCCAAGTCCACTTGTTCAT 540
 DB 526 CTGACCGTTAAAAAGACAGAGACTTATTAATATGATCCCAAGTCCACTTGTTCAT 585
 QY 541 GGGGAGCTTGGAGTCAAGCTTCACTTATGAGAGCTGTGCTTAAGTCCCGGGTGA 600
 DB 586 GGGGAGCTTGGAGTCAAGCTTCACTTATGAGAGCTGTGCTTAAGTCCCGGGTGA 645
 QY 601 TTGAGAGAAATCTTACTGAGAGCTGCAAAATACCAAGTTCGCGCAAACTTGGCGGCA 660
 DB 646 TTGAGAGAAATCTTACTGAGAGCTGCAAAATACCAAGTTCGCGCAAACTTGGCGGCA 705
 QY 661 CAATCCATGACTTGGAGAGATTTGAATGCAACAGAGTCTGGGCTTTGTCAT 720
 DB 706 CAATCCATGACTTGGAGAGATTTGAATGCAACAGAGTCTGGGCTTTGTCAT 765
 QY 721 GTGACTGATCAAGCCAAAGTGAAGCATGAGCATGAGCTTGTGCTTACTCAAA 780

DB 766 GTGACTGATCAAGCCAAAGTGAAGCATGAGCATGAGCTTGTGCTTACTCAAA 825
 QY 781 CTCTGA 786
 DB 826 CTCTGA 831

RESULT 12
 AAF55539
 ID AAF55539 standard; DNA; 879 BP.

AC AAF55539;

DT 29-MAY-2001 (first entry)

DE Nucleotide sequence of human gp39 protein, a CD40 ligand.

XX gp39; CD40 ligand; osteoblast cell death; apoptosis; bone loss;

KW osteoporosis; osteonecrosis; inflammatory arthritis; estrogen loss;

KW ovariectomy; hysterectomy; lupus nephritis; Takayasu's arteritis;

KW Wegener's granulomatosis; nephritis; myositis; scleroderma;

KW thrombocytopenia; asthma; lung disease; cancer; ss.

XX Homo sapiens.

OS 08-MAR-2001.

PD 24-AUG-2000; 2000WO-US23276.

PF 27-AUG-1999; 98US-0151250.

PR (TEXA) UNIV TEXAS SYSTEM.

PI Ahuja SS, Bonewald LF;

XX WPI; 2001-169007/17.

DR P-PSDB; AAB67612.

PT CD40 agonist containing composition, used to reduce bone cell death or

PT apoptosis associated with osteoporosis, osteonecrosis and inflammatory

PT arthritis -

PS Disclosure; Page 113; 118pp; English.

XX The present sequence encodes a gp39 protein. It is a CD40 ligand.

CC CD40 ligands are used for reducing osteoblast cell death or apoptosis,

CC at risk of, or undergoing, bone loss. The bone loss is associated with

CC osteoporosis, osteonecrosis, inflammatory arthritis, post-menopausal

CC osteoporosis, estrogen loss due to ovariectomy, total hysterectomy,

CC lupus nephritis, Takayasu's arteritis, Wegener's granulomatosis,

CC anti-idiopathic autoimmune thrombocytopenia, myositis, scleroderma,

CC idiopathic autoimmune thrombocytopenia, asthma, a chronic obstructive

CC lung disease, nephrotic/nephritic syndrome, or cancer. They may also be

CC used to treat or prevent bone loss in a subject undergoing, or scheduled

CC for, an organ or bone marrow transplant.

XX Sequence 879 BP; 274 A; 193 C; 190 G; 222 T; 0 other;

QY Query Match 97.2%; Score 763.6; DB 22; Length 879;
 Best Local Similarity 98.2%; Pred. No. 1.2e-212;
 Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

61 ATGAGATTTTGTATGTAATTAATTAATTTTCTTATCAACCAATGATTTGGTCAAC 120
 82 ATGAAATTTTATGATTAATTAATTAATTTTCTTATCAACCAATGATTTGGTCAAC 141
 121 CTTTGTCTGTATCTTATGATTAATTAATTTTCTTATCAACCAATGATTTGGTCAAC 180
 142 CTTTGTCTGTATCTTATGATTAATTAATTTTCTTATCAACCAATGATTTGGTCAAC 201
 181 GAAGATTTTGTATGTAATTAATTAATTTTCTTATCAACCAATGATTTGGTCAAC 240
 202 GAAGATTTTGTATGTAATTAATTAATTTTCTTATCAACCAATGATTTGGTCAAC 261
 241 TTAATGATTTGTATGTAATTAATTAATTTTCTTATCAACCAATGATTTGGTCAAC 300
 262 TTAATGATTTGTATGTAATTAATTAATTTTCTTATCAACCAATGATTTGGTCAAC 321
 301 AACAAAG 360
 322 AACAAAG 381
 361 CAAATTTGGGCAATGTCATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
 382 CAAATTTGGGCAATGTCATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 441
 421 GCTGAAAG 480
 442 GCTGAAAG 501
 481 CTGACCGTTTAAAG 540
 502 CTGACCGTTTAAAG 561
 541 CGGAAAG 600
 562 CGGAAAG 621
 601 TTGAG 660
 622 TTGAG 681
 661 CAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 720
 682 CAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 741
 721 GTGACTGATCAAGCCAAAGTGAAGCCAAAGTGAAGCCAAAGTGAAGCCAAAGTGA 780
 742 GTGACTGATCAAGCCAAAGTGAAGCCAAAGTGAAGCCAAAGTGAAGCCAAAGTGA 801
 781 CTCTGA 786
 802 CTCTGA 807

RESULT 13
 ID AAA51745 standard; cDNA; 1816 BP.
 AC AAA51745;
 DT 31-OCT-2000 (first entry)
 DE Human CD40 ligand cDNA.
 KW CD40 ligand; CD40; T cell; T cell receptor; rearrangement; maturation;
 KW anti-inflammatory; stress-induced; immunosuppressive; anti-thyroid;
 KW anti-inflammatory; anti-diabetic; anti-rheumatic; anti-anemic;
 KW dermatological; cytostatic; ss.
 OS Homo sapiens.
 FX Homo sapiens.
 FH Key Location/Qualifiers

FT CDS 40..825
 FT /*tag= a
 FT /product= Human_CD40_ligand
 FN MO200039283-A1.
 XX 06-JUL-2000.
 XX 22-DEC-1999; 99MO-US30930.
 XX 29-DEC-1998; 98US-0114106.
 XX (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.
 XX Newell MK, Wagner D, Newell E;
 DR MPI; 2000-452387/39.
 DR P-PSDB; AAY96993.
 PT Inducing T cell receptor gene rearrangement for treating autoimmune
 PS diseases comprises contacting T cells with a CD40-binding agent
 PS Disclosure; Page 46; 50pp; English.
 CC CD40 engagement on T cells can be used to induce T cell receptor
 CC rearrangement and enhance T cell affinity for a particular antigen. CD40
 CC engagement can be brought about by contacting CD40 with a CD40-binding
 CC agent, e.g. human CD40 ligand. The CD40-binding agents can also be used
 CC in methods for promoting T cell maturation, inhibiting T cell receptor
 CC rearrangement, inhibiting environmental stress-induced cell death
 CC altering the specificity of a T cell towards an antigen, inducing T cell
 CC reactivity towards an antigen or enhancing environmental stress-induced
 CC cell death (all claimed). T cell affinity maturation towards a specific
 CC antigen can be inhibited, especially for a self-antigen in an autoimmune
 CC disease, which includes rheumatoid arthritis, uveitis, insulin-dependent
 CC diabetes mellitus, hemolytic anaemias, rheumatic fever, Crohn's disease,
 CC Guillain-Barre syndrome, psoriasis, thyroiditis, Grave's disease,
 CC myasthenia gravis, glomerulonephritis, autoimmune hepatitis or systemic
 CC lupus erythematosus. Inducing environmental stress-induced T cell death
 CC is carried out in a cancerous T cell or a self-reactive T cell where the
 CC environmental stress is a chemotherapeutic agent (claimed).
 CC Sequence 1816 BP; 520 A; 461 C; 343 G; 492 T; 0 other;
 SQ
 Query Match 97.2%; Score 763.6; DB 21; Length 1816;
 Best Local Similarity 98.2%; Pred. No. 1.6e-212;
 Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
 QY 1 ATGATTAAG 60
 DB 40 ATGATTAAG 99
 QY 61 ATGATTAAG 120
 DB 100 ATGATTAAG 159
 QY 121 CTTTGTCTGTATCTTATGATTAATTAATTTTCTTATCAACCAATGATTTGGTCAAC 180
 DB 160 CTTTGTCTGTATCTTATGATTAATTAATTTTCTTATCAACCAATGATTTGGTCAAC 219
 QY 181 GAAGATTTTGTATGTAATTAATTAATTTTCTTATCAACCAATGATTTGGTCAAC 240
 DB 220 GAAGATTTTGTATGTAATTAATTAATTTTCTTATCAACCAATGATTTGGTCAAC 279
 QY 241 TTAATGATTTGTATGTAATTAATTAATTTTCTTATCAACCAATGATTTGGTCAAC 300
 DB 280 TTAATGATTTGTATGTAATTAATTAATTTTCTTATCAACCAATGATTTGGTCAAC 339
 QY 301 AACAAAG 360
 DB 340 AACAAAG 399
 QY 361 CAAATTTGGGCAATGTCATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420

Db 400 CAATTCGGGCACTGTCTATTAAGTAGGCGCCAGATTAAGATCTGTGTACAGTGG 459
Qy 421 GCTGAAAAAGGATCTACACATAGACAACTTGTGTAACCTTGGAAAAATGGAAACAG 480
Db 460 GCTGAAAAAGGATCTACACATAGACAACTTGTGTAACCTTGGAAAAATGGAAACAG 519
Qy 481 CTGACCGTTTAAAGACAGAGCTATATATATCTATGCGCAAGTCACTTGTGTCCAAAT 540
Db 520 CTGACCGTTTAAAGACAGAGCTATATATATCTATGCGCAAGTCACTTGTGTCCAAAT 579
Qy 541 CGGGAAGCTTTCAGATCAAGCTTCTTATATAGCCAGCTTCCCTTAAAGTCCCGGCTGA 600
Db 580 CGGGAAGCTTTCAGATCAAGCTTCTTATATAGCCAGCTTCTTAAAGTCCCGGCTGA 639
Qy 601 TTGAGAGAACTTCTATCTAGAGCTGCAATATCCCAAGTTCGCGCAAACTTGGCGGCA 660
Db 640 TTGAGAGAACTTCTATCTAGAGCTGCAATATCCCAAGTTCGCGCAAACTTGGCGGCA 699
Qy 661 CAATCCATTCATCTGGAGAGAGTATTTGAATTGCAACGAGTGGCTGGTGTTCAT 720
Db 700 CAATCCATTCATCTGGAGAGAGTATTTGAATTGCAACGAGTGGCTGGTGTTCAT 759
Qy 721 GTGACTGATCCAAAGCCAGTGGCCATGCGCACTGCTTCACTTGTGTCTTACTCAA 780
Db 760 GTGACTGATCCAAAGCCAGTGGCCATGCGCACTGCTTCACTTGTGTCTTACTCAA 819
Qy 781 CTCTGA 786
Db 820 CTCTGA 825

RESULT 14
AAS86571
ID AAS86571 standard; cDNA, 1816 BP.
XX
AC AAS86571;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #2375.
XX
XX Human: chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
XX 23-AUG-2000; 2000US-0649167.
XX
XX (HYSE-) HXSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI: 2001-639362/73.
XX
XX F-PSDB; ABG22384.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnosis, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity -
XX
XX Clajm 1; SEQ ID No 22375; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome

CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissues, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS9564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from Wipro
CC at ftp.wipro.int/pub/published_pcr_sequences.
XX
SQ Sequence 1816 BP; 520 A; 461 C; 343 G; 492 T; 0 other;
Query Match 97.2%; Score 763.6; DB 23; Length 1816;
Best Local Similarity 98.2%; Pred. No. 1.e-212;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
Qy 1 ATGATGAAACATACAGCAACCTTCCCGAGATCCGTGCAACTGACCTTCAGCGAGC 60
Db 40 ATGATGAAACATACAGCAACCTTCCCGAGATCCGTGCAACTGACCTTCAGCGAGC 99
Qy 61 ATGAAATTTTATGATATTTACTTACTGTTTCTTATCAACGAGTATGGTGCAGCA 120
Db 100 ATGAAATTTTATGATATTTACTTACTGTTTCTTATCAACGAGTATGGTGCAGCA 159
Qy 121 CTTTTCCTGTATCTTCTATAGAGGTTTGAAGATGATGAAAGATCTTCAT 180
Db 160 CTTTTCCTGTATCTTCTATAGAGGTTTGAAGATGATGAAAGATCTTCAT 219
Qy 181 GAAATTTTGTATCATGAAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
Db 220 GAAATTTTGTATCATGAAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 279
Qy 241 TTACTGAACTGTGAGAGATTTAAAGCCAGTTTGAAGCTTTGTGAAGATATATGTTA 300
Db 280 TTACTGAACTGTGAGAGATTTAAAGCCAGTTTGAAGCTTTGTGAAGATATATGTTA 339
Qy 301 AACAAAG 360
Db 340 AACAAAG 399
Qy 361 CAATTCGGGCACTGTCTATTAAGTAGGCGCCAGATTAAGATCTGTGTACAGTGG 420
Db 400 CAATTCGGGCACTGTCTATTAAGTAGGCGCCAGATTAAGATCTGTGTACAGTGG 459
Qy 421 GCTGAAAAAGGATCTACACATAGACAACTTGTGTAACCTTGGAAAAATGGAAACAG 480
Db 460 GCTGAAAAAGGATCTACACATAGACAACTTGTGTAACCTTGGAAAAATGGAAACAG 519
Qy 481 CTGACCGTTTAAAGACAGAGCTATATATATCTATGCGCAAGTCACTTGTGTCCAAAT 540
Db 520 CTGACCGTTTAAAGACAGAGCTATATATATCTATGCGCAAGTCACTTGTGTCCAAAT 579
Qy 541 CGGGAAGCTTTCAGATCAAGCTTCTTATATAGCCAGCTTCCCTTAAAGTCCCGGCTGA 600
Db 580 CGGGAAGCTTTCAGATCAAGCTTCTTATATAGCCAGCTTCCCTTAAAGTCCCGGCTGA 639
Qy 601 TTGAGAGAACTTCTATCTAGAGCTGCAATATCCCAAGTTCGCGCAAACTTGGCGGCA 660
Db 640 TTGAGAGAACTTCTATCTAGAGCTGCAATATCCCAAGTTCGCGCAAACTTGGCGGCA 699
Qy 661 CAATCCATTCATCTGGAGAGAGTATTTGAATTGCAACGAGTGGCTGGTGTTCAT 720
Db 700 CAATCCATTCATCTGGAGAGAGTATTTGAATTGCAACGAGTGGCTGGTGTTCAT 759

Qy 721 GTGACTGATCCAGCAAGTGAAGCATGCACTGGCTTCACTCTTGGCTTACTCAAA 780
 Db 760 GTGACTGATCCAGCAAGTGAAGCATGCACTGGCTTCACTCTTGGCTTACTCAAA 819
 Qy 781 CTCTGA 786
 Db 820 CTCTGA 825

RESULT 15

AA057984
 ID AA057984 standard; DNA; 840 BP.

XX AA057984;

DT 20-AUG-1994 (first entry)

XX Genomic sequence of human gp39.

XX gp39; T-cell antigen; CD40 ligand; B-cell proliferation;

XX B-cell differentiation; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX FT CDS 22..807

XX /*tag= a

XX EP85943-A.

XX PD 09-MAR-1994.

XX EF 03-SEP-1993; 93EP-0114153.

XX PR 04-SEP-1992; 92US-0940605.

XX PA (BRIM) BRISTOL-MYERS SQUIBB CO.

XX PI Aruffo AA, Hollenbaugh D, Ledbetter JA, Aruffo A;

XX DR WPI; 1994-076264/10.

XX DR P-PSDB; AAR59548.

XX XX New nucleic acid encoding human gp39 T cell antigen - which is a

XX PT ligand for the CD40 receptor, causing proliferation and

XX PT differentiation of B cells and some cancer cells

XX PS Claim 1; Fig 1; 3pp; English.

XX CC The complete nucleic acid sequence of human gp39 (hgp39) protein

XX CC (corresp. to cDNA) and the complete AA sequence of hgp39 are

XX CC presented in AA057984 and AAR49548 respectively and contd. in plasmid

XX CC CDW8-hgp39, deposited with the ATCC as E. coli; CDW8 MC1061/p3-hgp39

XX CC and assigned accession No. 69050. The human T cell antigen gp39 is a

XX CC ligand for the CD40 receptor. Soluble gp39 may be produced using the

XX CC expression vector CD8-gp39.

XX SQ Sequence 840 BP; 263 A; 180 C; 183 G; 214 T; 0 other;

XX Query Match 96.9%; Score 762; DB 15; Length 840;

XX Best Local Similarity 98.1%; Pred. No. 3.3e-212;

XX Matches 771; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1 ATGATAGAAACATACAGCCACCTTCCCGATCCGTCGCACTGACCTTCCAGCAGC 60

Db 22 ATGATAGAAACATACAGCCACCTTCCCGATCCGTCGCACTGACCTTCCAGCAGC 81

Qy 61 ATGAAGATTTTATGATTTACTTACTGTTTTTCTTATCACCAGATGATGGGTGACA 120

Db 82 ATGAAGATTTTATGATTTACTTACTGTTTTTCTTATCACCAGATGATGGGTGACA 141

Qy 121 CTTTGGCTGTATCTTCAATAGAGTTTGACAGATGATGAAGATCTTCAAT 180

Db 142 CTTTGGCTGTATCTTCAATAGAGTTTGACAGATGATGAAGATCTTCAAT 201
 Qy 181 GAAAGTTTGTATTTATCATGAAAACGATACAGATGTCACACAGAGAAATCTTATTC 240
 Db 202 GAAAGTTTGTATTTATCATGAAAACGATACAGATGTCACACAGAGAAATCTTATTC 261
 Qy 241 TTACTGAACTGTGAGAGATTTAAAGCACTTTGAGAGATTAATATGTTA 300
 Db 262 TTACTGAACTGTGAGAGATTTAAAGCACTTTGAGAGATTAATATGTTA 321
 Qy 301 AACAAAGAGAGACGAAAGAAAGAAACAGCTTTGAAATGCAAAAGGTATCAAAATCCT 360
 Db 322 AACAAAGAGAGACGAAAGAAAGAAACAGCTTTGAAATGCAAAAGGTATCAAAATCCT 381
 Qy 361 CAAATTTGGGACATGTCATTAAGTGAAGCCAGCAATTAACATCTGTGTACAGTGG 420
 Db 382 CAAATTTGGGACATGTCATTAAGTGAAGCCAGCAATTAACATCTGTGTACAGTGG 441
 Qy 421 GCTGAAAAAGATTTACTACACCTTGAAGCAACATTTGTAACCTTGGAAAAATGGAAACG 480
 Db 442 GCTGAAAAAGATTTACTACACCTTGAAGCAACATTTGTAACCTTGGAAAAATGGAAACG 501
 Qy 481 CTGACCGTTAAAGACAGACATCTATTATATCTATGCCAAGTCACTTCTGTCAAT 540
 Db 502 CTGACCGTTAAAGACAGACATCTATTATATCTATGCCAAGTCACTTCTGTCAAT 561
 Qy 541 CGGGAAGCTTCAGTCAAGCTTCATTTATGACAGCTTCTGCTTAAAGTCCCCGGTACA 600
 Db 562 CGGGAAGCTTCAGTCAAGCTTCATTTATGACAGCTTCTGCTTAAAGTCCCCGGTACA 621
 Qy 601 TTGAGAGAAATCTTACTCAGAGCTGCAATATACCAAGTCCGCAAACTTGGCGGCA 660
 Db 622 TTGAGAGAAATCTTACTCAGAGCTGCAATATACCAAGTCCGCAAACTTGGCGGCA 681
 Qy 661 CAATCATTCATCTTGGAGAGATTTTGAATTCGAAACAGAGTCTTGGTGTGCAAT 720
 Db 682 CAATCATTCATCTTGGAGAGATTTTGAATTCGAAACAGAGTCTTGGTGTGCAAT 741
 Qy 721 GTGACTGATCCAGCAAGTGAAGCATGCACTGGCTTCACTCTTGGCTTACTCAAA 780
 Db 742 GTGACTGATCCAGCAAGTGAAGCATGCACTGGCTTCACTCTTGGCTTACTCAAA 801
 Qy 781 CTCTGA 786
 Db 802 CTCTGA 807

Search completed: March 8, 2003, 22:12:52
 Job time : 167.215 secs

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OM nucleic - nucleic search, using sw model

Run on: March 9, 2003, 02:11:48 ; Search time 54.2612 Seconds
(without alignments)
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Title: US-08-982-272-6
Perfect score: 786
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 478924 seqs, 33395956 residues

Total number of hits satisfying chosen parameters: 957848

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	582.8	74.1	1250	9	US-10-182-093-1
2	135	17.2	2395	9	US-09-875-453-9
3	42.4	5.4	1352	9	US-09-938-8428-3149
4	42.4	5.4	1352	9	US-09-938-8428-5264
5	39.2	5.0	2000	9	US-09-938-8428-1756
6	38.6	4.9	424	10	US-09-960-352-11218
7	37.6	4.8	418	10	US-09-960-352-2222
8	35.8	4.6	10351	10	US-09-874-470-5
9	35	4.5	501	10	US-09-783-590-406
10	35	4.5	640681	10	US-09-790-988-1
11	34	4.3	451	10	US-09-960-352-10262
12	34	4.3	1073	9	US-10-063-547-95
13	34	4.3	1073	9	US-10-174-590-305
14	34	4.3	1073	9	US-10-176-758-305
15	34	4.3	1073	9	US-10-063-616-95
16	34	4.3	1073	9	US-10-175-737-305
17	34	4.3	1073	9	US-10-063-502-95
18	34	4.3	1073	9	US-10-173-706-305
19	34	4.3	1073	9	US-10-175-738-305

20	34	4.3	1073	9	US-10-175-752-305	Sequence 305, App
21	34	4.3	1073	9	US-10-176-482-305	Sequence 305, App
22	34	4.3	1073	9	US-10-176-757-305	Sequence 305, App
23	34	4.3	1073	9	US-10-176-913-305	Sequence 305, App
24	34	4.3	1073	9	US-10-180-552-305	Sequence 305, App
25	34	4.3	1073	9	US-10-180-557-305	Sequence 305, App
26	34	4.3	1073	9	US-10-173-700-305	Sequence 305, App
27	34	4.3	1073	9	US-10-174-572-305	Sequence 305, App
28	34	4.3	1073	9	US-10-174-579-305	Sequence 305, App
29	34	4.3	1073	9	US-10-174-582-305	Sequence 305, App
30	34	4.3	1073	9	US-10-174-588-305	Sequence 305, App
31	34	4.3	1073	9	US-10-175-739-305	Sequence 305, App
32	34	4.3	1073	9	US-10-175-740-305	Sequence 305, App
33	34	4.3	1073	9	US-10-175-743-305	Sequence 305, App
34	34	4.3	1073	9	US-10-176-488-305	Sequence 305, App
35	34	4.3	1073	9	US-10-176-492-305	Sequence 305, App
36	34	4.3	1073	9	US-10-176-747-305	Sequence 305, App
37	34	4.3	1073	9	US-10-176-750-305	Sequence 305, App
38	34	4.3	1073	9	US-10-176-985-305	Sequence 305, App
39	34	4.3	1073	9	US-10-176-987-305	Sequence 305, App
40	34	4.3	1073	9	US-10-176-991-305	Sequence 305, App
41	34	4.3	1073	9	US-10-176-992-305	Sequence 305, App
42	34	4.3	1073	9	US-10-176-993-305	Sequence 305, App
43	34	4.3	1073	9	US-10-184-658-305	Sequence 305, App
44	34	4.3	1073	9	US-10-227-884-99	Sequence 99, Appl
45	34	4.3	1073	9	US-10-173-695-305	Sequence 305, Appl

ALIGNMENTS

RESULT 1
US-10-182-093-1
; Sequence 1, Application US/10182093
; Publication No. US20030021808A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as represented by
; APPLICANT: The Secretary, Department of Health and Human Services,
; APPLICANT: c/o Center for Disease Control and Prevention
; APPLICANT: Tripp, Ralph
; APPLICANT: Jones, Les
; APPLICANT: Anderson, Larry
; APPLICANT: Brown, Michael
; TITLE OF INVENTION: Cyt40 ligand Adjuvant for Respiratory
; TITLE OF INVENTION: Syncytial Virus
; FILE REFERENCE: 14114.0301U2
; CURRENT APPLICATION NUMBER: US/10/182, 093
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/179, 905
; PRIOR FILING DATE: 2000-02-02
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1250
; TYPE: DNA
; ORGANISM: Murine
US-10-182-093-1
Query Match 74.1%; Score 582.8; DB 9; Length 1250;
Best Local Similarity 84.7%; Pred. No. 1.2e-153;
Matches 666; Conservative 0; Mismatches 117; Indels 3; Gaps 1;
QY 1 ATGATGAACATACAGCACTTCCCGAGTCGTCGCACTGACCTTCACGAGC 60
DB 13 ATGATGAACATACAGCACTTCCCGAGTCGTCGCACTGACCTTCACGAGC 72
QY 61 ATGGAAGTTTATGATTTCTTACCTGTTTCTTATCACCCGAGTGGGTCACCA 120
DB 73 ATGAAGATTTTATGATTTCTTACCTGTTTCTTATCACCCGAGTGGGTCACCA 132
QY 121 CTTTTCCTGTATCTTATGATGAGGTTGACCAAGATGAGTGAAGATGATTCAT 180
DB 133 CTTTTCCTGTATCTTATGATGAGGTTGACCAAGATGAGTGAAGATGATTCAT 192

		4.9%;	Score 38.6;	DB 10;	Length 424;	
		Best Local Similarity	47.9%;	Ped. No. 0.32;		
		Matches 145;	Conservative	0;	Mismatches 154;	Indels 4; Gaps 1;
Oy	68	TTTTTANGATTTACTTAACGTCTTTTCTTATCACCCAGTAGTGCGTCAGACCTTTTG	127			
Db	30	TT	89			
Oy	128	CTGTGATCTCATAGAGGTGGACAAGATAGAGATGAAGAATCTTCATGAGATT	187			
Db	90	TTTTTTTTTTTTAAATATAAATAATATAAATAAATAAATAAATAAATAAATAAATAA	149			
Oy	188	TGTGATTCAGAAAACGATCAAGATGCACACAGAGAAAGATCCTTATCCTACGA	247			
Db	150	TAAAAAATAAAAAAAAAATTAAAAATTAATTAATTTTAAATTTTGTGTTAA	209			
Oy	248	ACTGT---GAGAGATTAAACCAGTTTGAAAGCTTTGTGAAGATATATGTTAAC	303			
Db	210	AATATATAAAAAAAAAATATTATAGAAATTTTAAAAAATAAATAAAGAGATTTTAAAGA	269			
Oy	304	AAAGGAGACGAGAAAGAAAACAGCTTTGAATGCAAAAAGGTGATCGATCCTCAA	363			
Db	270	AAAAAAAAAATGAATTTTBAABAAAGATTAAAGTTATTTAAAAAAGATTTAAAA	329			
Oy	364	ATT 366				
Db	330	ATT 332				

RESULT 7

US-09-960-352-2222
; Sequence 2222, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511, 006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; NUMBER OF SEQ ID NOS: 2001-09-24
; SEQ ID NO 2222
; LENGTH: 418
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 10-LIB3058-040-Q1-K1-CS
US-09-960-352-2222

Query Match 4.8%; Score 37.6; DB 10; Length 418;
Best Local Similarity 47.5%; Pred. No. 0.61;
Matches 112; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

QY 238 TCCTTACTGAACCTGAGAGATTAAAGCCAGTTTGAAAGCTTTGAAAGATATATG 297
DB 6 TCTATCTTTACAGTGTGTAATAAATTGGAGTGTGTTCCAGAAAGCAGATA 65
QY 298 TTAACAAG 357
DB 66 CTCAAGTATGTGATCCAACTTACAGAAACAGAGAGAACTTCAGAAAGCAATCAGAG 125
QY 358 CCTCAATTCGGGCACATCTCATAGTGGCCAGCAGATTAACAACATCTGTATAG 417
DB 126 CAGTATCAG 185
QY 418 TGGCTGAAAAAGATCTACACCATGAGCAACATCTGTACCTGGAATG 473
DB 186 CAGAAAAATCTTGACGTGAGCAAAAAAGAACAAAGAGACACCTGGAATG 241

RESULT 8

US-09-874-470-5/C
; Sequence 5, Application US/09874470
; Patent No. US20020071842A1
; GENERAL INFORMATION:
; APPLICANT: Gumperz, Jenny E
; APPLICANT: Brenner, Michael B
; APPLICANT: Behar, Samuel M
; TITLE OF INVENTION: Soluble CD1 Compositions and Uses Thereof
; FILE REFERENCE: B00801/70212
; CURRENT APPLICATION NUMBER: US/09/874,470
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/209,416
; PRIOR FILING DATE: 2000-06-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 10351
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-874-470-5

Query Match 4.6%; Score 35.8; DB 10; Length 10351;
Best Local Similarity 47.5%; Pred. No. 9;
Matches 106; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

QY 164 ATGAAGAATCTTCATGAAGTTTGTATTCATGAAGCAATCAGAGATGCAACAG 223
DB 6762 ATGAAAGAAATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6703

QY 224 GAGAAAGATCTTATCTTACTGACCTGAGAGAGATTAAAGCCAGTTTGAAAGCTTTG 283
DB 6702 GAAAAATTTCTGGGAAATCATATGAGAGCTAGAGTTTACTGGCAAGGAGAAAAAT 6643
QY 284 TGAAGATATAATGTTTAAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 343
DB 6642 TGTGGAG 6583
QY 344 AAGGTATGAGATCTTCAATTCGCGGACATGTCATTAAGTGA 386
DB 6582 GATGGAGAGCTATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6540

RESULT 9

US-09-783-590-406/C
; Sequence 406, Application US/09783590
; Patent No. US20020110850A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Haseltine, William A.
; APPLICANT: Li, Haodong
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
; FILE REFERENCE: PO-16,2CI
; CURRENT APPLICATION NUMBER: US/09/783,590
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/420,856
; PRIOR FILING DATE: 1995-04-12
; PRIOR APPLICATION NUMBER: 08/346,731
; PRIOR FILING DATE: 1994-11-21
; NUMBER OF SEQ ID NOS: 12485
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 406
; LENGTH: 501
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (265)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (308)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (334)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (383)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (402)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (441)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (446)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (468)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (478)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-406

Query Match 4.5%; Score 35; DB 10; Length 501;
Best Local Similarity 56.5%; Pred. No. 3.6;
Matches 65; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 99 CACCAGATGATGGCTCAGCACTTTTGTGTATCTTCAATGAGAGTTGACAGAGAT 158

APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.

APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C42
CURRENT FILING DATE: 2002-06-18
Prior application removed - See file wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 305
LENGTH: 1073
TYPE: DNA
ORGANISM: Homo Sapien
US-10-174-590-305

Query Match 4.3%; Score 34; DB 9; Length 1073;
Best Local Similarity 54.9%; Pred. No. 9.8; Mismatches 0; Gaps 0;
Matches 67; Conservative 0; Indels 55; Indels 0; Gaps 0;

QY 224 GAGAAAGATCCTTATCTTACTGAACTGTGAGAGATTAAAGCCAGTTTGAAGCCTTTG 283
DB 939 GAAATATTAACATTATGCTGCTGATGATGATGATTAACATATTGGAAGAACTGGA 998
QY 284 TGAAGATATATGTTAAACAAAGAGAGACGAAAGAAAGAAAGAGCTTTGAAATGCAA 343
DB 999 AA 1058
QY 344 AA 345
DB 1059 AA 1060

RESULT 14
US-10-176-758-305
Sequence 305, Application US/10176758
Publication No. US20030008353A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C104
CURRENT FILING DATE: 2002-06-21
Prior application removed - See file wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 305
LENGTH: 1073
TYPE: DNA
ORGANISM: Homo Sapien
US-10-176-758-305

Query Match 4.3%; Score 34; DB 9; Length 1073;
Best Local Similarity 54.9%; Pred. No. 9.8; Mismatches 0; Gaps 0;
Matches 67; Conservative 0; Indels 55; Indels 0; Gaps 0;

QY 224 GAGAAAGATCCTTATCTTACTGAACTGTGAGAGATTAAAGCCAGTTTGAAGCCTTTG 283
DB 939 GAAATATTAACATTATGCTGCTGATGATGATGATTAACATATTGGAAGAACTGGA 998
QY 284 TGAAGATATATGTTAAACAAAGAGAGACGAAAGAAAGAAAGAGCTTTGAAATGCAA 343

DB 999 AA 1058
QY 344 AA 345
DB 1059 AA 1060

RESULT 15
US-10-063-616-95
Sequence 95, Application US/10063616
Publication No. US20030013855A1
GENERAL INFORMATION:
APPLICANT: Baton, Dan L.
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3230R1C1
CURRENT FILING DATE: 2002-05-03
Prior application removed - See file wrapper or Palm
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 95
LENGTH: 1073
TYPE: DNA
ORGANISM: Homo Sapien
US-10-063-616-95

Query Match 4.3%; Score 34; DB 9; Length 1073;
Best Local Similarity 54.9%; Pred. No. 9.8; Mismatches 0; Gaps 0;
Matches 67; Conservative 0; Indels 55; Indels 0; Gaps 0;

QY 224 GAGAAAGATCCTTATCTTACTGAACTGTGAGAGATTAAAGCCAGTTTGAAGCCTTTG 283
DB 939 GAAATATTAACATTATGCTGCTGATGATGATGATTAACATATTGGAAGAACTGGA 998
QY 284 TGAAGATATATGTTAAACAAAGAGAGACGAAAGAAAGAAAGAGCTTTGAAATGCAA 343
DB 999 AA 1058
QY 344 AA 345
DB 1059 AA 1060

Search completed: March 9, 2003, 09:51:39
Job time: 340.261 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: March 8, 2003, 21:49:58 ; Search time 33.6448 Seconds
(without alignments)
7164.491 Million cell updates/sec

Title: US-08-982-272-6

Perfect score: 786
Sequence: 1 ATGATGAAACATACAGCA.....TTGGCTTACTCAAACTTGA 786

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 862724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, NA:
1: /cgn2_6/prodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/prodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/prodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/prodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/prodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/prodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	763.6	97.2	786	1	US-08-446-922-3
2	763.6	97.2	786	5	PCT-US93-10034-3
3	763.6	97.2	840	1	US-07-940-605A-1
4	763.6	97.2	840	1	US-08-184-422-7
5	763.6	97.2	840	1	US-08-360-923A-1
6	763.6	97.2	840	1	US-08-431-055-3
7	763.6	97.2	840	2	US-08-630-096-1
8	763.6	97.2	840	2	US-08-249-189-11
9	763.6	97.2	840	2	US-08-484-624A-11
10	763.6	97.2	840	2	US-08-477-733B-11
11	763.6	97.2	840	3	US-08-763-995-1
12	763.6	97.2	840	3	US-08-088-913A-11
13	763.6	97.2	840	3	US-08-589-771B-7
14	763.6	97.2	840	4	US-08-769-819-11
15	763.6	97.2	840	4	US-08-770-974-11
16	763.6	97.2	840	4	US-08-858-197-3
17	763.6	97.2	840	4	US-08-770-981-11
18	763.6	97.2	840	4	US-09-399-106-11
19	638.2	81.2	1425	2	US-08-249-189-15
20	638.2	81.2	1425	2	US-08-484-624A-15
21	638.2	81.2	1425	2	US-08-477-733B-15
22	638.2	81.2	1425	3	US-09-088-913A-15
23	638.2	81.2	1425	4	US-08-769-819-15
24	638.2	81.2	1425	4	US-08-770-974-15
25	638.2	81.2	1425	4	US-08-770-981-15
26	638.2	81.2	1425	4	US-09-399-106-15
27	637.2	81.1	929	1	US-08-446-922-10

ALIGNMENTS

28	637.2	81.1	929	2	US-08-249-189-20	Sequence 20, Appl
29	637.2	81.1	929	2	US-08-484-624A-20	Sequence 20, Appl
30	637.2	81.1	929	2	US-08-477-733B-20	Sequence 20, Appl
31	637.2	81.1	929	3	US-09-088-913A-20	Sequence 20, Appl
32	637.2	81.1	929	4	US-08-769-819-20	Sequence 20, Appl
33	637.2	81.1	929	4	US-08-770-974-20	Sequence 20, Appl
34	637.2	81.1	929	4	US-08-770-981-20	Sequence 20, Appl
35	637.2	81.1	929	4	US-09-399-106-20	Sequence 20, Appl
36	584.4	74.4	783	1	US-08-446-922-5	Sequence 5, Appl
37	584.4	74.4	783	2	US-08-249-189-1	Sequence 1, Appl
38	584.4	74.4	783	2	US-08-484-624A-1	Sequence 1, Appl
39	584.4	74.4	783	2	US-08-477-733B-1	Sequence 1, Appl
40	584.4	74.4	783	3	US-09-088-913A-1	Sequence 1, Appl
41	584.4	74.4	783	4	US-08-769-819-1	Sequence 1, Appl
42	584.4	74.4	783	4	US-08-770-974-1	Sequence 1, Appl
43	584.4	74.4	783	4	US-08-770-981-1	Sequence 1, Appl
44	584.4	74.4	783	4	US-09-399-106-1	Sequence 1, Appl
45	584.4	74.4	783	5	PCT-US93-10034-5	Sequence 5, Appl

RESULT 1
US-08-446-922-3
; Sequence 3, Application US/08446922
; Patent No. 5716805
; GENERAL INFORMATION:
; APPLICANT: Spriggs, Melanje
; APPLICANT: Srivivasan, Subhashini
; TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.1
; SOFTWARE: Microsoft Word for Apple, Version 5.1a
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/446, 922
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/107,353
; FILING DATE: 08-13-93
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 1003-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 786 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Human
; STRAIN: CD40-L
; FEATURE:

NAME/KEY: CDS
LOCATION: 1..783
US-08-446-922-3

Query Match 97.2%; Score 763.6; DB 1; Length 786;
Best Local Similarity 98.2%; Pred. No. 1.3e-212;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGATGAGAAACATACAGCAAGCTTCCCGAGATCCGAGCACTGGACCTGACGAGC 60
DB 1 ATGATGAGAAACATACAGCAAGCTTCCCGAGATCCGAGCACTGGACCTGACGAGC 60
QY 61 ATGAAATTTTATGATTTTACTTACTGTTTTTTCTTATCACCAGATGATGGGTACCA 120
DB 61 ATGAAATTTTATGATTTTACTTACTGTTTTTTCTTATCACCAGATGATGGGTACCA 120
QY 121 CTTTTCGTGTATCTTCAATGAAAGTTGGAACAGATGAAAGATGAAAGATCTTAT 180
DB 121 CTTTTCGTGTATCTTCAATGAAAGTTGGAACAGATGAAAGATGAAAGATCTTAT 180
QY 181 GAAATTTTGTATTCATGAAACATACAGATGCAACAGAGAGAAAGATCTTATCC 240
DB 181 GAAATTTTGTATTCATGAAACATACAGATGCAACAGAGAGAAAGATCTTATCC 240
QY 241 TTAAGTAACTGTAGAGAGATTAAAGCAGTTTGAAGCTTTGTGAAGATTAATGTTA 300
DB 241 TTAAGTAACTGTAGAGAGATTAAAGCAGTTTGAAGCTTTGTGAAGATTAATGTTA 300
QY 301 AACAAAG 360
DB 301 AACAAAG 360
QY 361 CAAATTCGCGACATGTCTAATGAGGCGAGAGATTAACAGATCTGTGTACAGTGG 420
DB 361 CAAATTCGCGACATGTCTAATGAGGCGAGAGATTAACAGATCTGTGTACAGTGG 420
QY 421 GCTGAAAAAGATCTACACCAATGAGCAACATTTGTTACCTTGGAAAAATGGGAAA 480
DB 421 GCTGAAAAAGATCTACACCAATGAGCAACATTTGTTACCTTGGAAAAATGGGAAA 480
QY 481 CTGACCGTTAAAG 540
DB 481 CTGACCGTTAAAG 540
QY 541 CGGAGAGCTTCAGTCAAGCTTCATTTATGCGAGCTTCGCTAAAGTCCCGGTGGA 600
DB 541 CGGAGAGCTTCAGTCAAGCTTCATTTATGCGAGCTTCGCTAAAGTCCCGGTGGA 600
QY 601 TTCGAGAGATCTTACTCAGAGCTGCAAAATCCACAGTTCGCGCAAACTTGGCGG 660
DB 601 TTCGAGAGATCTTACTCAGAGCTGCAAAATCCACAGTTCGCGCAAACTTGGCGG 660
QY 661 CAATTCATTCATTTGGAGAGAGATTTGAAATGCAACAGAGTCTTGGGTGTCTCAT 720
DB 661 CAATTCATTCATTTGGAGAGAGATTTGAAATGCAACAGAGTCTTGGGTGTCTCAT 720
QY 721 GTGACTGATCAAGCCAAAGTGGCATGAGCACTGAGCTTCAAGCTTTGGCTTACTCAA 780
DB 721 GTGACTGATCAAGCCAAAGTGGCATGAGCACTGAGCTTCAAGCTTTGGCTTACTCAA 780
QY 781 CTCTGA 786
DB 781 CTCTGA 786

RESULT 2
PCT-US93-10034-3

Sequence 3, Application PC/TUS9310034

GENERAL INFORMATION:

APPLICANT: Spriggs, Melanie

APPLICANT: Srinivasan, Subhashini

TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric Proteins

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSER: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/10034

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia A

REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 1003

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 587-0430

TELEFAX: (206) 233-0644

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 786 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Human

STRAIN: CD40-L

FEATURE:

NAME/KEY: CDS

LOCATION: 1..783

PCT-US93-10034-3

Query Match 97.2%; Score 763.6; DB 5; Length 786;
Best Local Similarity 98.2%; Pred. No. 1.3e-212;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGATGAGAAACATACAGCAAGCTTCCCGAGATCCGAGCACTGGACCTGACGAGC 60
DB 1 ATGATGAGAAACATACAGCAAGCTTCCCGAGATCCGAGCACTGGACCTGACGAGC 60
QY 61 ATGAAATTTTATGATTTTACTTACTGTTTTTTCTTATCACCAGATGATGGGTACCA 120
DB 61 ATGAAATTTTATGATTTTACTTACTGTTTTTTCTTATCACCAGATGATGGGTACCA 120
QY 121 CTTTTCGTGTATCTTCAATGAAAGTTGGAACAGATGAAAGATGAAAGATCTTAT 180
DB 121 CTTTTCGTGTATCTTCAATGAAAGTTGGAACAGATGAAAGATGAAAGATCTTAT 180
QY 181 GAAATTTTGTATTCATGAAACATACAGATGCAACAGAGAGAAAGATCTTATCC 240
DB 181 GAAATTTTGTATTCATGAAACATACAGATGCAACAGAGAGAAAGATCTTATCC 240
QY 241 TTAAGTAACTGTAGAGAGATTAAAGCAGTTTGAAGCTTTGTGAAGATTAATGTTA 300
DB 241 TTAAGTAACTGTAGAGAGATTAAAGCAGTTTGAAGCTTTGTGAAGATTAATGTTA 300
QY 301 AACAAAG 360
DB 301 AACAAAG 360
QY 361 CAAATTCGCGACATGTCTAATGAGGCGAGAGATTAACAGATCTGTGTACAGTGG 420
DB 361 CAAATTCGCGACATGTCTAATGAGGCGAGAGATTAACAGATCTGTGTACAGTGG 420

QY 421 GCTGAAAAAGATCTACACATGAGCAACATGGTAACCTGGAAAAATGGGAAACAG 480
 DB 421 GCTGAAAAAGATCTACACATGAGCAACATGGTAACCTGGAAAAATGGGAAACAG 480
 QY 481 CTGACCGTTAAAGACAGAGACTCTATTATATCTATGCCCAGAGTCACTTGTTCAT 540
 DB 481 CTGACCGTTAAAGACAGAGACTCTATTATATCTATGCCCAGAGTCACTTGTTCAT 540
 QY 541 CGGGAAGCTTGAAGTCAATTTATAGCAGCTGCTGCTAAAGTCCCGGGTATA 600
 DB 541 CGGGAAGCTTGAAGTCAATTTATAGCAGCTGCTGCTAAAGTCCCGGGTATA 600
 QY 601 TTGAGAGATCTTACTCAGAGCTCAATATCCACAGTTCCGCAAACTTGGGGCA 660
 DB 601 TTGAGAGATCTTACTCAGAGCTCAATATCCACAGTTCCGCAAACTTGGGGCA 660
 QY 661 CAATCATTCTGGGAGAGATTTGAATTTGCAACAGAGTCTGGGGTTTGTCAAT 720
 DB 661 CAATCATTCTGGGAGAGATTTGAATTTGCAACAGAGTCTGGGGTTTGTCAAT 720
 QY 721 GTGACTGATCCAGCCAGAGTGAAGCATGCGCTTCACTGCTTTTGTCTTCAAA 780
 DB 721 GTGACTGATCCAGCCAGAGTGAAGCATGCGCTTCACTGCTTTTGTCTTCAAA 780
 QY 781 CTCTGA 786
 DB 781 CTCTGA 786

RESULT 3
 US-07-940-605A-1
 ; Sequence 1, Application US/07940605A
 ; Patent No. 5540926
 ; GENERAL INFORMATION:
 ; APPLICANT: ARUPPO, ALEJANDRO
 ; APPLICANT: HOLLENBAUGH, DIANE
 ; APPLICANT: LEDBETTER, JEFFREY A.
 ; TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/940.605A
 ; FILING DATE: 04-SEP-1992
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mistrock, S. Leslie
 ; REGISTRATION NUMBER: 18,872
 ; REFERENCE/DOCKET NUMBER: 5624-184
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212 790-9090
 ; TELEFAX: 212 869-8864/9741
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 840 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 22..807

US-07-940-605A-1
 Query Match 97.2%; Score 763.6; DB 1; Length 840;
 Best Local Similarity 98.2%; Prid. No. 1.4e-212;
 Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
 QY 1 ATGATTAAGAAACATACAGCCAACTTCCCGAGATCCGTGCAATGAGACTTCAGAGC 60
 DB 22 ATGATTAAGAAACATACAGCCAACTTCCCGAGATCCGTGCAATGAGACTTCAGAGC 81
 QY 61 ATGAAGATTTTATGATTTTACTTACTGTTTCTTATACCAAGATGATGGGTACCA 120
 DB 82 ATGAAGATTTTATGATTTTACTTACTGTTTCTTATACCAAGATGATGGGTACCA 141
 QY 121 CTTTTCCTGTGATCTTCAATAGAGGTTGCAAGATAGAGATGAGATGAGATCTTCAT 180
 DB 142 CTTTTCCTGTGATCTTCAATAGAGGTTGCAAGATAGAGATGAGATGAGATCTTCAT 201
 QY 181 GAAGATTTTGTATTCATGAAAACGATACAGAGATGCAACAGAGAAAGATCTTATCC 240
 DB 202 GAAGATTTTGTATTCATGAAAACGATACAGAGATGCAACAGAGAAAGATCTTATCC 261
 QY 241 TTACTGAATCTGTAGAGATTTAAAGCCAGTTTGAAGCTTGTGAAGATTAATGTTA 300
 DB 262 TTACTGAATCTGTAGAGATTTAAAGCCAGTTTGAAGCTTGTGAAGATTAATGTTA 321
 QY 301 AACAAAGAGAGACGAAAGAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAACTCT 360
 DB 322 AACAAAGAGAGACGAAAGAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAACTCT 381
 QY 361 CAAATTCGCGCATGTCATTAAGAGGCGAGCAGATTAACATCTGTGTTACATGCG 420
 DB 382 CAAATTCGCGCATGTCATTAAGAGGCGAGCAGATTAACATCTGTGTTACATGCG 441
 QY 421 GCTGAAAAAGATCTACACATGAGCAACATGGTAACCTGGAAAAATGGGAAACAG 480
 DB 442 GCTGAAAAAGATCTACACATGAGCAACATGGTAACCTGGAAAAATGGGAAACAG 501
 QY 481 CTGACCGTTAAAGACAGAGACTCTATTATATCTATGCCCAGAGTCACTTGTTCAT 540
 DB 502 CTGACCGTTAAAGACAGAGACTCTATTATATCTATGCCCAGAGTCACTTGTTCAT 561
 QY 541 CGGGAAGCTTGAAGTCAATTTATAGCAGCTGCTGCTAAAGTCCCGGGTATA 600
 DB 562 CGGGAAGCTTGAAGTCAATTTATAGCAGCTGCTGCTAAAGTCCCGGGTATA 621
 QY 601 TTGAGAGATCTTACTCAGAGCTCAATATCCACAGTTCCGCAAACTTGGGGCA 660
 DB 622 TTGAGAGATCTTACTCAGAGCTCAATATCCACAGTTCCGCAAACTTGGGGCA 681
 QY 661 CAATCATTCTGGGAGAGATTTGAATTTGCAACAGAGTCTGGGGTTTGTCAAT 720
 DB 682 CAATCATTCTGGGAGAGATTTGAATTTGCAACAGAGTCTGGGGTTTGTCAAT 741
 QY 721 GTGACTGATCCAGCCAGAGTGAAGCATGCGCTTCACTGCTTTTGTCTTCAAA 780
 DB 742 GTGACTGATCCAGCCAGAGTGAAGCATGCGCTTCACTGCTTTTGTCTTCAAA 801
 QY 781 CTCTGA 786
 DB 802 CTCTGA 807

RESULT 4
 US-08-184-422-7
 ; Sequence 7, Application US/08184422
 ; Patent No. 555321
 ; GENERAL INFORMATION:
 ; APPLICANT: ARMITAGE, RICHARD
 ; APPLICANT: DAVISON, BARRY
 ; APPLICANT: FANSLON, WILLIAM
 ; APPLICANT: RENSCH, BLAIR
 ; APPLICANT: SPRIGGS, MELANIE

TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46..831
US-08-360-923A-1

Query Match 97.2%; Score 763.6; DB 1; Length 840;
Best Local Similarity 98.2%; Pred. No. 1.4e-212;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1 ATGATGAAACATACGACCACTTCCCGAGATCGGTGCACTGACCTTCAGAGGAGC 60
Db 46 ATGATGAAACATACGACCACTTCCCGAGATCGGTGCACTGACCTTCAGAGGAGC 105
Qy 61 ATGAGATTTTATGATTTTACTTCTCTTTTCTTATCACCCAGATGTTGGTCAAGA 120
Db 106 ATGAGATTTTATGATTTTACTTCTCTTTTCTTATCACCCAGATGTTGGTCAAGA 165
Qy 121 CTTTGGCTGTATCTTCAATGAGGTTGGAAGAATGAGAGGATCTTCT 180
Db 166 CTTTGGCTGTATCTTCAATGAGGTTGGAAGAATGAGAGGATCTTCT 225
Qy 181 GAAGATTTTGTATCATGAAAAAGATGACAGATGCAACAGAGAAAGATCTTATCC 240
Db 226 GAAGATTTTGTATCATGAAAAAGATGACAGATGCAACAGAGAAAGATCTTATCC 285
Qy 241 TTAAGTGAAGTGTGAGAGATTTAAAGGCGATTTGAGGCTTTGTAAGATTTAATGTTA 300
Db 286 TTAAGTGAAGTGTGAGAGATTTAAAGGCGATTTGAGGCTTTGTAAGATTTAATGTTA 345
Qy 301 AACAAAG 360
Db 346 AACAAAG 405
Qy 361 CAAATTTGGGACATGCTAATGAGGCGAGAGTAAAGCAATCTGTGTTACAGTGG 420
Db 406 CAAATTTGGGACATGCTAATGAGGCGAGAGTAAAGCAATCTGTGTTACAGTGG 465
Qy 421 GCTGAAAAAGATGATGACCAATGAGCAACCTTGGTAACTTGGAAAAAG 480
Db 466 GCTGAAAAAGATGATGACCAATGAGCAACCTTGGTAACTTGGAAAAAG 525
Qy 481 CTGACCGTTTAAAGAGAGAGATTTATATCTATGAGGCAAGTACCTTCTGTCAAT 540
Db 526 CTGACCGTTTAAAGAGAGATTTATATCTATGAGGCAAGTACCTTCTGTCAAT 585
Qy 541 CGGGAAGCTTGAAGTCAAGCTCATTATTAAGCCAGCTTGTCTTAAATCCCGGTAGA 600
Db 586 CGGGAAGCTTGAAGTCAAGCTCATTATTAAGCCAGCTTGTCTTAAATCCCGGTAGA 645
Qy 601 TTGAGAGAGATCTTACTCAGAGCTCAATACCAAGTTCCGCAAACTTGGGGCA 660
Db 646 TTGAGAGAGATCTTACTCAGAGCTCAATACCAAGTTCCGCAAACTTGGGGCA 705
Qy 661 CAATCATTTCACTTGGAGAGATTTGAATTTGCAACAGGTCTTGGTGTTCAT 720
Db 706 CAATCATTTCACTTGGAGAGATTTGAATTTGCAACAGGTCTTGGTGTTCAT 765

Qy 721 GTGACTATCCAAAGCAAGTGAAGCATGAGGCTTCAAGTCTTGGCTTACTCAAA 780
Db 766 GTGACTATCCAAAGCAAGTGAAGCATGAGGCTTCAAGTCTTGGCTTACTCAAA 825
Qy 781 CTTCTGA 786
Db 826 CTTCTGA 831

RESULT 6
US-08-431-055-3
Sequence 3, Application US/08431055
Patent No. 5817516

GENERAL INFORMATION:
APPLICANT: KEHRY, MERILYN R
APPLICANT: CASTLE, BRIAN E
TITLE OF INVENTION: METHODS FOR PROLIFERATING AND
TITLE OF INVENTION: DIFFERENTIATING B CELLS, AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
STREET: 100 NEW YORK AVE. N.W. SUITE 600
CITY: WASHINGTON
STATE: D.C.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431, 055
FILING DATE: 28-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/234,580
FILING DATE: 28-APR-1994

ATTORNEY/AGENT INFORMATION:
NAME: MILLMAN, ROBERT A
REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 1011.1030000/RAM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2640

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 22..807
US-08-431-055-3

Query Match 97.2%; Score 763.6; DB 1; Length 840;
Best Local Similarity 98.2%; Pred. No. 1.4e-212;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1 ATGATGAAACATACGACCACTTCCCGAGATCGGTGCACTGACCTTCAGAGGAGC 60
Db 22 ATGATGAAACATACGACCACTTCCCGAGATCGGTGCACTGACCTTCAGAGGAGC 81
Qy 61 ATGAGATTTTATGATTTTACTTCTTTTCTTATCACCCAGATGTTGGTCAAGA 120
Db 82 ATGAGATTTTATGATTTTACTTCTTTTCTTATCACCCAGATGTTGGTCAAGA 141
Qy 121 CTTTGGCTGTATCTTCAATGAGGTTGGAAGAATGAGAGGATCTTCT 180
Db 142 CTTTGGCTGTATCTTCAATGAGGTTGGAAGAATGAGAGGATCTTCT 201
Qy 181 GAAGATTTTGTATCATGAAAAAGATGACAGATGCAACAGAGAAAGATCTTATCC 240

Db 202 GAGATTTTGTATTCATGAAACGATTCAGAGTGAACAGGAGAAAGATCTTATCC 261
Qy 241 TTACTGAATCTGAGAGATTTAAAGCACTTTGAAAGCTTTGAGAGATATATGTA 300
Db 262 TTACTGAATCTGAGAGATTTAAAGCACTTTGAAAGCTTTGAGAGATATATGTA 321
Qy 301 AACAAAG 360
Db 322 AACAAAG 381
Qy 361 CAAATGCGGACATCTCATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Db 382 CAAATGCGGACATCTCATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 441
Qy 421 GCTGAAAAAGATATCTACCAATGAGCAACATTTGTATACCTTGAAAAATGGAGAG 480
Db 442 GCTGAAAAAGATATCTACCAATGAGCAACATTTGTATACCTTGAAAAATGGAGAG 501
Qy 481 CTGACCGTTAAAG 540
Db 502 CTGACCGTTAAAG 561
Qy 541 CGGAGAGCTTGAAGTCAAGCTTCAATTTATAGCCAGCTTCTGCTTAAAGTCCCGGTAGA 600
Db 562 CGGAGAGCTTGAAGTCAAGCTTCAATTTATAGCCAGCTTCTGCTTAAAGTCCCGGTAGA 621
Qy 601 TTGAGAGAGATCTTACTGAGAGCTGCAAAATACCAAGTCCGCAAACTTTGCGGGGAA 660
Db 622 TTGAGAGAGATCTTACTGAGAGCTGCAAAATACCAAGTCCGCAAACTTTGCGGGGAA 681
Qy 661 CAATTCATTCATTTGGAGAGAGATTTGAATTTGCAACCAAGTCTTGTGTTTGTCAAT 720
Db 682 CAATTCATTCATTTGGAGAGAGATTTGAATTTGCAACCAAGTCTTGTGTTTGTCAAT 741
Qy 721 GTGACTGATCCAAAGCAAGTGAAGCAATGCACTGCTTCAAGCTTGTGCTTACTCAA 780
Db 742 GTGACTGATCCAAAGCAAGTGAAGCAATGCACTGCTTCAAGCTTGTGCTTACTCAA 801
Qy 781 CTCTGA 786
Db 802 CTCTGA 807

RESULT 7
US-08-690-096-1
Sequence 1, Application US/08690096
Patent No. 5945513
GENERAL INFORMATION:
APPLICANT: ARUPPO, ALEJANDRO
APPLICANT: HOLLENBAUGH, DIANE
APPLICANT: LEDBETTER, JEFFREY A.
TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/690,096
FILING DATE: 31-JUL-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/940,605
FILING DATE: 04-SEP-1992

ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-184
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 869-8644/9741
TELEFAX: 212 869-8644/9741
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 22..807
US-08-690-096-1

Query Match 97.2%; Score 763.6; DB 2; Length 840;
Best Local Similarity 98.2%; Pred. No. 1.4e-212;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

1 ATGATGAACATACAGCAACCTTCCCAAGATCCGTGCAACTGCACTTCCAGCGAGC 60
22 ATGATGAACATACATCAACCAACTTCTCCCAATCTGCGGCACTGCACTGCCATCAGC 81
Qy 61 ATGATGAATTTTAAATTTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 120
Db 82 ATGATGAATTTTAAATTTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 141
Qy 121 CTTTGTGCTGTATCTTCAATGAGAGTTGCAAGATGAGATGAGATGAGATGAGATGAGAT 180
Db 142 CTTTGTGCTGTATCTTCAATGAGAGTTGCAAGATGAGATGAGATGAGATGAGATGAGAT 201
Qy 181 GAAGATTTGTATCATGAG 240
Db 202 GAAGATTTGTATCATGAG 261
Qy 241 TTACTGAATCTGAGAGATTTAAAGCACTTTGAAAGCTTTGAGAGATATATGTA 300
Db 262 TTACTGAATCTGAGAGATTTAAAGCACTTTGAAAGCTTTGAGAGATATATGTA 321
Qy 301 AACAAAG 360
Db 322 AACAAAG 381
Qy 361 CAAATGCGGACATCTCATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Db 382 CAAATGCGGACATCTCATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 441
Qy 421 GCTGAAAAAGATATCTACCAATGAGCAACATTTGTATACCTTGAAAAATGGAGAG 480
Db 442 GCTGAAAAAGATATCTACCAATGAGCAACATTTGTATACCTTGAAAAATGGAGAG 501
Qy 481 CTGACCGTTAAAG 540
Db 502 CTGACCGTTAAAG 561
Qy 541 CGGAGAGCTTGAAGTCAAGCTTCAATTTATAGCCAGCTTCTGCTTAAAGTCCCGGTAGA 600
Db 562 CGGAGAGCTTGAAGTCAAGCTTCAATTTATAGCCAGCTTCTGCTTAAAGTCCCGGTAGA 621
Qy 601 TTGAGAGAGATCTTACTGAGAGCTGCAAAATACCAAGTCCGCAAACTTTGCGGGGAA 660
Db 622 TTGAGAGAGATCTTACTGAGAGCTGCAAAATACCAAGTCCGCAAACTTTGCGGGGAA 681
Qy 661 CAATTCATTCATTTGGAGAGAGATTTGAATTTGCAACCAAGTCTTGTGTTTGTCAAT 720
Db 682 CAATTCATTCATTTGGAGAGAGATTTGAATTTGCAACCAAGTCTTGTGTTTGTCAAT 741
Qy 721 GTGACTGATCCAAAGCAAGTGAAGCAATGCACTGCTTCAAGCTTGTGCTTACTCAA 780


```

? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/477,733B
? FILING DATE: June 07, 1995
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/249,189
? FILING DATE: May 24, 1994
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 07/969,703
? FILING DATE: October 23, 1992
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 07/805,723
? FILING DATE: December 5, 1991
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 07/783,707
? FILING DATE: October 25, 1991
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: Perkins, Patricia A.
? REGISTRATION NUMBER: 34,693
? REFERENCE/DOCKET NUMBER: 2802-D
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 2065870430
? TELEFAX: 2065870606
? INFORMATION FOR SEQ ID NO: 11:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 840 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? HYPOTHETICAL: NO
? ANTI-SENSE: NO
? ORIGINAL SOURCE:
? ORGANISM: Homo sapiens
? IMMEDIATE SOURCE:
? CLONE: CD40-L
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 46..831
? US-08-477-733B-11

Query Match 97.2%; Score 763.6; DB 2; Length 840;
Best Local Similarity 98.2%; Pred. No. 1,4e-212;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGATAGAAACATACACCCACCTTCCCGAGATCCGTGCAACTGAGCTCCAGGAGC 60
DB 46 ATGATAGAAACATACACCCACCTTCCCGAGATCCGTGCAACTGAGCTCCAGGAGC 105
QY 61 ATGAAAGATTTTATGATTTTACTGCTTTTCTTATTCACCCAGATGATGGGTGAGA 120
DB 106 ATGAAAGATTTTATGATTTTACTGCTTTTCTTATTCACCCAGATGATGGGTGAGA 165
QY 121 CTTTTCGTGTATCTTCTATGAAAGTTGACAAGATGAAAGATGAAATCTTCAT 180
DB 166 CTTTTCGTGTATCTTCTATGAAAGTTGACAAGATGAAAGATGAAATCTTCAT 225
QY 181 GAAGATTTTATTCATGAAAGATGATGATGCAACACGAGAAAGATCTTATTC 240
DB 226 GAAGATTTTATTCATGAAAGATGATGATGCAACACGAGAAAGATCTTATTC 285
QY 241 TTAAGAACTGTGAGAGATTAAGCAAGTTGAAGCTTTGTGAAGATATATGTTA 300
DB 286 TTAAGAACTGTGAGAGATTAAGCAAGTTGAAGCTTTGTGAAGATATATGTTA 345
QY 301 AACAAAGAGAGAGAAAGAAAGAAAGCACTTTGAATGCAAAAAGGTGATCAGATCT 360
DB 346 AACAAAGAGAGAGAAAGAAAGAAAGCACTTTGAATGCAAAAAGGTGATCAGATCT 405

QY 361 CAATTGGCGCAATGTCATAGTGAAGCCAGAGATTAACAACATCTGTTACAGTGC 420
DB 406 CAATTGGCGCAATGTCATAGTGAAGCCAGAGATTAACAACATCTGTTACAGTGC 465
QY 421 GCTGAAAAAGATATACACATGAGCAACAACCTTGTTAACCCTGAAAAATGGAAACG 480
DB 466 GCTGAAAAAGATATACACATGAGCAACAACCTTGTTAACCCTGAAAAATGGAAACG 525
QY 481 CTGACCTTTAAAGACAAAGACTATTTATATCTAGCCCAAGTCCCTGTTCCAT 540
DB 526 CTGACCTTTAAAGACAAAGACTATTTATATCTAGCCCAAGTCCCTGTTCCAT 585
QY 541 CGGAAAGCTTGAAGTCAAGCTTCATTTATAGCAAGCTTGTAAAGTCCCGGTAGA 600
DB 586 CGGAAAGCTTGAAGTCAAGCTTCATTTATAGCAAGCTTGTAAAGTCCCGGTAGA 645
QY 601 TTGAGAGAAATCTTACGAGACGTCGAAATACCAAGTCCGCAACCTTGCGGGCA 660
DB 646 TTGAGAGAAATCTTACGAGACGTCGAAATACCAAGTCCGCAACCTTGCGGGCA 705
QY 661 CAATCATTCATTTGGAGAGATTTTGAATTGCAACAGTGTCTGATTTGCAAT 720
DB 706 CAATCATTCATTTGGAGAGATTTTGAATTGCAACAGTGTCTGATTTGCAAT 765
QY 721 GTGACTGATCCAGCAAGTGAAGCAAGTGAAGTCAAGTGTCTGATTTGCAAT 780
DB 766 GTGACTGATCCAGCAAGTGAAGCAAGTGAAGTCAAGTGTCTGATTTGCAAT 825
QY 781 CTCTGA 786
DB 826 CTCTGA 831

RESULT 11
US-08-763-995-1
? Sequence 1, Application US/08763995
? Patent No. 6017527
? GENERAL INFORMATION:
? APPLICANT: MARASROVSKY, EUGENE
? TITLE OF INVENTION: METHOD OF ACTIVATING DENDRITIC CELLS
? NUMBER OF SEQUENCES: 4
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: IMMUNEX CORPORATION
? STREET: 51 UNIVERSITY STREET
? CITY: SEATTLE
? STATE: WASHINGTON
? COUNTRY: USA
? ZIP: 98101
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: Apple Operating System 7.5.5
? SOFTWARE: Microsoft Word for Macintosh, Version #6.0.1
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/763,995
? FILING DATE:
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: USN 08/677,762
? FILING DATE: 10 JUL 1996
? CLASSIFICATION:
? ATTORNEY/AGENT INFORMATION:
? NAME: Perkins, Patricia A.
? REGISTRATION NUMBER: 34,693
? REFERENCE/DOCKET NUMBER: 2845-A
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (206) 587-0430
? TELEFAX: (206) 233-0644
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 840 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
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TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE: NO
ORGANISM: Homo sapiens
IMMEDIATE SOURCE: NO
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46..831
US-08-763-995-1

Query Match 97.2%; Score 763.6; DB 3; Length 840;
Best Local Similarity 98.2%; Pred. No. 1.4e-212;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGATGAAACATACACCACTTCCCGATCCGTCGACATGAGCTTCACGAGC 60
DB 46 ATGATGAAACATACACCACTTCCCGATCCGTCGACATGAGCTTCACGAGC 105
QY 61 ATGAAAGTTTATATATATATATATATATATATATATATATATATATAT 120
DB 106 ATGAAAGTTTATATATATATATATATATATATATATATATATATATAT 165
QY 121 CTTTTCGTCGTCATCTCATAGAAAGTTGACAGATAGAAAGTAAAGATCTTCAT 180
DB 166 CTTTTCGTCGTCATCTCATAGAAAGTTGACAGATAGAAAGTAAAGATCTTCAT 225
QY 181 GAAAGTTTAT 240
DB 226 GAAAGTTTAT 285
QY 241 TTACTGAACTGTGAGAGATTAAGCCAGTTTGAAGCTTTGAGAGATTAAGTTTA 300
DB 286 TTACTGAACTGTGAGAGATTAAGCCAGTTTGAAGCTTTGAGAGATTAAGTTTA 345
QY 301 AACAAAG 360
DB 346 AACAAAG 405
QY 361 CAAATGCGGACATGTCTAAGTAGAGCCAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 406 CAAATGCGGACATGTCTAAGTAGAGCCAGAGAGAGAGAGAGAGAGAGAGAG 465
QY 421 GCTGAAAAGATATCTACATGAGCACAATGTTGTAACCTTGAGAAATGAGAAACAG 480
DB 466 GCTGAAAAGATATCTACATGAGCACAATGTTGTAACCTTGAGAAATGAGAAACAG 525
QY 481 CTGACCGTTAAAG 540
DB 526 CTGACCGTTAAAG 585
QY 541 CGGAGAGCTTCAGTCAAGCTCATTTATAGCCAGCTTGGCTTAAGTCCCGGTAGA 600
DB 586 CGGAGAGCTTCAGTCAAGCTCATTTATAGCCAGCTTGGCTTAAGTCCCGGTAGA 645
QY 601 TTGAGAGAAATCTTACTAGAGCTCAATATCCACAGTTCGCGCAAACTTTCGAGGCA 660
DB 646 TTGAGAGAAATCTTACTAGAGCTCAATATCCACAGTTCGCGCAAACTTTCGAGGCA 705
QY 661 CAATCATTCATCTTGGAGAGAGATTTGAATTCACACAGGTGCTTGGGTTCAT 720
DB 706 CAATCATTCATCTTGGAGAGAGATTTGAATTCACACAGGTGCTTGGGTTCAT 765
QY 721 GTGACTGATCAAGCAAGTAGAGCATGAGCTTCAAGCTCTTGGCTTACTCAAA 780
DB 766 GTGACTGATCAAGCAAGTAGAGCATGAGCTTCAAGCTCTTGGCTTACTCAAA 825
QY 781 CTCTGA 786
DB 826 CTCTGA 831

RESULT 12
US-09-088-913A-11
Sequence 11, Application US/09088913A

Patent No. 6087329
GENERAL INFORMATION:

APPLICANT: AMITAGE, RICHARD
APPLICANT: FANSLON, WILLIAM

APPLICANT: SPRIGGS, MELANIE
APPLICANT: SRINIVASAN, SUBHASHINI

APPLICANT: GIBSON, MARYLOU
APPLICANT: MORRIS, ARVIA E.

APPLICANT: MCGHEW, JEFFERY
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40

NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:

ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET

CITY: SEATTLE
STATE: WASHINGTON

COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5

SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/088,913A
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/484,624
FILING DATE:

APPLICATION NUMBER: 08/477,733
FILING DATE: June 07, 1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,703

FILING DATE: October 23, 1992
APPLICATION NUMBER: 07/805,723

PRIOR APPLICATION DATA:
FILING DATE: December 5, 1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/783,707

FILING DATE: October 25, 1991
ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2802-D
TELECOMMUNICATION INFORMATION:

TELEPHONE: 2065870606
TELEFAX: 2065870430

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:

LENGTH: 840 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: CDNA
HYPOTHETICAL: NO

ANTI-SENSE: NO
ORIGINAL SOURCE:

ORGANISM: Homo sapiens
IMMEDIATE SOURCE:

CLONE: CD40-L
FEATURE:

NAME/KEY: CDS
LOCATION: 46..831
US-09-088-913A-11

Query Match 97.2%; Score 763.6; DB 3; Length 840;
Best Local Similarity 98.2%; Pred. No. 1.4e-212;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

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QY 1 ATGATAGAAACATACAGCCAACTTCCCGAGATCGTGCAACTTCAGAGAGC 60
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Db 46 ATGATGAAACATACACAACTTCCCGATCTCGGCACTGCACTGCCATCAGC 105
QY 61 ATGAGATTTTATGATTTTACTTACTGTTTCTTATACCCAGATATGGGTGACA 120
   |||
Db 106 ATGAAATTTTATGATTTTACTTACTGTTTCTTATACCCAGATATGGGTGACA 165
QY 121 CTTTTCGTGTATCTTCAATAGAGTTGACAAAGATAGAGATGAAAGATCTTCAT 180
   |||
Db 166 CTTTTCGTGTATCTTCAATAGAGTTGACAAAGATAGAGATGAAAGATCTTCAT 225
QY 181 GAAGATTTTGTATCATGAAAGATACAGATGCAACAGAGAAAGATCTTATCC 240
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Db 226 GAAGATTTTGTATCATGAAAGATACAGATGCAACAGAGAAAGATCTTATCC 285
QY 241 TTACTGAATGTGAGAGATTAAGCCAGTTTGAAGGCTTGTGAAGATATATGTTA 300
   |||
Db 286 TTACTGAATGTGAGAGATTAAGCCAGTTTGAAGGCTTGTGAAGATATATGTTA 345
QY 301 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
   |||
Db 346 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 405
QY 361 CAAATTCGCGCACATGTCATATAGTGGCCAGAGTAAACAAATCTGTGTACAGTGG 420
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Db 406 CAAATTCGCGCACATGTCATATAGTGGCCAGAGTAAACAAATCTGTGTACAGTGG 465
QY 421 GCTGAAAAAGATCTACCATATGAGCAACATCTTGTAACCTTGAAATGGAGAA 480
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Db 466 GCTGAAAAAGATCTACCATATGAGCAACATCTTGTAACCTTGAAATGGAGAA 525
QY 481 CTGACCGTTTAAAGACAGAGACTTATATATATATATATATATATATATATATAT 540
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Db 526 CTGACCGTTTAAAGACAGAGACTTATATATATATATATATATATATATATATAT 585
QY 541 CGGGAAGCTTGAGATCAAGTCCATTTATACCGCTCTGCTTAAATGCCCGGTAGA 600
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Db 586 CGGGAAGCTTGAGATCAAGTCCATTTATACCGCTCTGCTTAAATGCCCGGTAGA 645
QY 601 TTGAGAGATCTTATACAGAGCTGCAATATACCAAGTTCGCGCAAACTTGGGCGCA 660
   |||
Db 646 TTGAGAGATCTTATACAGAGCTGCAATATACCAAGTTCGCGCAAACTTGGGCGCA 705
QY 661 CAATCCATTCCTTGGAGAGATTTTGAATTTGCAACAGGTGCTTCGGTGTTCAT 720
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Db 706 CAATCCATTCCTTGGAGAGATTTTGAATTTGCAACAGGTGCTTCGGTGTTCAT 765
QY 721 GTGACTGATCCAGCCAGATGAGCCATGSCATGCTTCAAGTCTTGGCTTACTCAA 780
   |||
Db 766 GTGACTGATCCAGCCAGATGAGCCATGSCATGCTTCAAGTCTTGGCTTACTCAA 825
QY 781 CTCTGA 786
   |||
Db 826 CTCTGA 831

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RESULT 13

US-08-589-771B-7

Sequence 7, Application US/08589771B

Patent No. 6106832

GENERAL INFORMATION:

APPLICANT: ARMITAGE, RICHARD

APPLICANT: DAVISON, BARRY

APPLICANT: FANSLON, WILLIAM

APPLICANT: RENSLOW, BLAIR

APPLICANT: SPRIGGS, MELANIE

APPLICANT: WIDMER, MICHAEL

TITLE OF INVENTION: TREATMENT OF INDIVIDUALS EXHIBITING

DEFECTIVE CD40L (as amended)

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

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ADDRESS: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS-DOS/Windows 95
SOFTWARE: Word for Windows 95, 7.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/589,771B
FILING DATE: January 22, 1996
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/009,258
FILING DATE: 01/22/93
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HENRY, JANIS C.
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2810-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ. ID NO. 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURES:
NAME/KEY: CDS
LOCATION: 46..831
US-08-589-771B-7
Query Match 97.2%; Score 763.6; DB 3; Length 840;
Best Local Similarity 98.2%; Pred. No. 1,4e-212;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 1 ATGATAGAAACATACAGCCAACTTCCCGAGATCGTGCAACTTCAGAGAGC 60
   |||
Db 46 ATGATGAAACATACACAACTTCCCGATCTCGGCACTGCACTGCCATCAGC 105
QY 61 ATGAGATTTTATGATTTTACTTACTGTTTCTTATACCCAGATATGGGTGACA 120
   |||
Db 106 ATGAAATTTTATGATTTTACTTACTGTTTCTTATACCCAGATATGGGTGACA 165
QY 121 CTTTTCGTGTATCTTCAATAGAGTTGACAAAGATAGAGATGAAAGATCTTCAT 180
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Db 166 CTTTTCGTGTATCTTCAATAGAGTTGACAAAGATAGAGATGAAAGATCTTCAT 225
QY 181 GAAGATTTTGTATCATGAAAGATACAGATGCAACAGAGAAAGATCTTATCC 240
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Db 226 GAAGATTTTGTATCATGAAAGATACAGATGCAACAGAGAAAGATCTTATCC 285
QY 241 TTACTGAATGTGAGAGATTAAGCCAGTTTGAAGGCTTGTGAAGATATATGTTA 300
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Db 286 TTACTGAATGTGAGAGATTAAGCCAGTTTGAAGGCTTGTGAAGATATATGTTA 345
QY 301 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
   |||
Db 346 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 405
QY 361 CAAATTCGCGCACATGTCATATAGTGGCCAGAGTAAACAAATCTGTGTACAGTGG 420

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Db	406	CAAAATTCGGGACATCTGTCATTAAGTAGAGCCAGACGTAATAACAATCTGTGTTACAGTGG	465
Qy	421	GCTGAAAAAGATATCTACACCATGAGCAACAATTGGTAACCTGGAAAAATGGAAACAG	480
Db	466	GCTGAAAAAGGATATCTACACCATGAGCAACAATTGGTAACCTGGAAAAATGGAAACAG	525
Qy	481	CTGACCGTTAAAAAGACAAGACTCTATTAATCTATGCCCCAAGTCACTCTGTGTCAT	540
Db	526	CTGACCGTTAAAAAGACAAGACTCTATTAATCTATGCCCCAAGTCACTCTGTGTCAT	585
Qy	541	CGGGAAGCTTGTGAGTCACTCCATCTTTATAGCAGCTTCCTGTAAGTCCCGCGGTGA	600
Db	586	CGGGAAGCTTGTGAGTCACTCCATCTTTATAGCAGCTTCCTGTAAGTCCCGCGGTGA	645
Qy	601	TTGAGAGAAATCTTACTCTAGAGCTGCAAAATCCACAGTTCGCGCAAACTGTGCGGCA	660
Db	646	TTGAGAGAAATCTTACTCTAGAGCTGCAAAATCCACAGTTCGCGCAAACTGTGCGGCA	705
Qy	661	CAATCCATTCCTTGGGAGAGATATTGCAATTCGCAACGAGGTCTTGCGGTGTGCAT	720
Db	706	CAATCCATTCCTTGGGAGAGATATTGCAATTCGCAACGAGGTCTTGCGGTGTGCAT	765
Qy	721	GTGACTGATCCAAAGCCAGTGAAGCCATGAGCACTGGCTTCAAGTCTTTTGACTTACTCAA	780
Db	766	GTGACTGATCCAAAGCCAGTGAAGCCATGAGCACTGGCTTCAAGTCTTTTGACTTACTCAA	825
Qy	781	CTCTGA 786	
Db	826	CTCTGA 831	

RESULT 14
US-08-769-819-11

Sequence 11, Application US/08769819
Patent No.66264951

GENERAL INFORMATION:

APPLICANT: ARMITAGE, RICHARD
APPLICANT: FANSLON, WILLIAM
APPLICANT: SPRIGGS, MELANIE
APPLICANT: SRINIVASAN, SUBHASHINI
APPLICANT: GISSON, MAYOLOU
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.1
SOFTWARE: Microsoft Word for Apple, version 5.1a

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/769,819
FILING DATE: 19-DEC-1996
CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/484,624
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: 08/249,189
FILING DATE: May 24, 1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/969,703
FILING DATE: October 23, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/805,723
FILING DATE: December 5, 1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/783,707

	FILING DATE:	October 25, 1991
	ATTORNEY/AGENT INFORMATION:	
	NAME:	Perkins, Patricia A.
	REGISTRATION NUMBER:	34,693
	REFERENCE/DOCKET NUMBER:	2802-B
	TELECOMMUNICATION INFORMATION:	
	TELEPHONE:	2065870430
	TELEFAX:	2065870606
	INFORMATION FOR SEQ ID NO:	11:
	SEQUENCE CHARACTERISTICS:	
	LENGTH:	840 base pairs
	TYPE:	nucleic acid
	STRANDEDNESS:	single
	TOPOLOGY:	linear
	MOLECULE TYPE:	cDNA
	HYPOTHETICAL:	NO
	ANTI-SENSE:	NO
	ORIGINAL SOURCE:	
	ORGANISM:	Homo sapiens
	IMMEDIATE SOURCE:	
	CLONE:	CD40-L
	FEATURE:	
	NAME/KEY:	CDS
	LOCATION:	46..831
	US-08-769-819-11	
	Query Match	97.2%; Score 763.6; DB 4; Length 840;
	Best local Similarity	98.2%; Pred. No. 1.4e-212;
	Matches 772; Conservative	0; Mismatches 14; Indels 0; Gaps 0;
Oy	1	ATGATAGAAACATACAGCCACTTTCCTCCCGAGATCCGTGGACAATCGAATCTTCACGAGC 60
Db	46	ATGATCAAAACATACACAACTCTCCCGATCTGGCACTGAATGAGCTGCCATGC 105
Oy	61	ATGAGAATTTTATGTAATTTACTTACTTGTTTTCTTATCACCCAGATGATGGGTACGA 120
Db	106	ATGAAAATTTTATGTAATTTACTTACTTGTTTTCTTATCACCCAGATGATGGGTACGA 165
Oy	121	CTTTTGTCTGTAATCTTCATATAAGTTGGACAAGATGAAATGAAGAAAGAAATCTCAT 180
Db	166	CTTTTGTCTGTAATCTTCATATAAGTTGGACAAGATGAAATGAAGAAAGAAATCTCAT 225
Oy	181	GAGATTTTGTATTCATGMAAACGATACAGATGCACACAGAGAAAGATCTTATCC 240
Db	226	GAGATTTTGTATTCATGMAAACGATACAGATGCACACAGAGAAAGATCTTATCC 285
Oy	241	TTCATGAACTGTGAGAAATTAAGCCAGTTTGAGGCTTGTGAGAGATTAATATGTA 300
Db	286	TTCATGAACTGTGAGAAATTAAGCCAGTTTGAGGCTTGTGAGAGATTAATATGTA 345
Oy	301	AACAAAGGAGACGMAAGAAAGAAAACACTTTGMAATCAAAAAGGTGATCAGAACTT 360
Db	346	AACAAAGGAGACGMAAGAAAGAAAACACTTTGMAATCAAAAAGGTGATCAGAACTT 405
Oy	361	CAAATTTGGGCAATGTCTATTAAGTAGGCGCAGACGTAAAAACAATCTGATTACAGTGG 420
Db	406	CAAATTTGGGCAATGTCTATTAAGTAGGCGCAGACGTAAAAACAATCTGATTACAGTGG 465
Oy	421	GCTGAAAAGGATATCTACACCATGAGCAAACTTGGTAACTCTTGAAAAATGGGAAACAG 480
Db	466	GCTGAAAAGGATATCTACACCATGAGCAAACTTGGTAACTCTTGAAAAATGGGAAACAG 525
Oy	481	CTGACCGTTAAAAGACAGAGCTCTTAATATATATGATGCCAAGTACACTTCTGTTCCAT 540
Db	526	CTGACCGTTAAAAGACAGAGCTCTTAATATATATGATGCCAAGTACACTTCTGTTCCAT 585
Oy	541	CGGGAAGCTTCAGTCAAGCTCCATTTATAGCAGCCTGTGCTAAAGTCCCCTGGATGA 600
Db	586	CGGGAAGCTTCAGTCAAGCTCCATTTATAGCAGCCTGTGCTAAAGTCCCCTGGATGA 645
Oy	601	TTTGAGGAAATCTTATCGAAGCTGGAAATCCACAGTTTCGGCAAACTTTCGGGGCAA 660
Db	646	TTTGAGGAAATCTTATCGAAGCTGGAAATCCACAGTTTCGGCAAACTTTCGGGGCAA 705

Oy 661 CAATCCATTCACTTGGAGAGATTGATTCGAACAGAGCTTGGCTTGTTCAT 720
 Db 706 CAATCCATTCACTTGGAGAGATTGATTCGAACAGAGCTTGGCTTGTTCAT 765
 Oy 721 GTGACTGATCCAAAGCAAGTGAAGCCATGCGCTTCACTGCTTGTTCATAA 780
 Db 766 GTGACTGATCCAAAGCAAGTGAAGCCATGCGCTTCACTGCTTGTTCATAA 825
 Oy 781 CTCTGA 786
 Db 826 CTCTGA 831

RESULT 15 US-08-770-974-11

Sequence 11, Application US/08770974
 Patent No. 6290972

GENERAL INFORMATION:

APPLICANT: ARMITAGE, RICHARD
 APPLICANT: FANSLON, WILLIAM
 APPLICANT: SPRIGGS, MELANIE
 APPLICANT: SRINIVASAN, SUBHASHINI
 APPLICANT: GIBSON, MARYLOU
 TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
 NUMBER OF SEQUENCES: 24
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: IMMUNEX CORPORATION
 STREET: 51 UNIVERSITY STREET
 CITY: SEATTLE
 STATE: WASHINGTON
 COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Apple Operating System 7.1

SOFTWARE: Microsoft Word for Apple, version 5.1a

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/770,974

FILING DATE: 20-DEC-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/477,733

FILING DATE: 02-AUG-1995

APPLICATION NUMBER: 08/249,189

FILING DATE: May 24, 1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/969,703

FILING DATE: October 23, 1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/805,723

FILING DATE: December 5, 1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/783,707

FILING DATE: October 25, 1991

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia A.

REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2802-D

TELECOMMUNICATION INFORMATION:

TELEPHONE: 2065870430

TELEFAX: 2065870606

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:
 LENGTH: 840 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:

ORGANISM: Homo sapiens
 IMMEDIATE SOURCE:
 CLONE: CD40-L
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 46..831
 US-08-770-974-11

Query Match 97.2%; Score 763.6; DB 4; Length 840;
 Best Local Similarity 98.2%; Pred. No. 1,4e-212;
 Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Oy 1 ATGATGAGAAATATACAGCAAGCTTCCCGCATCGTGGCAATGAGATTCAGAGC 60
 Db 46 ATGATGAGAAATATACAGCAAGCTTCCCGCATCGTGGCAATGAGATTCAGAGC 105
 Oy 61 ATGAGATTTTAT 120
 Db 106 ATGAGATTTTAT 165
 Oy 121 CTTTGTGTGTATCTTATATAGAGGTGACAGATAGAGATAGAGATATCTTAT 180
 Db 166 CTTTGTGTGTATCTTATATAGAGGTGACAGATAGAGATAGAGATATCTTAT 225
 Oy 181 GAAGATTTTAT 240
 Db 226 GAAGATTTTAT 285
 Oy 241 TTACTGAATCTGTAGAGATTTAAAGCACTTTGAAAGCTTTGAAAGATATATCT 300
 Db 286 TTACTGAATCTGTAGAGATTTAAAGCACTTTGAAAGCTTTGAAAGATATATCT 345
 Oy 301 AACAAAG 360
 Db 346 AACAAAG 405
 Oy 361 CAATTCGGGCAATGATCTAATAGAGGCGGCAAGTAAACATCTGTGTATACAG 420
 Db 406 CAATTCGGGCAATGATCTAATAGAGGCGGCAAGTAAACATCTGTGTATACAG 465
 Oy 421 GGTGAAAAGAGAT 480
 Db 466 GGTGAAAAGAGAT 525
 Oy 481 CTGACGTTAAAGACAGAGACTTATATATATATATATATATATATATATATAT 540
 Db 526 CTGACGTTAAAGACAGAGACTTATATATATATATATATATATATATATATAT 585
 Oy 541 CGGGAAGCTTGAAGTCAAGCTCAATTAATAGGAGCTCTGCGTAAAGTCCCGGTGA 600
 Db 586 CGGGAAGCTTGAAGTCAAGCTCAATTAATAGGAGCTCTGCGTAAAGTCCCGGTGA 645
 Oy 601 TTGAGAGAAATCTTATCTAGAGCTGCAATATACCAAGTTCCGCAACCTTGCAG 660
 Db 646 TTGAGAGAAATCTTATCTAGAGCTGCAATATACCAAGTTCCGCAACCTTGCAG 705
 Oy 661 CAATCCATTCACTTGGAGAGATTGATTCGAACAGAGCTTGGCTTGTTCAT 720
 Db 706 CAATCCATTCACTTGGAGAGATTGATTCGAACAGAGCTTGGCTTGTTCAT 765
 Oy 721 GTGACTGATCCAAAGCAAGTGAAGCCATGCGCTTCACTGCTTGTTCATAA 780
 Db 766 GTGACTGATCCAAAGCAAGTGAAGCCATGCGCTTCACTGCTTGTTCATAA 825
 Oy 781 CTCTGA 786
 Db 826 CTCTGA 831

Search completed: March 9, 2003, 04:46:17
 Job time : 36.6448 secs

11

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 8, 2003, 18:35:23 ; Search time 2048.61 Seconds

(without alignments)
1116.008 Million cell updates/sec

Title: US-08-982-272-7

Perfect score: 786

Sequence: 1 ATGATGAAACATACAGCA.....TTGGCTTACCAACTCTGA 786

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: gb_hcg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_stb:*

12: gb_sy:*

13: gb_un:*

14: gb_vi:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_ov:*

22: em_ov:*

23: em_ov:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_stb:*

28: em_un:*

29: em_vi:*

30: em_hcg_hum:*

31: em_hcg_inv:*

32: em_hcg_other:*

33: em_hcg_mus:*

34: em_hcg_pin:*

35: em_hcg_rtd:*

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37: em_hcg_vrt:*

38: em_sy:*

39: em_higo_hum:*

40: em_higo_mus:*

41: em_higo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	754	95.9	786	6	187864	187864 Sequence 3
2	754	95.9	840	6	AR044779	AR044779 Sequence
3	754	95.9	840	6	AR076926	AR076926 Sequence
4	754	95.9	840	6	AR078316	AR078316 Sequence
5	754	95.9	840	6	AR085419	AR085419 Sequence
6	754	95.9	840	6	AR103375	AR103375 Sequence
7	754	95.9	840	6	AR106246	AR106246 Sequence
8	754	95.9	840	6	AR169232	AR169232 Sequence
9	754	95.9	840	6	AR171647	AR171647 Sequence
10	754	95.9	840	6	123893	123893 Sequence 1
11	754	95.9	840	6	127345	127345 Sequence 7
12	754	95.9	840	6	167828	167828 Sequence 1
13	754	95.9	879	6	AX090039	AX090039 Sequence
14	754	95.9	879	6	HSCGP39MR	215017 H. sapiens m
15	754	95.9	1803	9	HSCD40	X67878 H. sapiens m
16	754	95.9	1816	9	HUMCD40L	L07414 Human CD40-
17	754	95.9	1822	9	HSTRAPA	X68550 H. sapiens T
18	744.4	94.7	1058	9	AF344841	AF344841 Cercopithec
19	744.4	94.7	1058	9	AF344859	AF344859 Macaca mu
20	736.8	94.0	839	9	HACD40L	X96710 H. sapiens m
21	723.6	92.1	974	9	AF344860	AF344860 Actin tcl
22	723.6	92.1	975	9	AF344844	AF344844 Callithrix
23	638.2	81.2	1425	6	AR076929	AR076929 Sequence
24	638.2	81.2	1425	6	AR078319	AR078319 Sequence
25	638.2	81.2	1425	6	AR085422	AR085422 Sequence
26	638.2	81.2	1425	6	AR103378	AR103378 Sequence
27	638.2	81.2	1425	6	AR169235	AR169235 Sequence
28	637.2	81.1	929	6	AR076932	AR076932 Sequence
29	637.2	81.1	929	6	AR078322	AR078322 Sequence
30	637.2	81.1	929	6	AR085425	AR085425 Sequence
31	637.2	81.1	929	6	AR103381	AR103381 Sequence
32	637.2	81.1	929	6	AR169238	AR169238 Sequence
33	637.2	81.1	929	6	187867	187867 Sequence
34	636	80.9	1566	6	AX455878	AX455878 Sequence 10
35	635.6	80.9	864	4	BTC401IG	Z49469 B. taurus mR
36	606.8	77.2	904	9	AF344853	AF344853 Macaca ne
37	603.6	76.8	788	4	AF079105	AF079105 Felis cat
38	600.4	76.4	786	4	AB040443	AB040443 Sus scrofa
39	594	75.6	783	6	AR076918	AR076918 Sequence
40	594	75.6	783	6	AR078308	AR078308 Sequence
41	594	75.6	783	6	AR085411	AR085411 Sequence
42	594	75.6	783	6	AR103367	AR103367 Sequence
43	594	75.6	783	6	AR169224	AR169224 Sequence
44	594	75.6	783	6	187865	187865 Sequence 5
45	594	75.6	1250	10	MMCD40	X65453 M. musculus

ALIGNMENTS

RESULT 1

187864

LOCUS 187864

DEFINITION Sequence 3 from patent US 5716805.

ACCESSION 187864

VERSION 187864.1 GI:3407804

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 786)

AUTHORS Strinivasan,S. and Spriggs,M.K.

TITLE Methods of preparing soluble, oligomeric proteins

JOURNAL Patent: US 5716805-A 3 10-FEB-1998;

FEATURES Location/Qualifiers

187864 bp DNA linear PAT 10-AUG-1998

source 1..786
/organism="unknown"
BASE COUNT 250 a 168 c 168 g 200 t
ORIGIN

Query Match 95.9%; Score 754; DB 6; Length 786;
Best Local Similarity 97.5%; Pred. No. 5.1e-191;
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ATGATGAAACATACGACCACTTCCCGAGTCGGGCACTGAGACTCCAGCGAGC 60
DB 1 ATGATGAAACATACGACCACTTCCCGAGTCGGGCACTGAGACTCCAGCGAGC 60
QY 61 ATGAGATTTTATGATTTTACTTACTGTTTCTTATCACCCTGATGATCTG 120
DB 61 ATGAGATTTTATGATTTTACTTACTGTTTCTTATCACCCTGATGATCTG 120
QY 121 CTTTTCCTGATCTTATGAGAGTTGAGAGATGAGATGAGATGAGATCTTAT 180
DB 121 CTTTTCCTGATCTTATGAGAGTTGAGAGATGAGATGAGATGAGATCTTAT 180
QY 181 GAAGATTTTATGATTTTACTTACTGTTTCTTATCACCCTGATGATCTG 240
DB 181 GAAGATTTTATGATTTTACTTACTGTTTCTTATCACCCTGATGATCTG 240
QY 241 TTAAGTAACTGAGAGATTTAAAGGCACTTGAAGCTTGTGAGATTAATGTTA 300
DB 241 TTAAGTAACTGAGAGATTTAAAGGCACTTGAAGCTTGTGAGATTAATGTTA 300
QY 301 AACAAAG 360
DB 301 AACAAAG 360
QY 361 CAATTTGGGCACTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 361 CAATTTGGGCACTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
QY 421 GCTGAAAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
DB 421 GCTGAAAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
QY 481 CTGACCGTTTAAAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
DB 481 CTGACCGTTTAAAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
QY 541 CGGAGAGCTTGAAGTCAATTTATGAGAGAGAGAGAGAGAGAGAGAG 600
DB 541 CGGAGAGCTTGAAGTCAATTTATGAGAGAGAGAGAGAGAGAGAGAG 600
QY 601 TTGAGAGAGATCTTATCTGAGAGCTGCAAAATGAGAGAGAGAGAGAG 660
DB 601 TTGAGAGAGATCTTATCTGAGAGCTGCAAAATGAGAGAGAGAGAGAG 660
QY 661 CAATTCATCTTGGAGAGAGATTTGAAATGCAACAGAGAGAGAGAGAG 720
DB 661 CAATTCATCTTGGAGAGAGATTTGAAATGCAACAGAGAGAGAGAGAG 720
QY 721 GTGAGATGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
DB 721 GTGAGATGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
QY 781 CTCTGA 786
DB 781 CTCTGA 786

RESULT 2
AR044779 840 bp DNA linear PAT 29-SEP-1999
LOCUS AR044779
DEFINITION Sequence 3 from patent US 5817516.
ACCESSION AR044779
VERSION AR044779.1 GI:596244
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 840)
AUTHORS Henry, M. and Castle, B.
TITLE Methods for proliferating and differentiating B cells with high density membrane CD40 ligand
JOURNAL Patent: US 5817516-A 3 06-Oct-1998;
FEATURES Location/Qualifiers
source 1..840
/organism="unknown"
BASE COUNT 263 a 182 c 181 g 214 t
ORIGIN

Query Match 95.9%; Score 754; DB 6; Length 840;
Best Local Similarity 97.5%; Pred. No. 5.1e-191;
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ATGATGAAACATACGACCACTTCCCGAGTCGGGCACTGAGACTCCAGCGAGC 60
DB 22 ATGATGAAACATACGACCACTTCCCGAGTCGGGCACTGAGACTCCAGCGAGC 81
QY 61 ATGAGATTTTATGATTTTACTTACTGTTTCTTATCACCCTGATGATCTG 120
DB 82 ATGAGATTTTATGATTTTACTTACTGTTTCTTATCACCCTGATGATCTG 141
QY 121 CTTTTCCTGATCTTATGAGAGTTGAGAGATGAGATGAGATGAGATCTTAT 180
DB 142 CTTTTCCTGATCTTATGAGAGTTGAGAGATGAGATGAGATGAGATCTTAT 201
QY 181 GAAGATTTTATGATTTTACTTACTGTTTCTTATCACCCTGATGATCTG 240
DB 202 GAAGATTTTATGATTTTACTTACTGTTTCTTATCACCCTGATGATCTG 261
QY 241 TTAAGTAACTGAGAGATTTAAAGGCACTTGAAGCTTGTGAGATTAATGTTA 300
DB 262 TTAAGTAACTGAGAGATTTAAAGGCACTTGAAGCTTGTGAGATTAATGTTA 321
QY 301 AACAAAG 360
DB 322 AACAAAG 381
QY 361 CAATTTGGGCACTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 382 CAATTTGGGCACTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 441
QY 421 GCTGAAAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
DB 442 GCTGAAAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 501
QY 481 CTGACCGTTTAAAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
DB 502 CTGACCGTTTAAAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 561
QY 541 CGGAGAGCTTGAAGTCAATTTATGAGAGAGAGAGAGAGAGAGAGAG 600
DB 562 CGGAGAGCTTGAAGTCAATTTATGAGAGAGAGAGAGAGAGAGAGAG 621
QY 601 TTGAGAGAGATCTTATCTGAGAGCTGCAAAATGAGAGAGAGAGAGAG 660
DB 622 TTGAGAGAGATCTTATCTGAGAGCTGCAAAATGAGAGAGAGAGAGAG 681
QY 661 CAATTCATCTTGGAGAGAGATTTGAAATGCAACAGAGAGAGAGAGAG 720
DB 682 CAATTCATCTTGGAGAGAGATTTGAAATGCAACAGAGAGAGAGAGAG 741
QY 721 GTGAGATGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
DB 742 GTGAGATGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 801
QY 781 CTCTGA 786
DB 802 CTCTGA 807

RESULT 3					
LOCUS	AR076926				
DEFINITION	Sequence 11 from patent US 5961974.	840 bp	DNA	linear	PAT 31-AUG-2000
ACCESSION	AR076926				
VERSION	AR076926.1				
KEYWORDS	Unknown.				
SOURCE	Unknown.				

REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES	source	BASE COUNT	ORIGIN
1 (bases 1 to 840)	Armitage,R.J., Panslow,W.C. and Spriggs,M.K.	Monoclonal antibodies to CD40 ligand, pharmaceutical composition comprising the same and hybridomas producing the same	US 5961974-A 11 05-OCT-1999;	Location/Qualifiers	1..840	266 a	185 c 175 g 214 t
					/organism="unknown"		

Query Match	95.9%	Score 754;	DB 6;	Length 840;
Best Local Similarity	97.5%	Pred. No. 5.1e-191;		
Matches 766; Conservative	0;	Mismatches 20;	Indels 0;	Gaps 0;

Qy	1	ATGATGAAAATCATACACCAACCTTCCCGAAGTCGTGGCAATCTGACCTTCAAGCAGAC	60
Db	46	ATGATGAAAATCATACCAACCAACTCTCCCGAATCTGGCGGCACTGGACTGGCCATCAAC	105
Qy	61	ATGGAAGATTTTAAATATTAATTTACTCTAATCTGTTCCTTATCAACCAATGATTTGATCTGTG	120
Db	106	ATGAAATATTTTAAATATTAATTTACTACTGTTCCTTATCAACCAAGATTTGGTTCAGCA	165
Qy	121	CTTTTGTCTGTATTCCTTACATGAAGGTTGGACAAGATGAAGATGAAGAAATCTTCAT	180
Db	166	CTTTTGTCTGTATTCCTTACATGAAGGTTGGACAAGATGAAGATGAAGAAATCTTCAT	225
Qy	181	GAGAATTTTGATTCATGAAGAAACGATACAGAGATGCACACAGAGAAAGATCTTATTC	240
Db	226	GAGAATTTTGATTCATGAAGAAACGATACAGAGATGCACACAGAGAAAGATCTTATTC	285
Qy	241	TTAATGAACTGTGAGAGATTTAAAGCCAGTTTGAAGGCTTTGGAGATTAATATGTTA	300
Db	286	TTACTGAATGTGGAGATTTAAAGCCAGTTTGAAGGCTTTGGAGATTAATATGTTA	345
Qy	301	AACAAAGAGAGACGAAGAAAGAAAACAGCTTTGAATGCAAAAGGTGATCAGATCCT	360
Db	346	AACAAAGAGAGAGACGAAGAAAGAAAACAGCTTTGAATGCAAAAGGTGATCAGATCCT	405
Qy	361	CAAAATGGCGCACATGTCATTAAGTAGGCGACAGAGATTAACCAATCTGTATTCACATGG	420
Db	406	CAAAATGGCGCACATGTCATTAAGTAGGCGCACAGATTAACCAATCTGTATTCACATGG	465
Qy	421	GCTGAAAAGGATCTACACACATGAGCAACAATCTGTATCCTCTGAAAATGGGAAACAG	480
Db	466	GCTGAAAAGGATCTACACACATGAGCAACAATCTGTATCCTCTGAAAATGGGAAACAG	525
Qy	481	CTGACCGTTAAAGACAAAGGACTCTATTATATCTATGCCCAAGTACCTTCTTCTCAAT	540
Db	526	CTGACCGTTAAAGACAAAGGACTCTATTATATCTATGCCCAAGTACCTTCTTCTCAAT	585
Qy	541	CGGGAAGCTTGAATCAAGCTCATTTATAGCCAGAGCTCTGCTTAAAGTCCCGCGGTAGA	600
Db	586	CGGGAAGCTTGAATCAAGCTCATTTATAGCCAGAGCTCTGCTTAAAGTCCCGCGGTAGA	645
Qy	601	TTGGAAGAAATCTTACTACAGAGCTGCAATTAACCAAGTCCCGCAAACTGGCGGGCA	666
Db	646	TTGGAAGAAATCTTACTACAGAGCTGCAATTAACCAAGTCCCGCAAACTGGCGGGCA	705
Qy	661	CAATCATTCATCTGGAGAGATTTTGAATGCAACAGGTCTCTGATTTTGTCAAT	720

Db	706	CAATCAATCACTTGGGAAGATATTGAATTCACAACCAAGGCTTGAGGATTGTCAAT	765
Qy	721	GTGACTGATCAAGCCAAAGTAGCATGAGCAGTGCTTCAGTCTCTTGGCTTACTCAAA	780
Db	766	GGAATGATCCAAAGCCAAATAGACCAATGAGCACTGGCTTCACTCTTGGCTTACTCAAA	825
Qy	781	CTCTGTA	786
Db	826	CTCTGTA	831

RESULT 4			
AR078316	AR078316	840 bp	linear
LOCUS	AR078316	840 bp	DNA
DEFINITION	Sequence 11 from patent US 5962406.		
ACCESSION	AR078316		
VERSION	AR078316.1	GI:10005062	

REFERENCE	AUTHORS	TITLE	JOURNAL FEATURES	source	BASE COUNT	ORIGIN
1 (bases 1 to 840)	Armitage, R. J., Fenslow, W. C., Springs, M. K., Srinivasan, S., Gibson, M. G., Morris, A. E. and McGee, J. T.	Recombinant soluble Cys4 ligand polypeptide and pharmaceutical composition containing the same	Patent: US 5962406-A 11/05-Oct-1999;	Location/Qualifiers		
				1..840		
				/organism="unknown"		
				266 a 185 c 175 g	214 t	

	Query Match	95.9%	Score 754	DB 6	Length 840	
	Best Local Similarity	97.5%	Pred. No. 5	Le-191		
	Matches 766	Conservative 0	Mismatches 20	Indels 0	Gaps 0	
Qy	1	ATGATGAAACATACAGCAACTTCCCGCATCTCGTGGCAATCGAATCTTCACGAGC	60			
Dh	46	ATGATGCAAAACATACACAACTTCTCCCGATCTCGGCGCATCGACCTGGCCATACGC	105			
Qy	61	ATGAGATTTTATGTATTTACTTACTCTCTTTCCCTATCACCCAAATGATGGATCTGTG	120			
Dh	106	ATGAAATTTTATGATGATTTACTTACTTCTTTCTTATCATCCAGATGATGGGCGACA	165			
Qy	121	CTTTTTCGTGTATCTTCAATGAGCTTGGACAATATGAAATGAAAGGAAATTTTCAAT	180			
Dh	166	CTTTTTCGTGTATCTTCAATGAGCTTGGACAATATGAAATGAAAGGAAATTTTCAAT	225			
Qy	181	GAAATTTTGTATCATGAAAGATACAGAGATGACACAGAGAAAGATCTTATACC	240			
Dh	226	GAAATTTTGTATCATGAAAGATACAGAGATGACACAGAGAAAGATCTTATACC	285			
Qy	241	TTAATGAACTGTGAGAGATTAAGGCAATTTGAAGCTTTTGAAGATATAATGTTA	300			
Dh	286	TTAATGAACTGTGAGAGATTAAGGCAATTTGAAGCTTTTGAAGATATAATGTTA	345			
Qy	301	AACAAAGAGACAGAGAAAGAAACGCTTTGAATGCAAAAAGGTGTCAGATCT	360			
Dh	346	AACAAAGAGACAGAGAAAGAAACGCTTTGAATGCAAAAAGGTGTCAGATCT	405			
Qy	361	CAATTTCCGCGCATGTCTAATGTAGGCCGACGATTAACACATCTGTGTACAGTGG	420			
Dh	406	CAATTTCCGCGCATGTCTAATGTAGGCCGACGATTAACACATCTGTGTACAGTGG	465			
Qy	421	GCTGAAAGAGATCTACACCATGAGCAACCTGTGAACCTGTGAAATGGGAAACAG	480			
Dh	466	GCTGAAAGAGATCTACACCATGAGCAACCTGTGAACCTGTGAAATGGGAAACAG	525			
Qy	481	CTGACGGTTAAAGCAAGGACCTTATATCTATGCCCAAGTCACTTTCTGTCCAAAT	540			
Dh	526	CTGACGGTTAAAGCAAGGACCTTATATCTATGCCCAAGTCACTTTCTGTCCAAAT	585			

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QY 541 CGGAGAGCTTCGAGTCAAGCTCCATTTATAGCAGAGCTCTGCTCCCTAAAGTCCCGGCTAGA 600
DB 586 CGGAGAGCTTCGAGTCAAGCTCCATTTATAGCAGAGCTCTGCTCCCTAAAGTCCCGGCTAGA 615
QY 601 TTGAGAGAAATTTACTGACAGCTGACCAATACCAAGTTCGCCCAACCTTGGCGGCA 660
DB 646 TTGAGAGAAATTTACTGACAGCTGACCAATACCAAGTTCGCCCAACCTTGGCGGCA 705
QY 661 CAATCCATTCATCTGGAGAGAGTATTTGAATTGCAACAGGCTGCTGGTGTTCAT 720
DB 706 CAATCCATTCATCTGGAGAGAGTATTTGAATTGCAACAGGCTGCTGGTGTTCAT 765
QY 721 GTGACTGATCCAGCCAAAGTGAAGCCATGCGCTTCAGGTCTTTGGCTTACATA 780
DB 766 GTGACTGATCCAGCCAAAGTGAAGCCATGCGCTTCAGGTCTTTGGCTTACATA 825
QY 781 CTCTGA 786
DB 826 CTCTGA 831

RESULT 5
AR085419 840 bp DNA linear PAT 01-SEP-2000
LOCUS Sequence 11 from patent US 5981724.
DEFINITION AR085419
ACCESSION AR085419
VERSION AR085419.1 GI:10012188
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 840)
AUTHORS Armitage,R.J., Fanslow,W.C., Spriggs,M.K., Srinivasan,S.,
Gibson,M.G., Morris,A.E. and McGraw,J.T.
TITLE DNA encoding CD40 ligand, a cytokine that binds CD40
JOURNAL Patent: US 5981724-A 11 09-NOV-1999;
FEATURES
location/Qualifiers
source 1..840
BASE COUNT 266 a 185 c 175 g 214 t
ORIGIN
Query Match 95.9%; Score 754; DB 6; Length 840;
Best Local Similarity 97.5%; Pred. No. 5.1e-191;
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ATGATAGAAACATACACCACTTCCCGCAATCCGTCGCACTTGACATCCAGCAGC 60
DB 46 ATGATAGAAACATACACCACTTCCCGCAATCCGTCGCACTTGACATCCAGCAGC 105
QY 61 ATGAGATTTTATGATTTACTTACTGTTTCTTATCACCCTAAATGATGGATCTGTG 120
DB 106 ATGAGATTTTATGATTTACTTACTGTTTCTTATCACCCTAAATGATGGATCTGTG 165
QY 121 CTTTTCGTGTATCTTATAGAGGTGGACAGATAGAGATAGAGATCTTAT 180
DB 166 CTTTTCGTGTATCTTATAGAGGTGGACAGATAGAGATAGAGATCTTAT 225
QY 181 GAAGATTTTATGATGAAACGATACAGATGCAACAGAGAAAGATCTTATCC 240
DB 226 GAAGATTTTATGATGAAACGATACAGATGCAACAGAGAAAGATCTTATCC 285
QY 241 TTACTGAACCTGAGAGATTTAAAGCCATTTGAAGGCTTTGGAGGATTAATGTTA 300
DB 286 TTACTGAACCTGAGAGATTTAAAGCCATTTGAAGGCTTTGGAGGATTAATGTTA 345
QY 301 AACAAAGAGAGAGAGAGAAAGAAACGCTTTGAATGCAAAAAGGTGATCAGATCCT 360
DB 346 AACAAAGAGAGAGAGAGAAAGAAACGCTTTGAATGCAAAAAGGTGATCAGATCCT 405
QY 361 CAAATGGCGCAATGTCATTAAGTGAAGCAGAGATTAACAAATCTGTTACAGTGG 420
DB 406 CAAATGGCGCAATGTCATTAAGTGAAGCAGAGATTAACAAATCTGTTACAGTGG 465

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QY 421 GCTGAAAAAGATCTACACATGAGCAACAACCTTGTAACCTGAAATAGGAAACAG 480
DB 466 GCTGAAAAAGATCTACACATGAGCAACAACCTTGTAACCTGAAATAGGAAACAG 525
QY 481 CTGACCTTTAAAGACAGAGATCTTATATCTATGCCCAGTCACTTGTGTCCAT 540
DB 526 CTGACCTTTAAAGACAGAGATCTTATATCTATGCCCAGTCACTTGTGTCCAT 585
QY 541 CGGAGAGCTTCGAGTCAAGCTCCATTTATAGCAGAGCTCTGCTCCCTAAAGTCCCGGCTAGA 600
DB 586 CGGAGAGCTTCGAGTCAAGCTCCATTTATAGCAGAGCTCTGCTCCCTAAAGTCCCGGCTAGA 645
QY 601 TTGAGAGAAATTTACTGACAGCTGCAAAATCCACAGTTCGCCCAACCTTGGCGGCA 660
DB 646 TTGAGAGAAATTTACTGACAGCTGCAAAATCCACAGTTCGCCCAACCTTGGCGGCA 705
QY 661 CAATCCATTCATCTGGAGAGAGTATTTGAATTGCAACAGGCTTCCGTGTTCAT 720
DB 706 CAATCCATTCATCTGGAGAGAGTATTTGAATTGCAACAGGCTTCCGTGTTCAT 765
QY 721 GTGACTGATCCAGCCAAAGTGAAGCCATGCGCTTCAGGTCTTTGGCTTACATA 780
DB 766 GTGACTGATCCAGCCAAAGTGAAGCCATGCGCTTCAGGTCTTTGGCTTACATA 825
QY 781 CTCTGA 786
DB 826 CTCTGA 831

RESULT 6
AR103375 840 bp DNA linear PAT 14-FEB-2001
LOCUS AR103375
DEFINITION Sequence 11 from patent US 6087329.
ACCESSION AR103375
VERSION AR103375.1 GI:12814963
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 840)
AUTHORS Armitage,R.J., Fanslow,W.C. and Spriggs,M.K.
TITLE CD40 ligand polypeptide
JOURNAL Patent: US 6087329-A 11 11-JUL-2000;
FEATURES
location/Qualifiers
source 1..840
BASE COUNT 266 a 185 c 175 g 214 t
ORIGIN
Query Match 95.9%; Score 754; DB 6; Length 840;
Best Local Similarity 97.5%; Pred. No. 5.1e-191;
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ATGATAGAAACATACACCACTTCCCGCAATCCGTCGCACTTGACATCCAGCAGC 60
DB 46 ATGATAGAAACATACACCACTTCCCGCAATCCGTCGCACTTGACATCCAGCAGC 105
QY 61 ATGAGATTTTATGATTTACTTACTGTTTCTTATCACCCTAAATGATGGATCTGTG 120
DB 106 ATGAGATTTTATGATTTACTTACTGTTTCTTATCACCCTAAATGATGGATCTGTG 165
QY 121 CTTTTCGTGTATCTTATAGAGGTGGACAGATAGAGATAGAGATCTTAT 180
DB 166 CTTTTCGTGTATCTTATAGAGGTGGACAGATAGAGATAGAGATCTTAT 225
QY 181 GAAGATTTTATGATGAAACGATACAGATGCAACAGAGAAAGATCTTATCC 240
DB 226 GAAGATTTTATGATGAAACGATACAGATGCAACAGAGAAAGATCTTATCC 285
QY 241 TTACTGAACCTGAGAGATTTAAAGCCATTTGAAGGCTTTGGAGGATTAATGTTA 300
DB 286 TTACTGAACCTGAGAGATTTAAAGCCATTTGAAGGCTTTGGAGGATTAATGTTA 345

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Qy	301	AACAAAGGAGACGAAAGAAAGAAAACACTTGAATATGCAAAAAAGATGATCAAGATCT	360
Dd	346	AACAAAGGAGACGAAAGAAAGAAAACACTTGAATATGCAAAAAAGATGATCAAGATCT	405
Qy	361	CAAAATGGGCAATCTCATATGAGAGGCGACAGATPAAAACAATCTGTGTTACATGGG	420
Dd	406	CAAAATGGGCAATCTCATATGAGAGGCGACAGATPAAAACAATCTGTGTTACATGGG	465
Qy	421	GCTGAAAAGGATATCAACCATAGCAACAACTTGTAACCTTGAAAAATGGAAAAAAG	480
Dd	466	GCTGAAAAGGATATCAACCATAGCAACAACTTGTAACCTTGAAAAATGGAAAAAAG	525
Qy	481	CTGACCGTTAAAAAGACAAGACTATATTATATCATGCCAAGTACCTTCTTTCAT	540
Dd	526	CTGACCGTTAAAAAGACAAGACTATATTATATCATGCCAAGTACCTTCTTTCAT	585
Qy	541	CGGGAAGCTTCAGATCAGCTCCATTTATAGCAAGCTCTGCTPAAAGTCCCGGGTGA	600
Dd	586	CGGGAAGCTTCAGATCAGCTCCATTTATAGCAAGCTCTGCTPAAAGTCCCGGGTGA	645
Qy	601	TTGAGAGAAATCTTACTGAGAGCTGCAAAATCCACAAGTTCCGCCAAAACCTTGCGGCA	660
Dd	646	TTGAGAGAAATCTTACTGAGAGCTGCAAAATCCACAAGTTCCGCCAAAACCTTGCGGCA	705
Qy	661	CAATCAATTCATCTTGGAGAGAGTATTTGAATATGCAACAGAGTCTTCGAGTGTTCAT	720
Dd	706	CAATCAATTCATCTTGGAGAGAGTATTTGAATATGCAACAGAGTCTTCGAGTGTTCAT	765
Qy	721	GTGAATGATCAAGCCAGATAGCAATGCAATGGCTTCAACGCTTGGCTTACATCAAA	780
Dd	766	GTGAATGATCAAGCCAGATAGCAATGCAATGGCTTCAACGCTTGGCTTACATCAAA	825
Qy	781	CTCTGA 786	
Dd	826	CTCTGA 831	

RESULT 7	LOCUS	840 bp	DNA	linear	PAT 14-FEB-2001
AR106246	Sequence 7 from patent US 6106832.				
DEFINITION	AR106246				
ACCESSION	AR106246.1	GI:12820776			
VERSION					
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 840)				
AUTHORS	Spijgs, M.K., Armillage, R.J., Fanslow, W.C. III and Widmer, M.B.				
TITLE	Treatment of individuals exhibiting defective CP40L				
JOURNAL	Patent: US 6106832-A 7 22-AUG-2000;				
FEATURES	location/Qualifiers				
source	1..840				
	/organism="unknown"				
BASE COUNT	266 a 185 c 175 g	214 t			
ORIGIN					
Query Match	95.9%; Score 754; DB 6; Length 840;				
Best Local Similarity	97.5%; Pred. No. 5.1e-191;				
Matches 766; Conservative	0; Mismatches 20; Indels 0; Gaps 0;				
QY	1 ATGATAGAAACATACAGCCACCTCCGCCGAGATCTCGSGCAATCGACCTTCGACGAGC 60				
Db	46 ATGATCGAAACATACACCAAACTCTCCCGGATCTCGSGCACTGACCTGCCATCAGC 105				
QY	61 ATGAAGATTTTATATGATTTATTTACTTACTCTGTTTTCCTATACCCCAAGATGATCTGTG 120				
Db	106 ATGAAAATTTTATATGATTTATTTACTTACTCTGTTTTCCTATACCCCAAGATGATGSGTGACA 165				
QY	121 CTTTTCGTGTGATCTTCATAGAGGTTGGACAAGATAGAGATGAAGAAATTTTCAT 180				
Db	166 CTTTTCGTGTGATCTTCATAGAGGTTGGACAAGATAGAGATGAAGAAATTTTCAT 225				

Qy	181	GAGGTTTTTGTATTCATGAAAAAGATACAGAGATGCAACAGGAGAAAAATCTTATCC	240
Db	226	GAGGATTTTGTATTCATGAAAAAGATACAGAGATGCAACAGGAGAAAAATCTTATCC	285
Qy	241	TTATCTGAACCTGTGAGAGATTTAAAGCCGATTTGAAGCTTTGTGAAGATTAATGTTA	300
Db	286	TTATCTGAACCTGTGAGAGATTTAAAGCCGATTTGAAGCTTTGTGAAGATTAATGTTA	345
Qy	301	AACAAAGAGGACGAAAGAAAAAGAAACAGCTTTGAATCAAAAAGGTGACAGATCTCT	360
Db	346	AACAAAGAGGACGAAAGAAAAAGAAACAGCTTTGAATCAAAAAGGTGATCAGATCTCT	405
Qy	361	CAAAATTCGGGCACATGTCATTAAGTGAGCCACAGCTTAACAAACATCTGTGTTACAGTG	420
Db	406	CAAAATTCGGGCACATGTCATTAAGTGAGCCACAGCTTAACAAACATCTGTGTTACAGTG	465
Qy	421	GCTGAAAAAGATACTAACCAAGAGCAACAACTGGTGAACCTGGAATAAGGAGAAACAG	480
Db	466	GCTGAAAAAGATACTAACCAAGAGCAACAACTGGTGAACCTGGAATAAGGAGAAACAG	525
Qy	481	CTGACCGCTTAAAGCAAGGACCTTATTAATCTAAGCCCAAGTCACTTCTGTTCAT	540
Db	526	CTGACCGCTTAAAGCAAGGACCTTATTAATCTAAGCCCAAGTCACTTCTGTTCAT	585
Qy	541	CGGGAAGCTTCCGAGTCAAGCTTCATTTAAGCCAGGCTCTGCTTAAGTCCCCCGGTAGA	600
Db	586	CGGGAAGCTTCCGAGTCAAGCTTCATTTAAGCCAGGCTCTGCTTAAGTCCCCCGGTAGA	645
Qy	601	TTCCGAGAGATCTTATCTCAGAGGTGAATAATCCACAGTTCGGGCCAAACCTTGCGGGGAA	660
Db	646	TTCCGAGAGATCTTATCTCAGAGGTGAATAATCCACAGTTCGGGCCAAACCTTGCGGGGAA	705
Qy	661	CAATTCATTCACCTTGGAGAGATTTGAATTGCAACCAAGGTGCTTCGATGTTTGTCAAT	720
Db	706	CAATTCATTCACCTTGGAGAGATTTGAATTGCAACCAAGGTGCTTCGATGTTTGTCAAT	765
Qy	721	GTGACATATCAAGCAAGTGAGCCATGGGCACTGGCTTCAAGTCTTGTGGCTTATCTCAAA	780
Db	766	GTGACATATCAAGCAAGTGAGCCATGGGCACTGGCTTCAAGTCTTGTGGCTTATCTCAAA	825
Qy	781	CTCTGA 786	
Db	826	CTCTGA 831	

	RESULT	8		
	LOCUS	ARI69232		
	DEFINITION	Sequence	11 from patent US 6290972.	DNA
	ACCESSION	ARI69232		linear
	VERSION	ARI69232.1		PAT 17-DEC-2001
	KEYWORDS	GI:17907047		
	SOURCE	Unknown.		
	ORGANISM	Unknown.		
	REFERENCE	Unclassified.		
	AUTHORS	1 (bases 1 to 840)		
	TITLE	Amitage,R.J., Fanslow,W.C., Spriggs,M.K., Srinivasan,S. and Gibson,M.G.		
	JOURNAL	Method of augmenting a vaccine response by administering CD40 ligand		
	FEATURES	Patent: US 6290972-A 11 18-SEP-2001;		
	SOURCE	Location/Qualifiers 1..840		
	BASE COUNT	/organism="unknown"		
	ORIGIN	266 a 185 c 175 g 214 t		
	Query Match	95.9%; Score 754; DB 6; Length 840;		
	Best Local Similarity	97.5%; Pred. NO.5.1e-191;		
	Matches 766; Conservative	0; Mismatches 20; Indels		
		0; Gaps		
		0;		
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ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 840)
AUTHORS Aruffo, A., Hollenbaugh, D. and Ledbetter, J. A.
TITLE Soluble and its use in B cell stimulation
JOURNAL Patent: US 5540926-A 1 30-JUL-1996;
FEATURES Location/Qualifiers
source 1..840
BASE COUNT 263 a 182 c 181 g 214 t
ORIGIN

Query Match 95.9%; Score 754; DB 6; Length 840;
Best Local Similarity 97.5%; Pred. No. 5.1e-191;
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ATGATGAAACATACAGCAACCTTCCCGAATCCGTGGCAACTGACCTCCAGGAGC 60
DB 22 ATGATGAAACATACAGCAACCTTCCCGAATCCGTGGCAACTGACCTCCAGGAGC 81

QY 61 ATGAGATTTTATGATATTTACTTACTGTTTTCTTATCAACCAATGATGATCTGTG 120
DB 82 ATGAAATTTTATGATATTTACTTACTGTTTTCTTATCAACCAATGATGATGATCTGTG 141

QY 121 CTTTGGCTGTGATCTTCTATAGAGTTGGACAAGATAGAGATGAAAGGATCTTCAT 180
DB 142 CTTTGGCTGTGATCTTCTATAGAGTTGGACAAGATAGAGATGAAAGGATCTTCAT 201

QY 181 GAAGATTTTATGATATTTACTTACTGTTTTCTTATCAACCAATGATGATCTGTG 240
DB 202 GAAGATTTTATGATATTTACTTACTGTTTTCTTATCAACCAATGATGATCTGTG 261

QY 241 TTACTGAACCTGTGAGAGATTTAAAGCCAGTTGAAGCTTTGTGAAGATATATGTTA 300
DB 262 TTACTGAACCTGTGAGAGATTTAAAGCCAGTTGTGAAGCTTTGTGAAGATATATGTTA 321

QY 301 AACAAAGAGAGACGAAGAAAGAAACAGCTTTGAAATGCAAAAAGTGATCAGATCTT 360
DB 322 AACAAAGAGAGACGAAGAAAGAAACAGCTTTGAAATGCAAAAAGTGATCAGATCTT 381

QY 361 CAAATTTGGCGCACATGTCATAGTGAGGCGACAGTAAACCAATCTGTGTTCAGGTG 420
DB 382 CAAATTTGGCGCACATGTCATAGTGAGGCGACAGTAAACCAATCTGTGTTCAGGTG 441

QY 421 GCTGAAAAAGATCTACACATGAGCAACAATTGGTAAACCTGGAATATGGAAACAG 480
DB 442 GCTGAAAAAGATCTACACATGAGCAACAATTGGTAAACCTGGAATATGGAAACAG 501

QY 481 CTGACCGTTAAAGACAAAGAGCTATTATATCTATGCCAAGTCACTTCTGTTCAT 540
DB 502 CTGACCGTTAAAGACAAAGAGCTATTATATCTATGCCAAGTCACTTCTGTTCAT 561

QY 541 CGGGAAGCTTGGAGTCAAGTCACTTATATAGCCAGCTTCTGCTTAAATCCCGGTGAG 600
DB 562 CGGGAAGCTTGGAGTCAAGTCACTTATATAGCCAGCTTCTGCTTAAATCCCGGTGAG 621

QY 601 TTGAGAGAACTTACTCAGAGCTGCAAAATCCCAAGTTCGCAAACTTGGGGCA 660
DB 622 TTGAGAGAACTTACTCAGAGCTGCAAAATCCCAAGTTCGCAAACTTGGGGCA 681

QY 661 CAATCCATTCACTTGGAGAGATTTTGAATTTGAACCAAGTGTCTTGGTGTTCAT 720
DB 682 CAATCCATTCACTTGGAGAGATTTTGAATTTGAACCAAGTGTCTTGGTGTTCAT 741

QY 721 GTGACTGATCCAGCCAAAGTGAGCCATGGCACTGGCTTCACTCTTGGCTTACTCAA 780
DB 742 GTGACTGATCCAGCCAAAGTGAGCCATGGCACTGGCTTCACTCTTGGCTTACTCAA 801

QY 781 CTCTGA 786
DB 802 CTCTGA 807

RESULT 11
LOCUS 127345
DEFINITION Sequence 7 from patent US 5565321.
ACCESSION 127345
VERSION 127345.1 GI:1818121
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 840)
AUTHORS Spriggs, M.K., Armitage, R.J. and Fanslow, W.C. III.
TITLE Detection of mutations in a CD40 ligand gene
JOURNAL Patent: US 5565321-A 7 15-OCT-1996;
FEATURES Location/Qualifiers
source 1..840
BASE COUNT 266 a 185 c 175 g 214 t
ORIGIN

Query Match 95.9%; Score 754; DB 6; Length 840;
Best Local Similarity 97.5%; Pred. No. 5.1e-191;
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ATGATGAAACATACAGCAACCTTCCCGAATCCGTGGCAACTGACCTCCAGGAGC 60
DB 46 ATGATGAAACATACAGCAACCTTCCCGAATCCGTGGCAACTGACCTCCAGGAGC 105

QY 61 ATGAGATTTTATGATATTTACTTACTGTTTTCTTATCAACCAATGATGATCTGTG 120
DB 106 ATGAAATTTTATGATATTTACTTACTGTTTTCTTATCAACCAATGATGATCTGTG 165

QY 121 CTTTGGCTGTGATCTTCTATAGAGTTGGACAAGATAGAGATGAAAGGATCTTCAT 180
DB 166 CTTTGGCTGTGATCTTCTATAGAGTTGGACAAGATAGAGATGAAAGGATCTTCAT 225

QY 181 GAAGATTTTATGATATTTACTTACTGTTTTCTTATCAACCAATGATGATCTGTG 240
DB 226 GAAGATTTTATGATATTTACTTACTGTTTTCTTATCAACCAATGATGATCTGTG 285

QY 241 TTACTGAACCTGTGAGAGATTTAAAGCCAGTTGAAGCTTTGTGAAGATATATGTTA 300
DB 286 TTACTGAACCTGTGAGAGATTTAAAGCCAGTTGTGAAGCTTTGTGAAGATATATGTTA 345

QY 301 AACAAAGAGAGACGAAGAAAGAAACAGCTTTGAAATGCAAAAAGTGATCAGATCTT 360
DB 346 AACAAAGAGAGACGAAGAAAGAAACAGCTTTGAAATGCAAAAAGTGATCAGATCTT 405

QY 361 CAAATTTGGCGCACATGTCATAGTGAGGCGACAGTAAACCAATCTGTGTTCAGGTG 420
DB 406 CAAATTTGGCGCACATGTCATAGTGAGGCGACAGTAAACCAATCTGTGTTCAGGTG 465

QY 421 GCTGAAAAAGATCTACACATGAGCAACAATTGGTAAACCTGGAATATGGAAACAG 480
DB 466 GCTGAAAAAGATCTACACATGAGCAACAATTGGTAAACCTGGAATATGGAAACAG 525

QY 481 CTGACCGTTAAAGACAAAGAGCTATTATATCTATGCCAAGTCACTTCTGTTCAT 540
DB 526 CTGACCGTTAAAGACAAAGAGCTATTATATCTATGCCAAGTCACTTCTGTTCAT 585

QY 541 CGGGAAGCTTGGAGTCAAGTCACTTATATAGCCAGCTTCTGCTTAAATCCCGGTGAG 600
DB 586 CGGGAAGCTTGGAGTCAAGTCACTTATATAGCCAGCTTCTGCTTAAATCCCGGTGAG 645

QY 601 TTGAGAGAACTTACTCAGAGCTGCAAAATCCCAAGTTCGCAAACTTGGGGCA 660
DB 646 TTGAGAGAACTTACTCAGAGCTGCAAAATCCCAAGTTCGCAAACTTGGGGCA 705

QY 661 CAATCCATTCACTTGGAGAGATTTTGAATTTGAACCAAGTGTCTTGGTGTTCAT 720
DB 706 CAATCCATTCACTTGGAGAGATTTTGAATTTGAACCAAGTGTCTTGGTGTTCAT 765

QY 721 GTGACTGATCCAGCCAAAGTGAGCCATGGCACTGGCTTCACTCTTGGCTTACTCAA 780

Db 766 GTGACTGATCCAAAGCCAAAGTGAAGCCATGCACTGGCTTCAAGTCTTTGGCTTACTCAAA 825

Qy 781 CTCTGA 786
Db 826 CTCTGA 831

RESULT 12

LOCUS 167828

DEFINITION Sequence 1 from patent US 5674492. 840 bp DNA linear PAT 04-FEB-1998

ACCESSION 167828

VERSION 167828.1

KEYWORDS GI:2829950

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 840)

AUTHORS Amitage,R.J., Fanslow,W.C. III, Longo,D.L. and Murphy,W.J.

TITLE Method of preventing or treating disease characterized by

JOURNAL neoplastic cells expressing CD40

FEATURES Patent: US 5674492-A 1 07-OCT-1997;

Location/Qualifiers

source 1..840

BASE COUNT 266 a 185 c 175 g 214 t

ORIGIN /organism="unknown"

Query Match 95.9%; Score 754; DB 6; Length 840;

Best Local Similarity 97.5%; Pred. No. 5,1e-191;

Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ATGATAGAAACATACAGCAACCTCCCGATCGTGGCACTGGACTTCACGAGC 60

Db 46 ATGATGAAACATACAGCAACCTCCCGATCGTGGCACTGGACTTCACGAGC 105

Qy 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATACCCCAATGATGATCTGTG 120

Db 106 ATGAAATTTTATGATTTACTTACTGTTTCTTATACCCCAATGATGATCTGTG 165

Qy 121 CTTTTCGTGATCTTATGAAAGTTGACAAATGAAAGTGAAGTCTTCAT 180

Db 166 CTTTTCGTGATCTTATGAAAGTTGACAAATGAAAGTGAAGTCTTCAT 225

Qy 181 GAAGATTTTATGATTTACTTACTGTTTCTTATACCCCAATGATGATCTGTG 240

Db 226 GAAGATTTTATGATTTACTTACTGTTTCTTATACCCCAATGATGATCTGTG 285

Qy 241 TTAAGTAACTGAGAGATTTAAAGCAGTTGAGAGCTTTGAGAGATTAATGTTA 300

Db 286 TTAAGTAACTGAGAGATTTAAAGCAGTTGAGAGCTTTGAGAGATTAATGTTA 345

Qy 301 AACAAAG 360

Db 346 AACAAAG 405

Qy 361 CAAATTCGCGACATGTCATTAAGTGAAGCCAGAGTAAACAATCTGTGTTACGTG 420

Db 406 CAAATTCGCGACATGTCATTAAGTGAAGCCAGAGTAAACAATCTGTGTTACGTG 465

Qy 421 GGTGAAAAAGGATTAACACATGAGCAACAATTTGTAACCTTGAAAAATGGAAAAAG 480

Db 466 GGTGAAAAAGGATTAACACATGAGCAACAATTTGTAACCTTGAAAAATGGAAAAAG 525

Qy 481 CTGACCGTTAAAG 540

Db 526 CTGACCGTTAAAG 585

Qy 541 CGGGAAGCTTGAAGTCAAGTCAATTAAGCAAGCTTGGCTTAAGTCCCGGTGAGA 600

Db 586 CGGGAAGCTTGAAGTCAAGTCAATTAAGCAAGCTTGGCTTAAGTCCCGGTGAGA 645

Qy 601 TTGAGAGATCTTACTCAGAGCTGCAAAATCCAGAGTTCCGCCAAAAGCTTGGAGGCA 660

Db 646 TTGAGAGATCTTACTCAGAGCTGCAAAATCCAGAGTTCCGCCAAAAGCTTGGAGGCA 705

Qy 661 CAATTCATCTTGGAGAGAGATTTGATTTGCAACAGAGTCTCGTGTGTTGTCAT 720

Db 706 CAATTCATCTTGGAGAGAGATTTGATTTGCAACAGAGTCTCGTGTGTTGTCAT 765

Qy 721 GTGACGATCCAAAGCAGAGTGAAGCCATGAGCACTGGCTTCAAGTCTTGGCTTCAAA 780

Db 766 GTGACGATCCAAAGCAGAGTGAAGCCATGAGCACTGGCTTCAAGTCTTGGCTTCAAA 825

Qy 781 CTCTGA 786

Db 826 CTCTGA 831

RESULT 13

LOCUS AX090039

DEFINITION Sequence 1 from Patent WO0116180. 879 bp DNA linear PAT 21-MAR-2001

ACCESSION AX090039

VERSION AX090039.1

KEYWORDS GI:13444004

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 879)

AUTHORS Ahuja,S.U. and Bonewald,L.U.

TITLE Cd40 agonist compositions and methods of use

JOURNAL Patent: WO 0116180-A 1 08-MAR-2001;

BOARD OF RESEARCH THE UNIVERSITY OF TEXAS SYSTEM (US)

Location/Qualifiers

source 1..879

BASE COUNT 274 a 193 c 190 g 222 t

ORIGIN /organism="Homo sapiens"

Query Match 95.9%; Score 754; DB 6; Length 879;

Best Local Similarity 97.5%; Pred. No. 5,1e-191;

Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ATGATGAAACATACAGCAACCTCCCGATCGTGGCACTGGACTTCAGAGC 60

Db 22 ATGATGAAACATACAGCAACCTCCCGATCGTGGCACTGGACTTCAGAGC 81

Qy 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATACCCCAATGATGATCTGTG 120

Db 82 ATGAAATTTTATGATTTACTTACTGTTTCTTATACCCCAATGATGATCTGTG 141

Qy 121 CTTTTCGTGATCTTATGAAAGTTGACAAATGAAAGTGAAGTCTTCAT 180

Db 142 CTTTTCGTGATCTTATGAAAGTTGACAAATGAAAGTGAAGTCTTCAT 201

Qy 181 GAAGATTTTATGATTTACTTACTGTTTCTTATACCCCAATGATGATCTGTG 240

Db 202 GAAGATTTTATGATTTACTTACTGTTTCTTATACCCCAATGATGATCTGTG 261

Qy 241 TTAAGTAACTGAGAGATTTAAAGCAGTTGAGAGCTTTGAGAGATTAATGTTA 300

Db 262 TTAAGTAACTGAGAGATTTAAAGCAGTTGAGAGCTTTGAGAGATTAATGTTA 321

Qy 301 AACAAAG 360

Db 322 AACAAAG 381

Qy 361 CAAATTCGCGACATGTCATTAAGTGAAGCCAGAGTAAACAATCTGTGTTACGTG 420

Db 382 CAAATTCGCGACATGTCATTAAGTGAAGCCAGAGTAAACAATCTGTGTTACGTG 441

Qy 421 GGTGAAAAAGGATTAACACATGAGCAACAATTTGTAACCTTGAAAAATGGAAAAAG 480


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442 GCTGAAAAAGTACTACACCATGAGCAACAACCTTGGTAACTCGTGAAGTGGAAAAAG 501
QY 481 CTGACCGTTAAAGCAAGACCTCTATTATATCTATGCGCAAGTCACTCTGTTCAT 540
Db 502 CTGACCGTTAAAGCAAGACCTCTATTATATCTATGCGCAAGTCACTCTGTTCAT 561
QY 541 CGGGAAGCTTCGAGTCAAGCTCATTATAGCAGCCTGTCTAAAGTCCCGGTAGA 600
Db 562 CGGGAAGCTTCGAGTCAAGCTCATTATAGCAGCCTGTCTAAAGTCCCGGTAGA 621
QY 601 TTGAGAGAAATCTTACTCAAGAGCTGCAAAATCCCAAGTCCGCAACCTTGGGCA 660
Db 622 TTGAGAGAAATCTTACTCAAGAGCTGCAAAATCCCAAGTCCGCAACCTTGGGCA 681
QY 661 CAATCCATTCACCTGGAGAGATTTGAATTTGCAACAGAGTCTCGTGTTCAT 720
Db 682 CAATCCATTCACCTGGAGAGATTTGAATTTGCAACAGAGTCTCGTGTTCAT 741
QY 721 GTGACTGATCCAAAGCAAGTGAAGCCATGGCACTGGCTTCACTCTTGGCTTACTCAA 780
Db 742 GTGACTGATCCAAAGCAAGTGAAGCCATGGCACTGGCTTCACTCTTGGCTTACTCAA 801
QY 781 CTCTGA 786
Db 802 CTCTGA 807

RESULT 14
HSGP39MR 879 bp mRNA linear PRI 01-SEP-1996
LOCUS HSGP39MR
DEFINITION H.sapiens mRNA for glycoprotein 39 (GP39).
ACCESSION Z15017.1 S49392
VERSION Z15017.1 GI:38483
KEYWORDS glycoprotein 39.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 879)
Hollenbaugh, D., Grosmaire, L.S., Kullas, C.D., Chalupny, N.J.,
Braesch-Andersen, S., Noelle, R.J., Stamenkovic, I., Ledbetter, J.A.
and Aruffo, A.
The human T cell antigen GP39, a member of the TNF gene family, is
a ligand for the CD40 receptor: expression of a soluble form of
GP39 with B cell co-stimulatory activity
EMBO J. 11 (12), 4313-4321 (1992)

JOURNAL
MEDLINE 93049181
PUBMED 1385114
REFERENCE 2 (bases 1 to 879)
AUTHORS Hollenbaugh, D.L.
TITLE Direct Submission
JOURNAL Submitted (27-AUG-1992) Diane L Hollenbaugh, Bristol-Myers Squibb
PRI, Seattle, WA, 98121
3 (bases 1 to 879)
REFERENCE 3
AUTHORS Hollenbaugh, D.
TITLE Direct Submission
JOURNAL Submitted (21-SEP-1992) Diane L Hollenbaugh, Bristol-Myers Squibb
PRI, Seattle, WA, 98121
COMMENT The original submission [1] reported 934bp.
FEATURES
Location/Qualifiers
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BASE COUNT 274 a 193 c 190 g 222 t
ORIGIN
Query Match 95.9%; Score 754; DB 9; Length 879;
Best Local Similarity 97.5%; Pred. No. 5, 1e-191;
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
1 ATGATGAAACATACAGCCAACTTCCCGAGATCCGTGCACTGAACTTCCAGGAGC 60
22 ATGATGAAACATACAGCCAACTTCCCGAGATCCGTGCACTGAACTGCACTGCAAC 81
QY 61 ATGAGATTTTATGATTTTATCTTCTGTTTCTTATACCCAAAGATGATGATG 120
Db 82 ATGAAATTTTATGATTTTATCTTCTGTTTCTTATACCCAAAGATGATGATG 141
QY 121 CTTTTCCTGTGTATCTTCAATGAAAGTTGACAAAGATGAAAGATGAAATCTTCAT 180
Db 142 CTTTTCCTGTGTATCTTCAATGAAAGTTGACAAAGATGAAAGATGAAATCTTCAT 201
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Db 202 GAAAGATTTTGAATTCATGAAACATACAGAGATGCAACAGAGAAAGATCTTATCC 261
QY 241 TTAATGAACTGTGAGAGATTTAAAGCCAGTTTGAAGCTTTTGAAGATATATGTTA 300
Db 262 TTAATGAACTGTGAGAGATTTAAAGCCAGTTTGAAGCTTTTGAAGATATATGTTA 321
QY 301 AACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
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QY 361 CAATTTGGGCGCATGCTCTAAATGAGGCGCAGCATGAAACATCTGTGTACAGTGG 420
Db 382 CAATTTGGGCGCATGCTCTAAATGAGGCGCAGCATGAAACATCTGTGTACAGTGG 441
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Db 562 CGGGAAGCTTCGAGTCAAGCTCATTATAGCAGCCTGTCTAAAGTCCCGGTAGA 621
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Db 622 TTGAGAGAAATCTTACTCAAGAGCTGCAAAATCCCAAGTCCGCAACCTTGGGCA 681
QY 661 CAATCCATTCACCTGGAGAGATTTGAATTTGCAACAGAGTCTCGTGTTCAT 720
Db 682 CAATCCATTCACCTGGAGAGATTTGAATTTGCAACAGAGTCTCGTGTTCAT 741
QY 721 GTGACTGATCCAAAGCAAGTGAAGCCATGGCACTGGCTTCACTCTTGGCTTACTCAA 780
Db 742 GTGACTGATCCAAAGCAAGTGAAGCCATGGCACTGGCTTCACTCTTGGCTTACTCAA 801
QY 781 CTCTGA 786
Db 802 CTCTGA 807

RESULT 15
HSCD40 1803 bp mRNA linear PRI 06-JUN-1997
LOCUS HSCD40
DEFINITION H.sapiens mRNA for CD40 ligand.
ACCESSION X67878.1 GI:38411
VERSION X67878.1 GI:38411

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KEYWORDS

glycoprotein.
Homo sapiens.
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 1803)

REFERENCE

1 Spriggs, M.
Direct Submision
Submitted (28-JUL-1992) M. Spriggs, Immunex Res & Development
Corporation, 51 University Street, Seattle WA 98101, USA
2 (bases 1 to 1803)

AUTHORS

Spriggs, M.K., Armistage, R.J., Strockbine, L., Clifford, K.N.,
Macdoff, B.M., Sato, T.A., Maliszewski, C.R. and Fenslow, W.C.
Recombinant human CD40 ligand stimulates B cell proliferation and
immunoglobulin E secretion
J. Exp. Med. 176 (6), 1543-1550 (1992)

JOURNAL

93094757

MEDLINE

1281209

PUBMED

1281209

FEATURES

Location/Qualifiers
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/organism="Homo sapiens"
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/db_xref="GI:38412"
/db_xref="SWISS-PROT:P29965"

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112..183
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sig_peptide

BASE COUNT 510 a 456 c 344 g 493 t

ORIGIN

Query Match

Best Local Similarity 95.9%; Score 754; DB 9; Length 1803;
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ATGATAGAAACATACAGCAACCTTCCCGAGTCCGTGGCACTGAGCTTCCAGGAGC 60
Db 46 ATGATCGAAACATACAGCAACCTTCCCGAGTCCGTGGCACTGAGCTTCCAGGAGC 105
Qy 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCAGATGATGATGATG 120
Db 106 ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCAGATGATGATGATG 165
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Db 166 CTTTGGCTGATCTTATGAAAGTTGAGCAAGATGAAAGATCTTCAAT 225
Qy 181 GAAGATTTTATGATTTACTTACTGTTTCTTATCACCAGATGATGATGATG 240
Db 226 GAAGATTTTATGATTTACTTACTGTTTCTTATCACCAGATGATGATGATG 285
Qy 241 TTAAGTAACTGAGAGATTTAAAGCAAGTTGAGCTTGTGAAGATATATATGTTA 300
Db 286 TTAAGTAACTGAGAGATTTAAAGCAAGTTGAGCTTGTGAAGATATATATGTTA 345
Qy 301 AACAAAG 360
Db 346 AACAAAG 405
Qy 361 CAAATTCGAGCATGATCATAGTGGCCAGCAGTAAACAACTGTTACAGTGG 420
Db 406 CAAATTCGAGCATGATCATAGTGGCCAGCAGTAAACAACTGTTACAGTGG 465
Qy 421 GCTGAAAAAGAGATCTACACATGAGCAACAATTGTAACCTGGAATGGGAAACG 480

Db 466 GCTGAAAAAGAGATCTACACATGAGCAACAATTGTAACCTGGAATGGGAAACG 525
Qy 481 CTAACCGTTAAAG 540
Db 526 CTAACCGTTAAAG 585
Qy 541 CGGAAAGCTTGGAGTCAAGCTCATTTATAGCCAGCTCTGCTTAAAGTCCCCGGTAA 600
Db 586 CGGAAAGCTTGGAGTCAAGCTCATTTATAGCCAGCTCTGCTTAAAGTCCCCGGTAA 645
Qy 601 TTCGAGAGATCTTACTCAGAGCTGCAATACCAAGTTCGCGCAAACTTGGCGGCA 660
Db 646 TTCGAGAGATCTTACTCAGAGCTGCAATACCAAGTTCGCGCAAACTTGGCGGCA 705
Qy 661 CAATCATTCATCTTGGAGAGATTTGAAATTTGCAACAGAGCTTGGTGTTCAT 720
Db 706 CAATCATTCATCTTGGAGAGATTTGAAATTTGCAACAGAGCTTGGTGTTCAT 765
Qy 721 GTGACTGATCCAGCAAGTGAAGCCATGAGCACTGCTTCACTTGGCTTACTCA 780
Db 766 GTGACTGATCCAGCAAGTGAAGCCATGAGCACTGCTTCACTTGGCTTACTCA 825
Qy 781 CTCTGA 786
Db 826 CTCTGA 831

Search completed: March 9, 2003, 02:11:38
Job time : 2052.61 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 8, 2003, 21:32:03 ; Search time 1291.53 Seconds
(without alignments)
9856.249 Million cell updates/sec

Title: US-08-982-272-7

Perfect score: 786
Sequence: 1 ATGATGAAACATACAGCCA.....TTGGCTTACTCAACTCTGA 786

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
EST:
1: em_estbda:*
2: em_estbda:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_estro:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	352.6	44.9	492	12	BF599437 263218 MA
2	277.2	35.3	398	10	AW486605 75217 MAR
3	69.6	8.9	638	9	AI982044 pat.pK007
4	50.2	6.4	1027	17	AZ166561 SP_0088_B
5	48.8	6.2	412	14	BM854912 K-EST0137
6	48.8	6.2	997	17	CNS0057E AL060767 Drosophila

Result	Score	Query Match	Length	ID	Description
7	48.8	6.2	999	14	BQ935454 AGENCOURT
8	48.4	6.2	1443	17	CNS0145P AL103735 Drosophila
9	47.2	6.0	396	12	BF820152 MRL-R002
10	47.2	6.0	486	10	AV174252 AV174252
11	47.2	6.0	578	10	AV724813 AV724813
12	47.2	6.0	583	13	BI713130 BI713130
13	47.2	6.0	586	12	BF791160 BF791160
14	47.2	6.0	797	9	AL534423 AL534423
15	47.2	6.0	845	12	BI601432 BI601432
16	47.2	6.0	845	13	BI601432 BI601432
17	47.2	6.0	861	12	BF573761 BF573761
18	47.2	6.0	873	12	BI616023 BI616023
19	47.2	6.0	874	12	BI616023 BI616023
20	47.2	6.0	874	12	BI616023 BI616023
21	46.8	6.0	553	9	AA312300 AA312300
22	46.6	5.9	458	9	AL514085 AL514085
23	46.4	5.9	562	9	AL564525 AL564525
24	46.2	5.9	433	9	AA115682 AA115682
25	46.2	5.9	772	12	BI676329 BI676329
26	46.2	5.9	777	13	BI598192 BI598192
27	46.2	5.9	877	14	BO643814 BO643814
28	46.2	5.9	432	12	BE888601 BE888601
29	46.2	5.9	636	12	BI671854 BI671854
30	46.2	5.9	1101	17	CNS0039G AL063921 Drosophila
31	45.8	5.8	382	9	AA352023 AA352023
32	45.6	5.8	302	9	AA852210 AA852210
33	45.6	5.8	385	14	T08274 T08274
34	45.6	5.8	389	10	AV704993 AV704993
35	45.6	5.8	434	9	AA081760 AA081760
36	45.6	5.8	437	10	AV729112 AV729112
37	45.6	5.8	460	13	BI598293 BI598293
38	45.6	5.8	479	14	BO130442 BO130442
39	45.6	5.8	494	13	BI698324 BI698324
40	45.6	5.8	508	10	AA08255 AA08255
41	45.6	5.8	512	10	AA372979 AA372979
42	45.6	5.8	515	12	BE895474 BE895474
43	45.6	5.8	523	10	BE397964 BE397964
44	45.6	5.8	560	12	BI639029 BI639029
45	45.6	5.8	565	9	AI929671 AI929671

ALIGNMENTS

RESULT 1
BF599437 492 bp mRNA linear EST 25-Apr-2001
LOCUS 263218 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
DEFINITION BF599437
ACCESSION BF599437.1 GI:11695919
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
Smith,T.P.L., Grose,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Caas,E., Wray,J.E., White,J., Chu,D., Fahrenkrug,S.C., Bennett,
G.L., Heaton,M.P., Laegreid,W.M., Kohrer,G.A., Chitko-Mckown,C.G.,
Petter,G., Holt,I., Karanycheva,S., Liang,F., Quackenbush,J. and
Keeler,J.W.

Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
2180013
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt_trimmed with phred

v0.980904.e. Vector identified by cross_match with the -minscore 18 and -mismatch 12 options.

PCR Primers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCCGACGACGACG
Plate: 33 row: N column: 5
Seq primer: ATTTAGTGACACTATAG.

FEATURES

source
1..492
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 350V"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: PCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendinosus muscle, and fetal
longissimus muscle."
BASE COUNT 163 a 103 c 104 g 122 t
ORIGIN

Query Match 44.9%; Score 352.6; DB 12; Length 492;
Best Local Similarity 86.8%; Pred. No. 4,4e-77;
Matches 388; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 1 ATGATGAAACATACAGCCACCTTCCCGACATCCGCGGACATGAGCTTCCAGCGAGC 60
DB 46 ATGATGAAACATACAGCTTCTTCCCGCTCCGCGGACATGAGCTTCCAGCTTCA 105
QY 61 ATGAAAGATTTTATGATTTACTTACTGTTTCTTATCACCCTAATGATGATCTGTG 120
DB 106 ATGAAAGATTTTATGATTTACTTACTGTTTCTTATCACCCTAATGATGATCTGTG 165
QY 121 CTTTGTGCTGATCTTCTTCAAGAGTGAACAATGAAAGATCTTCAAT 180
DB 166 CTTTGTGCTGATCTTCTTCAAGAGTGAACAATGAAAGATCTTCAAT 225
QY 181 GAAGATTTTGTATTCATGAAACGATACAGATGCAACAGAGAAAGATCTTATCC 240
DB 226 GAAGATTTTGTATTCATGAAACGATACAGATGCAATGAAAGAGAGGCTTATCC 285
QY 241 TTAAGTAACTGTAGAGATTTAAAGCAAGTTGAAGCTTTGTAAGATTAATGTTA 300
DB 286 TTAAGTAACTGTAGAGATTTAAAGCAAGTTGTAAGCTTTGTAAGATTAATGTTA 345
QY 301 AACAAAGAGAGACGAAAGAAAGAAACGCTTTGAATGCAAAAAGTATCAATCTT 360
DB 346 AACAAAGAGAGAAAGAAAGAAAGAAACGCTTTGAATGCAAAAAGTATCAAGAGCT 405
QY 361 CAATGCGGACATGTCATAGTAGGCGGACGAGTAAACAATCTGTGTTACAGTGG 420
DB 406 CAGATAGGCGGACATGTCATAGTAGGCGGAGTAAACAATCTGTGTTCCAGTGG 465
QY 421 GCTGAAAAAGATCTACACCTAGC 447
DB 466 GCCCCCAAGGATCTACACCTAGC 492

RESULT 2
LOCUS AM486605 398 bp mRNA linear EST 25-APR-2001
DEFINITION 75217 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION AM486605
VERSION AM486605.1 GI:7056711
KEYWORDS EST.
SOURCE
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
Smith,T.P., Grose,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Cebas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett

TITLE
JOURNAL
MEDLINE
COMMENT
G.L., Heaton,M.P., Laegreid,W.M., Rohrer,G.A., Chilko-McKown,C.G.,
Perea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
Keeler,J.W.
Sequence evaluation of four pooled tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
21180013
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smitth@mail.marc.usda.gov

Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 20
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCCGACGACGACG
Plate: 34 row: F column: 23
Seq primer: ATTTAGTGACACTATAG.
Location/Qualifiers
1..398
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 1BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: PCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from lymph node, ovary,
fat, hypothalamus, and pituitary."
BASE COUNT 134 a 77 c 82 g 105 t
ORIGIN

Query Match 35.3%; Score 277.2; DB 10; Length 398;
Best Local Similarity 87.6%; Pred. No. 2.3e-58;
Matches 303; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 1 ATGATGAAACATACAGCCACCTTCCCGACATCCGCGGACATGAGCTTCCAGCGAGC 60
DB 53 ATGATGAAACATACAGCTTCTTCCCGCTCCGCGGACATGAGCTTCCAGCTTCA 112
QY 61 ATGAAAGATTTTATGATTTACTTACTGTTTCTTATCACCCTAATGATGATCTGTG 120
DB 113 ATGAAAGATTTTATGATTTACTTACTGTTTCTTATCACCCTAATGATGATCTGTG 172
QY 121 CTTTGTGCTGATCTTCTTCAAGAGTGAACAATGAAAGATCTTCAAT 180
DB 173 CTTTGTGCTGATCTTCTTCAAGAGTGAACAATGAAAGATCTTCAAT 232
QY 181 GAAGATTTTGTATTCATGAAACGATACAGATGCAACAGAGAAAGATCTTATCC 240
DB 233 GAAGATTTTGTATTCATGAAACGATACAGATGCAATGAAAGAGGCTTATCC 292
QY 241 TTAAGTAACTGTAGAGATTTAAAGCAAGTTGAAGCTTTGTAAGATTAATGTTA 300
DB 293 TTAAGTAACTGTAGAGATTTAAAGCAAGTTGTAAGCTTTGTAAGATTAATGTTA 352
QY 301 AACAAAGAGAGACGAAAGAAAGAAACGCTTTGAATGCAAAAAG 346
DB 353 AACAAAGAGAGAAAGAAAGAAAGAAACGCTTTGAATGCAAAAAG 398

RESULT 3
LOCUS A1982044 638 bp mRNA linear EST 07-MAY-2001
DEFINITION pat.pK0072.c9.f chicken activated T cell cDNA Gallus gallus cDNA
clone pat.pK0072.c9.f 5' similar to CD40 ligand, mRNA sequence.
ACCESSION A1982044
VERSION A1982044.1 GI:5885072
KEYWORDS EST.
SOURCE
ORGANISM Gallus gallus

52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409

FEATURES

```

1. 412
/organism="Homo sapiens"
db_xref="taxon:9606"
clone="S21SNUS20-58-D01"
clone_1b="S21SNUS20"
sex="F"
tissue_type="Stomach"
cell_type="Floating aggregates"
cell_line="SNU-520"
lab_host="Top10F"

```

BASE COUNT
ORIGIN

147 a	72 c	119 g	74 e
-------	------	-------	------

Query Match	6.28;	Score 48.8;	DB 14;	Length 412;
Best Local Similarity	50.4;	Pred. No. 0.12;		

Qy	238	TCCTTACGAACTGTAGGAGATTTAAAGCACTTTGAAGCCTTTGAGAGATTTAATG	297
Db	171	TTCTATCATTTTCAGTGTGTTGGAATTTAAATTTGGATGATGGTTTCGGAGAGCACTA	230
Qy	298	TTAAACAAAGGAGACGAGAAAGAAACGCTTTGAAATGCAAAAAGGTATCAGAT	357
Db	231	CTCAAAATTCGTGGACACCAATTTGCAGAAACACCGAATCTCAAAAAGCAATCAGAG	290
Qy	358	CCTCAAAATTGGGCACATCTCATTAAGTAGGCGCAGCATAAACACATCTGTGTTCAG	417
Db	291	CAGTAGCATTTGGGGAAGATGTGAGGGCTGTCCCAAGAAAGAGACATCTGCTCGCA	350
Qy	418	TGGGCTGAAAAAGATATCACCAATAGGACAAATTGTGTATCCCTCGAAAATGG	473
Db	351	CAGAAAAATGTGCAATGTAAACCAAAACAAACAGAAAAACCTCGGAATGG	406

RESULT	6
CNS005TE/c	
LOCUS	CNS005TE
DEFINITION	Drosophila melanogaster genome survey sequence TERC end of BAC # BACR1XK2 of RPEC-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION	AL060767
VERSION	AL060767.1 GI:4943573
KEYWORDS	GSS.
SOURCE	Drosophila melanogaster.
ORGANISM	Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Epnyuroidea; Drosophilidae; Drosophila. 1. (baaes 1 to 997)
REFERENCE	

AUTHORS	Genoscope.
TITLE	Direct Submission
JOURNAL	Submitted (02-JUN-1999)
	Genoscope - Centre National de Sequencage :

COMMENT

collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the *Drosophila melanogaster* genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP *Drosophila melanogaster* BAC library was prepared by Kazutoyo Oosawa and Aaron Mammone in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCL-98 and was constructed by partial EcoRI digestion of *Drosophila* DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

BASE COUNT	89 a	99 c	13 g	258 t	538 others
ORIGIN					

Query Match	6.2%	Score 48.8;	DB 17;	Length 997;
Best Local Similarity	16.3%	Pred. No. 0.12;		
Matches 59;	Conservative 143;	Mismatches 160;	Indels 0;	Gaps 0;

[illegible]

RESULT	7
B0935454	
LOCUS	B0935454
DEFINITION	B0935454
ACCESSION	B0935454
VERSION	B0935454
KEYWORDS	B0935454.1 GI:22350837
SOURCE	EST.
ORGANISM	human.
	Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
1 (bases 1 to 999) Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
Tissue Procurement: DCTD/DRP/Gasdar
CDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L10M2548 row: e column: 05
High quality sequence start: 309
High quality sequence stop: 663.

FEATURES
source
1..999
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6372460"
/clone_id="NIH_MGC_18"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."

BASE COUNT 328 a 190 c 254 g 227 t
ORIGIN

Query Match 6.2%; Score 48.8; DB 14; Length 999;
Best Local Similarity 50.4%; Pred. No. 0.12;
Matches 119; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

Qy 238 TCCTTACTGAACTGTGAGAGATTAAAGCCATTGAAGCTTTGTGAAGATATATG 297
Db 223 TTCTATCATTTACAGTGTGATTAATAATTTGGATTAATGGCTTCGGAGACAGATG 282
Qy 298 TTTAAACAAGAT 357
Db 283 CTCGAATACGTGACACCAATTTGCGAATTTTGAATCTTCAAAAAGCCATCAGAG 342
Qy 358 CCTCAAAATTCGCGACATGTCATTAAGTGAAGCCAGAGTAAACAACATCTGTGTACAG 417
Db 343 CAGTATGCGAGAGGGAAGATGAGGGGCTGCCCGAGAAAGAGACATCTGTCTCCAA 402
Qy 418 TGGGCTGAAAAAGATCTACACATGACACCACTTGTGTAACCTTGAAATGG 473
Db 403 CAGAAAAATGTTGAAGTGAAGAAAGAAACAAACAGAAACACCTGGAATGG 458

RESULT 8
LOCUS CNS0145P/c 1043 bp DNA linear GSS 26-JUL-1999
DEFINITION Drosophila melanogaster genome survey sequence 17 end of BAC
BAC11G11 of Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL103735.1 GI:5615346
VERSION AL103735
KEYWORDS Drosophila melanogaster.
SOURCE Drosophila melanogaster.
ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 1043)

AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage;
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr)
Web: www.genoscope.cns.fr

COMMENT Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
<http://www.edgp.ebi.ac.uk> - This Drosophila melanogaster BAC
library (du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelOBAC11.

FEATURES
source
1..1043
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="BACN11G11"
/clone_id="DrosBAC"
/plasmid="pBelOBAC11"
/note="end: 17"

BASE COUNT 277 a 96 c 121 g 382 t 167 others
ORIGIN

Query Match 6.2%; Score 48.4; DB 17; Length 1043;
Best Local Similarity 35.1%; Pred. No. 0.15;
Matches 113; Conservative 51; Mismatches 158; Indels 0; Gaps 0;
Qy 61 ATGAAGATTTTATGATTTACTTACTGTTTCTTATCACCAGATATGATGATCTG 120
Db 916 WTADATWTKATTTTGTGATTTTATTTTATTTTATTTTATTTTATTTTATTTT 857
Qy 121 CTTTGTGTGATTTCTGATGAAGATGAGAGAGAGAGAGAGAGAGAGATCTGAT 180
Db 856 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 797
Qy 181 GAAGATTTTGTATTCATGAAAACATACAGAGATGCAACAGAGAGAGATCTTATCC 240
Db 796 WWWWTT 737
Qy 241 TTACGAACTGTGAGAGATTTAAAGCACTTTGAAGCTTTGGAAGATATATGTA 300
Db 736 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 677
Qy 301 AACAAAGATCTT 360
Db 676 TAAWAAAAAAMWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWATA 617
Qy 361 CAATTCGGCAGCATGCTATAA 382
Db 616 WATATTTTATTTATTTATTTA 595

RESULT 9
LOCUS BF820152 396 bp mRNA linear EST 13-JAN-2001
DEFINITION MR1-R10025-171100-003-c06 R10025 Homo sapiens CDNA, mRNA sequence.
ACCESSION BF820152
VERSION BF820152.1 GI:12158440
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 396)
Dias Neto E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, P.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags

JOURNAL
MEDLINE
20202663
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
Contact: Simpson A.J.G.
COMMENT

BASE COUNT	138 a	73 c	112 g	73 t
ORIGIN				

RESULT 10	
AV714252	
LOCUS	486 bp mRNA linear EST 11-OCT-2000
DEFINITION	AV714252 DCB Homo sapiens cDNA clone DCBAD07 5', mRNA sequence.
ACCESSION	AV714252
VERSION	AV714252.1 GI:10795769
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euteria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 486)
AUTHORS	Xu,X., Gu,J., Liu,F., Qu,J., Zhao,M., Li,Y., Huang,Q., Zhou,T., Song,H., Gu,Y., Yang,Y., Gao,G., Xiao,H., Li,N., Qian,B., Gao,X., Cheng,Z., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu ,G., Cheng,Z. and Han,Z.
TITLE	Homo sapiens cDNA DCB clones
JOURNAL	Unpublished (2000)
COMMENT	Contact: Zeguang Han

Chinese National Human Genome Center at Shanghai
351 Guo Shouling Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex. 45)
Fax: 86-21-50801932
Email: hanzgc@chgc.sh.cn
This clone is available at CHGC in Shanghai.

BASE COUNT	182 a	87 c	124 g	93 t
ORIGIN				

	Query Match	Score	DB 10	Length	486
	Best Local Similarity	5.08	Pred. No. 0.3		
	Matches 118	Conservative 0	Mismatches 118	Indels 0	Gaps 0
QY	238	TCCTTACGAACTGAGAGAGATTAAACCAGTTTGAAGCGTTTGGAAGATATAATG	297		
Db	139	TTCAATCTTACAGTGAGTGAATATTAATTTGATGATGTTCCGAGACAAATTA	198		
QY	298	TAAACAAAGAGAGACAGAAAGAAACAGCTTTGAATCAAAAAGGATCTCAGAT	357		
Db	199	CTCAATATCTGACACCAATTTGCAAGAACAGGAACTTCAAAAAGCCATCATGAG	258		
QY	358	CCTCAATTTCCGCACATGTCATTAATGAGCGACAGTAAACAATCTGTGTTAAG	417		
Db	259	CAGTATGCAAGGGAAGATAGAGGGCTGCCAGAAAGAAACATCTGATCTGGAA	318		
QY	418	TGGCGTAAAAAGATCTACATCAGACCAACTTGGTAACTCTGGAAAAATG	473		
Db	319	CAGAAAAATGTTAAGTAAACGAAAGAAACCAACAGAAACCTCGAAAAATGG	374		

[illegible]


```

/issue_type="Hypothalamus"
/adv_stage="Adult"
/lab_host="SOLR"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"
BASE COUNT      206 a      98 c      148 g      126 t
ORIGIN
Query Match      6.0%; Score 47.2; DB 10; Length 578;
Best Local Similarity 50.0%; Pred. No. 0.3; Indels 0; Gaps 0;
Matches 118; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

QY 238 TCCTTACTGAACTGTGAGAGATTAAAGCCAGTTTGAAGCTTTGTGAGAGATATATG 297
Db 28 TTCTATCATTTACAGTGTGATTAATAATTTGGATGAATGGGTTCCGAGACAGATG 87

QY 298 TTAAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 357
Db 88 CTCGAATAGTGGACACCAATTTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 147

QY 358 CTTCAAAATTGGCGCACTGTCTAATAGTGGCGAGAGAGAGAGAGAGAGAGAGAG 417
Db 148 CAGTATGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 207

QY 418 TGGGCTGAAAAAGATCTACACCATGAGCAAACTTGTGTAACCTGGAAATGG 473
Db 208 CAGAAAAATGTTGAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 263

RESULT 12
LOCUS      B1713130      583 bp      mRNA      linear      EST 11-MAR-2002
DEFINITION      ie02f03.y1 HR85 islet Homo sapiens cDNA clone IMAGE:5085845 5'
ACCESSION      B1713130
VERSION      B1713130
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 583)
Mellon, D., Brown, J., Kenty, G., Permut, A., Lee, C., Kaestner, K.,
Lemishka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifford, S.,
Hillier, L., Maitre, M., Page, D., Wylie, F., Martin, J., Blisstein, A.,
Schmitt, A., Theising, B., Ritzer, E., Ronko, I., Bennett, J., Cardenas
, M., Gibbons, M., McCann, R., Cole, R., Tsagarashvili, R., Williams, T.
, Jackson, Y. and Bowers, Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Other ESTs: ie02f03.x1
Contact: Douglas Mellon, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmellon@biohpc.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center for information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Seq primer: -40RP from Glibco
High quality sequence stop: 471.
Location/Qualifiers
1. 583
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5085845"
/clone_lib="HR85 islet"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"

/issue_type="Hypothalamus"
/adv_stage="Adult"
/lab_host="SOLR"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"
BASE COUNT      206 a      98 c      148 g      126 t
ORIGIN
Query Match      6.0%; Score 47.2; DB 10; Length 578;
Best Local Similarity 50.0%; Pred. No. 0.3; Indels 0; Gaps 0;
Matches 118; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

QY 238 TCCTTACTGAACTGTGAGAGATTAAAGCCAGTTTGAAGCTTTGTGAGAGATATATG 297
Db 28 TTCTATCATTTACAGTGTGATTAATAATTTGGATGAATGGGTTCCGAGACAGATG 87

QY 298 TTAAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 357
Db 88 CTCGAATAGTGGACACCAATTTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 147

QY 358 CTTCAAAATTGGCGCACTGTCTAATAGTGGCGAGAGAGAGAGAGAGAGAGAGAG 417
Db 148 CAGTATGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 207

QY 418 TGGGCTGAAAAAGATCTACACCATGAGCAAACTTGTGTAACCTGGAAATGG 473
Db 208 CAGAAAAATGTTGAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 263

RESULT 13
LOCUS      BF791160      586 bp      mRNA      linear      EST 12-JAN-2001
DEFINITION      602251255f1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4338636 5'
ACCESSION      BF791160
VERSION      BF791160
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 586)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strauberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LNCM1214 row: n column: 13
High quality sequence stop: 582.
Location/Qualifiers
1. 586
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4338636"
/clone_lib="NIH MGC 81"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: muscle (skeletal); Vector: pDNR-LIB
(Clontech); Site_1: SfiI (ggccgctcgcc); Site_2: SfiI
(ggcatcagcc); 5' and 3' adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CACGCGCATTAATGCGC-3'
and 3' adaptor sequence:
5'-ATTCTAGAGCGGAGGCGCGGCGAGCATG-dt(30)BN-3' (where B = A,

```

C, or G and N = A, C, G, or T). Average insert size 1.55 kb (range 1.0-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

BASE COUNT 198 a 107 c 163 g 118 t

Query Match 6.0%; Score 47.2; DB 12; Length 586;

Best Local Similarity 50.0%; Pred. No. 0.3;

Matches 118; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

QY 238 TCCTTACTGAACTGTGAGAGATTAAAGCCAGTTGAAAGCTTGTGAAGATTAATG 297
 DB 144 TTCAATACATTCAGTGTGTTGATTAATACTGGATGATGTTCCGGAGAGAGATA 203
 QY 298 TTAACAAAG 357
 DB 204 CTCATTAATCGTGACACCAATTTGCAAGAAACAGAGAACTTCAAAAGCCATCAGAG 263
 QY 358 CCTCAATTCGGCACATGTCATTAAGTGAAGCCAGAGTAAACATCTGTCTTACAG 417
 DB 264 CAGTATGACAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 323
 QY 418 TGGCGTAAAAAGATATACACCATGAGCAACACTTGTAACTCGGAAATGG 473
 DB 324 CAGAAAAATGTGAAGTAAACGAAAAAGAACAAACGAAAAACCTCGAAATGG 379

RESULT 14

AL534423

LOCUS AL534423 LIT FL013 FBm1 Homo sapiens cDNA clone CS0DF004YD24 5

DEFINITION prime, mRNA sequence.

ACCESSION AL534423

VERSION AL534423.1 GI:12797916

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 797)

Li, W. B., Gruber, C., Jessee, J., and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 Evry cedex - France

Email: segre@genoscope.cns.fr; Web : www.genoscope.cns.fr.

Location/Qualifiers

1. 797

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="CS0DF004YD24"

/clone_lib="LIT_FL013_FBm1"

/dev_stage="pooled tissue from post conception fetuses (20

week, 24 week and 26 week)"

/lab_host="DH10B"

/note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand

cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-stranded cDNA was digested with Not I

and cloned into the Not I and Eco RV sites of the

pCMVSPORT 6 vector. Library was constructed by Life

Technologies. Contact : Feng Liang Life Technologies, a

division of Invitrogen 9800 Medical Center Drive Rockville

, Maryland 20850, USA Fax : (1) 301 610 8371 Email :

fliang@lifetechn.com URL :

http://fulllength.invitrogen.com"

BASE COUNT

407 a 43 c 120 g 152 t 75 others

Query Match 6.0%; Score 47.2; DB 9; Length 797;

Best Local Similarity 39.6%; Pred. No. 0.31;

Matches 168; Conservative 37; Mismatches 215; Indels 4; Gaps 1;

QY 151 GAGAAATGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 210
 DB 244 GAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 303
 QY 211 AGATGCAACAG 270
 DB 304 AAATTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 363
 QY 271 TTGAAGGCTTTGTAAGAGAT----ATAATGTTAAACAAAGAGAGAGAGAGAGAGAA 326
 DB 364 AAAG 423
 QY 327 CAGCTTGAATGCAAAAG 386
 DB 424 AAGTAAAG 483
 QY 387 GGCACAGTAAACCAATCTGTGTACAGGGGTGAGAGAGAGAGAGAGAGAGAGAGAG 446
 DB 484 AATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 543
 QY 447 CAACAACTGTTACCTCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 506
 DB 544 AAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 603
 QY 507 TTAATCTATGCGCAAGTCACTTCTGTTCATCGGAGAGAGAGAGAGAGAGAGAGAGAG 566
 DB 604 TTGTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 663
 QY 567 TATA 570
 DB 664 MMTA 667

RESULT 15

BC715238

LOCUS BC715238 845 bp mRNA linear EST 08-MAY-2001

DEFINITION 6026/6117/1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:479872 5',

mRNA sequence.

ACCESSION BC715238

VERSION BC715238.1 GI:13994417

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 845)

NIH-MGC http://mgs.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cga@bde-remail.nih.gov

Tissue Procurement: Miklos Palokovits, M.D., Ph.D.

cDNA Library Preparation: Michael J. Brownstein (NIGRI), Shitaki

Toshitaki and Piero Carninci (RIKEN)

CDNA library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

http://image.llnl.gov

Plate: LLM10686 row: b column: 05

High quality sequence strip: 830.

FEATURES

source

1. 845

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:479872"

/clone_lib="NIH_MGC_96"

/tissue_type="hypothalamus"

/lab_host="DH10B"

/note="Organ: Brain; Vector: pBluescriptR (modified

pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gcccag

); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTVN-3',
size-selected for average insert size 2.3 kb and
normalized to ROT 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carlini, in preparation). Library
constructed by M. Brownstein (NIMH/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT 284 a 151 c 228 g 182 t
ORIGIN

Query Match 6.0%; Score 47.2; DB 12; Length 845;
Best Local Similarity 50.0%; Pred. No. 0.31;
Matches 118; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

OY 238 TCCTTACTGAACCTGTGAGAGATTAAAGCCAGTTTGAAGCTTTGTGAGAGATATATG 297
Db 177 TTCATACATTACAGTGTGTAATTAATTCGGGATGATGGGTTCCGGAGCAGAGTA 236
OY 298 TTAACCAAG 357
Db 237 CTCATATAGTGAACCAATTTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 296
OY 358 CCTCAATTCGGGCAATGTCATAGTGAAGCCAGCAGTAAACCAATCTGTGTACAG 417
Db 297 CAGTATGACAGAGGAGAGATGAGAGGGGCTGCCAGAGAGAGAGAGAGAGAGAG 356
OY 418 TGGGCTGAG 473
Db 357 CAG 412

Search completed: March 9, 2003, 04:42:27
Job time : 1295.53 secs

100

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 8, 2003, 18:30:53 ; Search time 164.215 Seconds
(without alignments)
10778.963 Million cell updates/sec

Title: US-08-982-272-7

Sequence: 1 ATGATGAGAAACATACAGCCA.....TTGGCTTACTCAAACTCTGA 786

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapept 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : N.Geneseq.101002.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	786	100.0	786	19 AAV39003	Exemplary CD40 lig
2	776.4	98.8	786	19 AAV39002	Exemplary CD40 lig
3	763.6	97.2	786	19 AAV39000	Exemplary CD40 lig
4	754	95.9	786	15 AAO63959	Human CD40-L type
5	754	95.9	786	19 AAV38997	CD40 ligand gene u
6	754	95.9	786	19 AAV12852	CD40 ligand coding
7	754	95.9	840	14 AAO41506	CD40-L DNA. Homo
8	754	95.9	840	15 AAO67123	CD40 ligand gene.
9	754	95.9	840	16 AAT05763	Human CD40 ligand

10	754	95.9	840	18 AAT93782	CDNA of CD40L, a n
11	754	95.9	840	19 AAO61063	Human CD40 ligand
12	754	95.9	840	20 AAO27525	Human CD40-L codin
13	754	95.9	879	22 AAF55539	Nucleotide sequenc
14	754	95.9	1816	21 AAO51745	Human CD40 ligand
15	754	95.9	1816	23 AAO86571	DNA encoding novel
16	752.4	95.7	840	15 AAO57984	Genomic sequence o
17	751	95.5	840	18 AAO58122	Human CD40L mutain
18	749.2	95.3	840	15 AAO94091	Human CD40-L CDNA.
19	694.8	88.4	783	19 AAV42184	Exemplary nucleoti
20	648.2	82.5	1552	22 AAF55525	Nucleotide sequenc
21	642.8	81.8	865	22 AAF82933	HIV-1 gp120 V3 100
22	642.8	81.8	906	22 AAF82932	HIV-1 gp120 V3 100
23	642.8	81.8	2209	22 AAF82929	HIV-1 gp120-human
24	642.8	81.8	2252	22 AAF82928	HIV-1 gp120-human
25	638.2	81.2	1425	14 AAO41516	Human CD40-L/FC fu
26	638.2	81.2	1425	20 AAO27534	Human CD40-L/FC fu
27	637.2	81.1	929	18 AAT58123	CDNA encoding yeast
28	637.2	81.1	929	20 AAT58123	Human trimeric CD4
29	636	80.9	1566	24 AAK12874	Chimeric SA-CD40L
30	635.6	80.9	864	19 AAV39004	CD40 ligand gene u
31	598.8	76.2	885	21 AAZ55540	Feline CD154 CDNA.
32	598.8	76.2	885	21 AAZ55541	Feline CD154 CDNA.
33	595.8	75.8	780	21 AAZ55542	Feline CD154 CDNA
34	595.8	75.8	780	21 AAZ55543	Feline CD154 CDNA
35	594	75.6	783	15 AAO63960	Mouse CD40-L type
36	594	75.6	783	19 AAV12853	CD40 ligand coding
37	594	75.6	783	20 AAO27524	Mouse CD40-L codin
38	592.4	75.4	783	19 AAV38998	CD40 ligand gene u
39	592.4	75.4	818	19 AAV61062	Murine CD40 ligand
40	589.8	75.0	782	14 AAO41507	Murine CD40-L DNA.
41	576.4	73.3	1878	21 AAZ55534	Canine CD154 CDNA.
42	576.4	73.3	1878	21 AAZ55535	Canine CD154 CDNA
43	573.4	73.0	780	21 AAZ55536	Canine CD154 CDNA
44	573.4	73.0	780	21 AAZ55537	Canine CD154 CDNA
45	570	72.5	783	19 AAV39001	Exemplary CD40 lig

ALIGNMENTS

AAV39003	standard; DNA; 786 BP.
AAV39003;	
23-SEP-1998 (first entry)	
Exemplary CD40 ligand gene used in the course of the invention.	
CD40 ligand; alteration; immunoreactivity; human cell;	
accessory molecule ligand; AM; gene therapy; treatment; neoplasia;	
autoimmune disorder; rheumatoid arthritis; vaccine; chimera; ss.	
Chimeric - Mus sp.	
Chimeric - Homo sapiens.	
WO9826061-A2.	
18-JUN-1998.	
08-DEC-1997; 97WO-US22740.	
01-DEC-1997; 97US-0982272.	
PR 09-DEC-1996; 96US-0032145.	
(REBC) UNIV CALIFORNIA.	
Cantwell M, Kipps TJ, Sharma S;	
WPI; 1998-348521/30.	

PT Vectors containing accessory molecule ligand genes - used for
 CC altering immunoreactivity of cells, particularly for treatment of
 PT neoplasia or autoimmune disorders, e.g. rheumatoid arthritis
 XX
 XX
 PS Disclosure; Page 107; 167bp; English.

XX The present sequence represents an exemplary CD40 ligand gene,
 CC comprising nucleotides encoding the extracellular domains (Domains III
 CC and IV) of the human CD40 ligand gene (AAV38998) operatively linked to
 CC nucleotides encoding the cytoplasmic domain (Domain I) and transmembrane
 CC domain (Domain II) of the murine CD40 ligand gene (AAV38997). The
 CC sequence is used to exemplify the method of the invention. The
 CC specification describes a method for altering the immunoreactivity of
 CC human cells which comprises introducing a gene encoding an accessory
 CC molecule ligand (AML) into the cells so that the AML is expressed on the
 CC surface of the cells. Vectors containing the AML genes can be used in
 CC gene therapy for treating neoplasia or autoimmune disorders such as
 CC rheumatoid arthritis. They can also be used for vaccination to produce
 CC immunity against a virus cell, bacteria, protein, fungus or neoplasia.
 XX
 XX Sequence 786 BP; 250 A; 166 C; 170 G; 200 T; 0 other;

Query Match 100.0%; Score 786; DB 19; Length 786;
 Best Local Similarity 100.0%; Pred. No. 5,7e-216;
 Matches 786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGAAACATACACGCAACCTCCGAGATCCGAGCACTGACCTTCCAGCAGC 60
 DB 1 ATGATGAAACATACACGCAACCTCCGAGATCCGAGCACTGACCTTCCAGCAGC 60
 QY 61 ATGAAAGATTTTATGATTTTACTTACTGTTTCTTATCACCCTAATGATGATCTGTG 120
 DB 61 ATGAAAGATTTTATGATTTTACTTACTGTTTCTTATCACCCTAATGATGATCTGTG 120
 QY 121 CTTTGGCTGATCTTATGAGAGGTTGACAAATATGAAAGATCTTAT 180
 DB 121 CTTTGGCTGATCTTATGAGAGGTTGACAAATATGAAAGATCTTAT 180
 QY 181 GAAATTTTATTCATGAAACGATACAGAGATGCAACAGAGAAAGATCTTATTC 240
 DB 181 GAAATTTTATTCATGAAACGATACAGAGATGCAACAGAGAAAGATCTTATTC 240
 QY 241 TTACTGAACGTGAGAGATTTAAAGCAGTTTGAAGGATTAATATGTTA 300
 DB 241 TTACTGAACGTGAGAGATTTAAAGCAGTTTGAAGGATTAATATGTTA 300
 QY 301 AACAAAGAGAGACGAAAGAAAGAAACGTTGAATGCAAAAAGGTGATCAGATCT 360
 DB 301 AACAAAGAGAGACGAAAGAAAGAAACGTTGAATGCAAAAAGGTGATCAGATCT 360
 QY 361 CAATATGCGGACATGTCATTAAGAGGCGAGAGTAAACAACTCTGTTACAGTGG 420
 DB 361 CAATATGCGGACATGTCATTAAGAGGCGAGAGTAAACAACTCTGTTACAGTGG 420
 QY 421 GCTGAAAAAGATATCAACCATGAGCAACATCTGTGTAATCTTGAATAATGGAACG 480
 DB 421 GCTGAAAAAGATATCAACCATGAGCAACATCTGTGTAATCTTGAATAATGGAACG 480
 QY 481 CTGACCGTTAAAGACAGAGACTATATATCTAATGCCAAGTCACTTCTTCCAT 540
 DB 481 CTGACCGTTAAAGACAGAGACTATATATCTAATGCCAAGTCACTTCTTCCAT 540
 QY 541 CGGGAAGCTTGAGTCAAGCTTCATTTATGACCACTTGTCTTAAAGTCCCGGTGAA 600
 DB 541 CGGGAAGCTTGAGTCAAGCTTCATTTATGACCACTTGTCTTAAAGTCCCGGTGAA 600
 QY 601 TTGAGAGATCTTACTGAGAGCTCAATATCCACAGTTCCGCAAACTTTCGAGGCA 660
 DB 601 TTGAGAGATCTTACTGAGAGCTCAATATCCACAGTTCCGCAAACTTTCGAGGCA 660
 QY 661 CAATCATTCATCTTGGAGAGATTTGAATGCAACAGTGTCTTGGTGTTCAT 720
 DB 661 CAATCATTCATCTTGGAGAGATTTGAATGCAACAGTGTCTTGGTGTTCAT 720

QY 721 GTGACTGATCCAGGCAAGTGAAGCCATGSCATGCTTACGCTTTGGCTTACTGAA 780
 DB 721 GTGACTGATCCAGGCAAGTGAAGCCATGSCATGCTTACGCTTTGGCTTACTGAA 780
 QY 781 CTCCTGA 786
 DB 781 CTCCTGA 786
 RESULT 2
 ID AAV39002 standard; DNA; 786 BP.
 XX AAV39002;
 AC AAV39002;
 XX 23-SEP-1998 (first entry)
 DT Exemplary CD40 ligand gene used in the course of the invention.
 XX
 DE
 XX CD40 ligand; alteration; immunoreactivity; human cell;
 KW accessory molecule ligand; AML; gene therapy; treatment; neoplasia;
 KW autoimmune disorder; rheumatoid arthritis; vaccine; chimera; ss.
 XX
 OS Chimeric - Mus sp.
 OS Chimeric - Homo sapiens.
 XX
 PN W09826061-A2.
 XX
 PD 18-JUN-1998.
 XX
 XX 08-DEC-1997; 97W0-US22740.
 PF 01-DEC-1997; 97US-0382272.
 PR 09-DEC-1996; 96US-0032145.
 XX
 PR (REGC) UNIV CALIFORNIA.
 PA
 PI Cantwell M, Kipps TJ, Sharma S;
 PI WPI; 1998-348521/30.
 DR
 XX
 PT Vectors containing accessory molecule ligand genes - used for
 PT altering immunoreactivity of cells, particularly for treatment of
 PT neoplasia or autoimmune disorders, e.g. rheumatoid arthritis
 XX
 XX
 PS Disclosure; Page 106; 167bp; English.

XX The present sequence represents an exemplary CD40 ligand gene,
 CC comprising nucleotides encoding the extracellular domains (Domains III
 CC and IV) and transmembrane domain (Domain II) of human CD40 ligand gene
 CC (AAV38998) operatively linked to nucleotides encoding the cytoplasmic
 CC domain (Domain I) of the murine CD40 ligand gene (AAV38997). The sequence
 CC is used to exemplify the method of the invention. The specification
 CC describes a method for altering the immunoreactivity of human cells which
 CC comprises introducing a gene encoding an accessory molecule ligand (AML)
 CC into the cells so that the AML is expressed on the surface of the cells.
 CC Vectors containing the AML genes can be used in gene therapy for
 CC treating neoplasia or autoimmune disorders such as rheumatoid arthritis.
 CC They can also be used for vaccination to produce immunity against a virus
 CC cell, bacteria, protein, fungus or neoplasia.
 XX
 XX Sequence 786 BP; 250 A; 166 C; 171 G; 199 T; 0 other;

Query Match 98.8%; Score 776.4; DB 19; Length 786;
 Best Local Similarity 99.2%; Pred. No. 3.3e-213;
 Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGATGAAACATACACGCAACCTCCGAGATCCGAGCACTGACCTTCCAGCAGC 60
 DB 1 ATGATGAAACATACACGCAACCTCCGAGATCCGAGCACTGACCTTCCAGCAGC 60
 QY 61 ATGAAAGATTTTATGATTTTACTTACTGTTTCTTATCACCCTAATGATGATCTGTG 120

Db 61 ATGAGATTTTATGATTTACTTACTGTTTTCTTTATCCCAATGATGGTCAACA 120
 Qy 121 CTTTGTGCTGTGATCTTCTATAGAGTTTGAACAATAGAGATGAAATCTTCAAT 180
 Db 121 CTTTGTGCTGTGATCTTCTATAGAGTTTGAACAATAGAGATGAAATCTTCAAT 180
 Qy 181 GAAGATTTGTATCATGAAAAAGATAGAGATGCAACAAGAGAAATCTTATCC 240
 Db 181 GAAGATTTGTATCATGAAAAAGATAGAGATGCAACAAGAGAAATCTTATCC 240
 Qy 241 TTACTGAAGTGTGAGAGATTAAGCCAGTTTGAAGCTTTGTAGAGATATATGTTA 300
 Db 241 TTACTGAAGTGTGAGAGATTAAGCCAGTTTGAAGCTTTGTAGAGATATATGTTA 300
 Qy 301 AACCAAG 360
 Db 301 AACCAAG 360
 Qy 361 CAATTTGGCGGCACTGTCTATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
 Db 361 CAATTTGGCGGCACTGTCTATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
 Qy 421 GCTGAAAAAGAGATCTACACATGAGCAAACTTGTGTAACCTGGAAGATGGAACAG 480
 Db 421 GCTGAAAAAGAGATCTACACATGAGCAAACTTGTGTAACCTGGAAGATGGAACAG 480
 Qy 481 CTGACCGTTTAAAG 540
 Db 481 CTGACCGTTTAAAG 540
 Qy 541 CGGGAAGCTTGAAGTCAAGCTCCATTTATAGCCAGCTTGTGCTAAATGCCCGGAG 600
 Db 541 CGGGAAGCTTGAAGTCAAGCTCCATTTATAGCCAGCTTGTGCTAAATGCCCGGAG 600
 Qy 601 TTGAGAGAGATCTTACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
 Db 601 TTGAGAGAGATCTTACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
 Qy 661 CAATCATTCATTGGAGAGAGATTTGATTTGCAACAGAGTGTCTTGGTTTGTCAAT 720
 Db 661 CAATCATTCATTGGAGAGAGATTTGATTTGCAACAGAGTGTCTTGGTTTGTCAAT 720
 Qy 721 GTGAGTGAATCCAG 780
 Db 721 GTGAGTGAATCCAG 780
 Qy 781 CTCTGA 786
 Db 781 CTCTGA 786
 RESULT 3
 ID AAV39000 standard; DNA; 786 BP.
 XX AAV39000;
 XX AAV39000;
 XX 23-SEP-1998 (first entry)
 DE Exemplary CD40 ligand gene used in the course of the invention.
 XX
 KW CD40 ligand; alteration; immunoreactivity; human cell;
 KW accessory molecule ligand; AMU; gene therapy; treatment; neoplasia;
 KW autoimmune disorder; rheumatoid arthritis; vaccine; chimera; ss.
 XX Chimeric - Mus sp.
 OS Chimeric - Homo sapiens.
 XX
 XX WO9826061-A2.
 XX
 XX 18-JUN-1998.
 XX

PF 08-DEC-1997; 97WO-US22740.
 XX
 PR 01-DEC-1997; 97US-0982272.
 PR 09-DEC-1996; 96US-0032145.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Cantwell M, Kipps TJ, Sharma S;
 DR WPI; 1998-348521/30.
 XX
 PT Vectors containing accessory molecule ligand genes - used for
 PT altering immunoreactivity of cells, particularly for treatment of
 PT neoplasia or autoimmune disorders, e.g. rheumatoid arthritis
 XX
 PS Disclosure; Page 105; 167pp; English.
 CC
 CC The present sequence represents an exemplary CD40 ligand gene,
 CC comprising nucleotides encoding the extracellular domains (domains III
 CC and IV) of human CD40 ligand gene (AAV38998) are operatively linked to
 CC nucleotides encoding the murine CD40 ligand transmembrane domain (Domain
 CC I) (AAV38997) which is operatively linked to the human CD40 ligand gene
 CC cytoplasmic domain (Domain I). The sequence is used to exemplify the
 CC method of the invention. The specification describes a method for
 CC altering the immunoreactivity of human cells which comprises introducing
 CC a gene encoding an accessory molecule ligand (AMU) into the cells so that
 CC the AMU is expressed on the surface of the cells. Vectors containing the
 CC AMU genes can be used in gene therapy for treating neoplasia or
 CC autoimmune disorders such as rheumatoid arthritis. They can also be used
 CC for vaccination to produce immunity against a virus cell, bacteria,
 CC protein, fungus or neoplasia.
 XX
 SQ Sequence 786 BP; 250 A; 168 C; 167 G; 201 T; 0 other;
 Query Match 97.2%; Score 763.6; DB 19; Length 786;
 Best Local Similarity 98.2%; Pred. No. 1.6e-209;
 Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
 Qy 1 ATGATAG 60
 Db 1 ATGATAG 60
 Qy 61 ATGAGAGATTTTATGATTTACTTACTGTTTTCTTTATCCCAATGATGGTCAACA 120
 Db 61 ATGAGAGATTTTATGATTTACTTACTGTTTTCTTTATCCCAATGATGGTCAACA 120
 Qy 121 CTTTGTGCTGTGATCTTCTATAGAGTTTGAACAATAGAGATGAAATCTTCAAT 180
 Db 121 CTTTGTGCTGTGATCTTCTATAGAGTTTGAACAATAGAGATGAAATCTTCAAT 180
 Qy 181 GAAGATTTGTATCATGAAAAAGATAGAGATGCAACAAGAGAAATCTTATCC 240
 Db 181 GAAGATTTGTATCATGAAAAAGATAGAGATGCAACAAGAGAAATCTTATCC 240
 Qy 241 TTACTGAAGTGTGAGAGATTAAGCCAGTTTGAAGCTTTGTAGAGATATATGTTA 300
 Db 241 TTACTGAAGTGTGAGAGATTAAGCCAGTTTGAAGCTTTGTAGAGATATATGTTA 300
 Qy 301 AACCAAG 360
 Db 301 AACCAAG 360
 Qy 361 CAATTTGGCGGCACTGTCTATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
 Db 361 CAATTTGGCGGCACTGTCTATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
 Qy 421 GCTGAAAAAGAGATCTACACATGAGCAAACTTGTGTAACCTGGAAGATGGAACAG 480
 Db 421 GCTGAAAAAGAGATCTACACATGAGCAAACTTGTGTAACCTGGAAGATGGAACAG 480
 Qy 481 CTGACCGTTTAAAG 540
 Db 481 CTGACCGTTTAAAG 540

QY 541 CGGGAAGCTTCGAGTCAAGCTTCATTATAGCCAGCTTCGCTTAAGTCCCGGCTAGA 600
 DB 541 CGGGAAGCTTCGAGTCAAGCTTCATTATAGCCAGCTTCCTTAAGTCCCGGCTAGA 600
 QY 601 TTGAGAGAACTTCTACTCAGAGCTGCAAAATCCCAAGTTCGCGCAAACTTCGCGGCA 660
 DB 601 TTGAGAGAACTTCTACTCAGAGCTGCAAAATCCCAAGTTCGCGCAAACTTCGCGGCA 660
 QY 661 CAATCCATTCCTTGGGAGGAGTATTTGATTTGCAACGAGGCTTCGCTTGTGCAAT 720
 DB 661 CAATCCATTCCTTGGGAGGAGTATTTGATTTGCAACGAGGCTTCGCTTGTGCAAT 720
 QY 721 GTGACTGATCCAAAGCCAAAGTCCATGAGCACTGCTTCACGCTCTTGTGCTTAA 780
 DB 721 GTGACTGATCCAAAGCCAAAGTCCATGAGCACTGCTTCACGCTCTTGTGCTTAA 780
 QY 781 CTCTGA 786
 DB 781 CTCTGA 786

RESULT 4
 AA063959
 ID AA063959 standard; cDNA to mRNA; 786 BP.

XX AA063959;
 DT 11-JAN-1995 (first entry)

XX Human CD40-L type II transmembrane protein coding sequence.
 DE Leucine zipper; trimerization; trimeric CD40-L; fusion protein;
 KM hetero-oligomer; homo-oligomer; type II transmembrane protein;
 KW soluble CD40-L; tumour necrosis factor family; ss.

XX Homo sapiens.

OS
 FH Key Location/Qualifiers
 FT 1..786
 FT CDS /product= human CD40-L
 FT /note= "nucleotides 148-783 code for the
 FT extracellular region (amino acids 50-261)"

PN MO9410308-A.

XX 11-MAY-1994.

XX 20-OCT-1993; 93WO-US10034.

XX 23-OCT-1992; 92US-0969703.

XX 13-AUG-1993; 93US-0107353.

XX (IMMV) IMPDNEK CORP.

XX Spriggs MK, Srinivasan S;

XX WPI, 1994-167465/20.

XX P-FSDB; AARS3969.

PT Prepn. of soluble oligomeric mammalian proteins - using host
 PT cells to express a fusion protein comprising a leucine zipper
 PT domain and a heterologous mammalian protein

XX Example 1; Page 22-23; 35pp; English.

XX A DNA fragment encoding the extracellular (soluble) region of human
 CC CD40-L was ligated to a synthetic oligonucleotide sequence coding
 CC for a leader peptide, a 33 amino acid leucine zipper sequence
 CC (AARS3968) and the flag (Rm) linker sequence. Cells expressing the
 CC fusion construct are grown to accumulate oligomeric, soluble CD40-L
 CC in the supernatant. The leucine zipper sequence spontaneously

CC trimers in solution and fusion proteins comprising
 CC the sequence fused to a heterologous mammalian protein also form
 CC oligomers.

XX Sequence 786 BP; 250 A; 168 C; 168 G; 200 T; 0 other;

Query Match 95.9%; Score 754; DB 15; Length 786;
 Best Local Similarity 97.5%; Pred. No. 9.2e-207;
 Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ATGATGAAACATACACCACTCCCGAGATCCGCGCAACTGCACTTCGAGGAG 60
 DB 1 ATGATGAAACATACACCACTTCCTCCGATTCGCGCACTGCACTTCGAGGAG 60
 QY 61 ATGAGATTTTATGATATTTACTTACTGTTTCTTATCCCAATGATGATCTG 120
 DB 61 ATGAGATTTTATGATATTTACTTACTGTTTCTTATCCCAATGATGATCTG 120
 QY 121 CTTTGGCTGTGATCTTCATAGAGGTTGACAGATGAGATGAGAAAGATCTT 180
 DB 121 CTTTGGCTGTGATCTTCATAGAGGTTGACAGATGAGATGAGAAAGATCTT 180
 QY 181 GAAAGATTTTATGATGAAACGATACAGATGCAACAGAGAAAGATCTTATCC 240
 DB 181 GAAAGATTTTATGATGAAACGATACAGATGCAACAGAGAAAGATCTTATCC 240
 QY 241 TTACTGATCTGTGAGGAGATTTAAAGCCGTTGAGGCTTGTGAGATGATAT 300
 DB 241 TTACTGATCTGTGAGGAGATTTAAAGCCGTTGAGGCTTGTGAGATGATAT 300
 QY 301 AACAAAGAGACGAGAAAGAAAGAAAGCTTTGAAATGCAAAAGGATGATCT 360
 DB 301 AACAAAGAGACGAGAAAGAAAGAAAGCTTTGAAATGCAAAAGGATGATCT 360
 QY 361 CAAATTGCGGACATGCTATAGAGGCGAGAGTAAACATCTGTCTACAGT 420
 DB 361 CAAATTGCGGACATGCTATAGAGGCGAGAGTAAACATCTGTCTACAGT 420
 QY 421 GCTGAAAGATGATCTACACCATGAGCAACCTTGTATCCCTGAAATGGGAA 480
 DB 421 GCTGAAAGATGATCTACACCATGAGCAACCTTGTATCCCTGAAATGGGAA 480
 QY 481 CTGACGCTTAAAGCAAGAGCTCTATATCTATGCTCCAGTCACTTCTGTCC 540
 DB 481 CTGACGCTTAAAGCAAGAGCTCTATATCTATGCTCCAGTCACTTCTGTCC 540
 QY 541 CGGGAAGCTTCGAGTCAAGCTTCATTATAGCCAGCTTCGCTTAAGTCCCG 600
 DB 541 CGGGAAGCTTCGAGTCAAGCTTCATTATAGCCAGCTTCGCTTAAGTCCCG 600
 QY 601 TTGAGAGAACTTCTACTCAGAGCTGCAAAATCCCAAGTTCGCGCAAACT 660
 DB 601 TTGAGAGAACTTCTACTCAGAGCTGCAAAATCCCAAGTTCGCGCAAACT 660
 QY 661 CAATCCATTCCTTGGGAGGAGTATTTGATTTGCAACGAGGCTTCGCTTGT 720
 DB 661 CAATCCATTCCTTGGGAGGAGTATTTGATTTGCAACGAGGCTTCGCTTGT 720
 QY 721 GTGACTGATCCAAAGCCAAAGTCCATGAGCACTGCTTCACGCTCTTGTG 780
 DB 721 GTGACTGATCCAAAGCCAAAGTCCATGAGCACTGCTTCACGCTCTTGTG 780
 QY 781 CTCTGA 786
 DB 781 CTCTGA 786

RESULT 5
 AA063997
 ID AA063997 standard; DNA; 786 BP.
 XX AA063997;
 AC

DT 23-SEP-1998 (first entry)
 XX CD40 ligand gene used in the course of the invention.
 DE CD40 ligand; alteration; immunoreactivity; human cell;
 XX CD40 ligand; alteration; immunoreactivity; human cell;
 KW accessory molecule ligand; AMU; gene therapy; treatment; neoplasia;
 KW autoimmune disorder; rheumatoid arthritis; vaccine; ss.
 XX Mus sp.
 OS Mus sp.
 PN WO9826061-A2.
 XX 18-JUN-1998.
 XX 08-DEC-1997; 97WO-US22740.
 XX 01-DEC-1997; 97US-0982272.
 PR 09-DEC-1996; 96US-0032145.
 XX (REGC) UNIV CALIFORNIA.
 XX Cantwell M, Kipps TJ, Sharma S;
 DR WPI; 1998-348521/30.
 PT Vectors containing accessory molecule ligand genes - used for
 PT altering immunoreactivity of cells, particularly for treatment of
 PT neoplasia or autoimmune disorders, e.g. rheumatoid arthritis
 PS Disclosure; Page 104; 167pp; English.
 XX The present sequence represents the CD40 ligand gene. The sequence is
 CC used to exemplify the method of the invention. The specification
 CC describes a method for altering the immunoreactivity of human cells
 CC which comprises introducing a gene encoding an accessory molecule
 CC ligand (AMU) into the cells so that the AMU is expressed on the surface
 CC of the cells. Vectors containing the AMU genes can be used in gene
 CC therapy for treating neoplasia or autoimmune disorders such as rheumatoid
 CC arthritis. They can also be used for vaccination to produce immunity
 CC against a virus cell, bacteria, protein, fungus or neoplasia.
 XX
 SQ Sequence 786 BP; 250 A; 168 C; 168 G; 200 T; 0 other;
 Query Match 95.9%; Score 754; DB 19; Length 786;
 Best Local Similarity 97.5%; Pred. No. 9,2e-207;
 Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
 QY 1 ATGATAGAAACATACAGCAACCTTCCCGAGATCCGTGGCAACTGATCCAGGAGC 60
 DB 1 ATGATCGAAACATACCAAACTTCTCCGAGTCGTGGCCACTGAGCTGCCATCAGC 60
 QY 61 ATGAAGATTTTATGATTTTACTCTGTTTCTTATCAACCAAGATTTGATCTGTG 120
 DB 61 ATGAAATTTTATGATTTTACTCTGTTTCTTATCAACCAAGATTTGATCTGTG 120
 QY 121 CTTTTCCTGTGATCTTCAATGAAAGTTTGACAAAGATGAAAGATCTTCAT 180
 DB 121 CTTTTCCTGTGATCTTCAATGAAAGTTTGACAAAGATGAAAGATCTTCAT 180
 QY 181 GAAGATTTTATGATTTTACTCTGTTTCTTATCAACCAAGATTTGATCTGTG 240
 DB 181 GAAGATTTTATGATTTTACTCTGTTTCTTATCAACCAAGATTTGATCTGTG 240
 QY 241 TTAAGATTTTATGATTTTACTCTGTTTCTTATCAACCAAGATTTGATCTGTG 300
 DB 241 TTAAGATTTTATGATTTTACTCTGTTTCTTATCAACCAAGATTTGATCTGTG 300
 QY 301 AACCAAG 360
 DB 301 AACCAAG 360
 QY 361 CAAATTCGGGACATGTCATTAAGTGAAGCCAGAGTAAACCAATCTGTGTACAGTG 420
 DB 361 CAAATTCGGGACATGTCATTAAGTGAAGCCAGAGTAAACCAATCTGTGTACAGTG 420

DB 361 CAAATTCGGGACATGTCATTAAGTGAAGCCAGAGTAAACCAATCTGTGTACAGTG 420
 QY 421 GCTGAAAAAGATATCTACACCATGAGCAACACTTGTGTAACCTGTGAAAAAGAG 480
 DB 421 GCTGAAAAAGATATCTACACCATGAGCAACACTTGTGTAACCTGTGAAAAAGAG 480
 QY 481 CTGACCGTTTAAAGACAGAGACTCTATATATATGAGCCAGTCACTTCTGTCCAT 540
 DB 481 CTGACCGTTTAAAGACAGAGACTCTATATATATGAGCCAGTCACTTCTGTCCAT 540
 QY 541 CCGGAAAGCTTCAGAGTCAAGCTTCATTTATGACCAAGCTTCCTTAAAGTCCCGTGA 600
 DB 541 CCGGAAAGCTTCAGAGTCAAGCTTCATTTATGACCAAGCTTCCTTAAAGTCCCGTGA 600
 QY 601 TTGAGAGAAATCTTATCTCAGAGCTGCAAAATACCAAGTTCGCGCAAACTTGGGCA 660
 DB 601 TTGAGAGAAATCTTATCTCAGAGCTGCAAAATACCAAGTTCGCGCAAACTTGGGCA 660
 QY 661 CAATCATTCATCTTGGAGAGATTTGAAATTTGCAACCAAGTCTTGGTGTTCAT 720
 DB 661 CAATCATTCATCTTGGAGAGATTTGAAATTTGCAACCAAGTCTTGGTGTTCAT 720
 QY 721 GTGACTGATCCAGCAAGTGAAGCATGAGCACTGCTTCAAGTCTTGGCTTATCAAA 780
 DB 721 GTGACTGATCCAGCAAGTGAAGCATGAGCACTGCTTCAAGTCTTGGCTTATCAAA 780
 QY 781 CTCTGA 786
 DB 781 CTCTGA 786
 RESULT 6
 AA12852
 ID AA12852 standard; cDNA to mRNA; 786 BP.
 XX AA12852;
 AC
 AC
 DT 13-MAY-1998 (first entry)
 XX
 DE CD40 ligand coding sequence.
 XX
 KW Leucine zipper; fusion protein production; soluble oligomeric protein;
 KW heterologous mammalian type II transmembrane protein; activated T cell;
 KW heterologous mammalian type I transmembrane protein; antibody production;
 KW CD40-L; B-cell proliferation; CD27-L; lymphocyte antigen; ss.
 XX Homo sapiens.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 1..786
 FT /*tag= a
 PN US5716805-A.
 PD 10-FEB-1998.
 PF 18-MAY-1995; 95US-0446922.
 PR 18-MAY-1995; 95US-0446922.
 PR 25-OCT-1991; 91US-0783707.
 PR 05-DEC-1991; 91US-0805723.
 PR 23-OCT-1992; 92US-0969703.
 PR 13-AUG-1993; 93US-0107353.
 PA (IMMUNEX) IMMUNEX CORP.
 XX
 XX Spriggs MK, Strinivasan S;
 XX WPI; 1998-144799/13.
 DR P-PSDB; AAW1178.
 DR
 XX Soluble oligomeric fusion proteins - comprising leucine zipper fused
 PT to extracellular region of transmembrane protein

XX Example 1; column 19-20; 21bp; English.

CC This sequence is the coding sequence for the human CD40 ligand (CD40-L).
 CC The encoded protein can be used in a fusion protein produced using the
 CC method of the invention. The method is for preparing soluble oligomeric
 CC protein by culturing a host cell transfected with a vector for the
 CC fusion protein. The soluble oligomeric proteins comprise a leucine zipper
 CC fused to the N terminus of the extracellular region of a heterologous
 CC mammalian type II transmembrane protein or to the C terminus of the
 CC extracellular region of a heterologous mammalian type I transmembrane
 CC protein, where the leucine zipper is a peptide comprising at least part
 CC of AA41171 or AA41172, optionally with conservative amino acid
 CC substitutions, provided that the peptide trimerizes in solution. A
 CC soluble fusion protein comprising the leucine zipper of AA41171 linked
 CC to the extracellular region of CD40-L (a type II transmembrane protein
 CC that is found on activated T cells and acts as a ligand for the B-cell
 CC antigen CD40) stimulates B-cell proliferation and antibody production in
 CC a similar manner to membrane-bound CD40-L. A soluble fusion protein
 CC comprising the leucine zipper of AA41172 linked to the extracellular
 CC region of CD27-L (a type II transmembrane protein that binds to the
 CC lymphocyte antigen CD27) inhibits binding of CD27c (a fusion protein
 CC comprising the extracellular region of CD27 and a human IgG1 Fc region)
 CC to EBV-transformed B cells expressing CD27-L.

SQ Sequence 786 BP; 250 A; 168 C; 168 G; 200 T; 0 other;

Query Match 95.9%; Score 754; DB 19; Length 786;

Best Local Similarity 97.5%; Pred. No. 9.2e-207;

Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ATGATGAGAAACATACAGCCACCTTCCCGAGTCGGGCACTGACCTTCCAGCGAGC 60
 DB 1 ATGATGAGAAACATACAGCCACCTTCCCGAGTCGGGCACTGACCTTCCAGCGAGC 60
 QY 61 ATGAGAGATTTTATGATTTCTTACTGTTTCTTATCACCAGCAATGGATCTGTG 120
 DB 61 ATGAGAGATTTTATGATTTCTTACTGTTTCTTATCACCAGCAATGGATCTGTG 120
 QY 121 CTTTTCCTGTGATCTTATGAGAGGTTGACAGATGAGAGATGAGAGATCTTCAT 180
 DB 121 CTTTTCCTGTGATCTTATGAGAGGTTGACAGATGAGAGATGAGAGATCTTCAT 180
 QY 181 GAAGATTTTGTATTCATGAGAAACGATACAGATGAGCAACAGAGAGAGATCTTATCC 240
 DB 181 GAAGATTTTGTATTCATGAGAAACGATACAGATGAGCAACAGAGAGAGATCTTATCC 240
 QY 241 TTACTGAACTGTGAGAGATTTAAAGCCAGTTTGAAGGCTTGTGAAGATATATGTTA 300
 DB 241 TTACTGAACTGTGAGAGATTTAAAGCCAGTTTGAAGGCTTGTGAAGATATATGTTA 300
 QY 301 AACAAAG 360
 DB 301 AACAAAG 360
 QY 361 CAAATGGGCGACATGTCATTAAGTGAAGCCAGAGTAAGAAACAATCTGTGTTACAGTGG 420
 DB 361 CAAATGGGCGACATGTCATTAAGTGAAGCCAGAGTAAGAAACAATCTGTGTTACAGTGG 420
 QY 421 GGTGAAAAAGATATACACATGAGCAACAATGTTGTAACCTGGAAAAATGGGAAACAG 480
 DB 421 GGTGAAAAAGATATACACATGAGCAACAATGTTGTAACCTGGAAAAATGGGAAACAG 480
 QY 481 CTGACCGTTAAAGACAGAGACTTATATATATATATATATATATATATATATATATAT 540
 DB 481 CTGACCGTTAAAGACAGAGACTTATATATATATATATATATATATATATATATATAT 540
 QY 541 CGGAGAGCTTGAAGTCAAGCTCATTATATATATATATATATATATATATATATATATAT 600
 DB 541 CGGAGAGCTTGAAGTCAAGCTCATTATATATATATATATATATATATATATATATATAT 600
 QY 601 TTGAGAGAAATCTTACTGAGAGCTGCAAAATACCAAGTTCCGCAAACTTTCGGGCAAA 660
 DB 601 TTGAGAGAAATCTTACTGAGAGCTGCAAAATACCAAGTTCCGCAAACTTTCGGGCAAA 660

DB 601 TTGAGAGAAATCTTACTGAGAGCTGCAAAATACCAAGTTCCGCAAACTTTCGGGCAAA 660
 QY 661 CAATTCATCTTGGGAGAGAGATTTGAAATGGCAACAGAGCTTCCGATGTTGCAAT 720
 DB 661 CAATTCATCTTGGGAGAGAGATTTGAAATGGCAACAGAGCTTCCGATGTTGCAAT 720
 QY 721 GTGACGATTCAGAGCAAGTGAAGCCATGCGCTTCCGCTTACTGCAAA 780
 DB 721 GTGACGATTCAGAGCAAGTGAAGCCATGCGCTTCCGCTTACTGCAAA 780
 QY 781 CTCTGA 786
 DB 781 CTCTGA 786

RESULT 7
 AAQ41506
 ID AAQ41506 standard; DNA; 840 BP.

AC AAQ41506;
 XX
 XX 12-AUG-1993 (first entry)
 DT
 XX
 DE CD40-L DNA.

KW Human; CD40-L; CD40; type II; membrane; polypeptide; extracellular;
 KW transmembrane; region; intracellular; soluble; activity; B cell;
 KW proliferation; induction; antibody; secretion; IGF; agonist;
 KW antagonist; binding assay; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH CDS 46..831
 FT /*tag= a

PN MO308207-A.

XX 29-APR-1993.

PF 23-OCT-1992; 92MO-US08990.

PR 25-OCT-1991; 91US-0783707.

PR 05-DEC-1991; 91US-0805723.

XX (IMMV) IMMUNEX CORP.

PI Armitage RJ, Fanslow WC, Spriggs MK;

DR WPI: 1993-152417/18.

DR P-PSDB: AAR36701.

PT New cytokine CD40-L as CD40 agonist and antagonist - is used for
 PT treating allergies, lupus, rheumatoid arthritis,
 PT graft-versus-host disease and insulin-dependent diabetes mellitus
 XX
 XX Claim 1; Fig 2; 80bp; English.

PS This sequence encodes a human CD40-L polypeptide which binds to CD40.
 CC CD40-L is a type II membrane polypeptide which has an extracellular
 CC region at its C-terminus, a transmembrane region and an
 CC intracellular region at its N-terminus. A soluble form of CD40-L
 CC lacks the transmembrane domain. CD40-L activity is mediated by
 CC binding with CD40 and induces B cell proliferation and induction of
 CC antibody secretion, including IGF. Membrane bound CD40-L acts as a
 CC CD40 agonist and soluble CD40-L acts as a CD40 antagonist. CD40-L
 CC can be used in a binding assay to detect cells expressing CD40.

SQ Sequence 840 BP; 266 A; 185 C; 175 G; 214 T; 0 other;

Query Match 95.9%; Score 754; DB 14; Length 840;

Best Local Similarity 97.5%; Pred. No. 9.5e-207;

Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Oy 1 ATGATAGAAACATACAGCAACCTTCCCGAGATCCGTGGCAACTGACCTTCAGCAGC 60
 Db 46 ATGATAGAAACATACAGCAACCTTCCCGAGATCCGTGGCAACTGACCTTCAGCAGC 105
 Oy 61 ATGATAGAAACATACAGCAACCTTCCCGAGATCCGTGGCAACTGACCTTCAGCAGC 120
 Db 106 ATGATAGAAACATACAGCAACCTTCCCGAGATCCGTGGCAACTGACCTTCAGCAGC 165
 Oy 121 CTTTGGCTGTGTATCTTCAATAGAGTTGCAAGATGAGTAAAGATGATCTTCAT 180
 Db 166 CTTTGGCTGTGTATCTTCAATAGAGTTGCAAGATGAGTAAAGATGATCTTCAT 225
 Oy 181 GAAGATTTTGTATTCATGAGAAACGATACAGATGACCAACAGAGAAAGATCTTATCC 240
 Db 226 GAAGATTTTGTATTCATGAGAAACGATACAGATGACCAACAGAGAAAGATCTTATCC 285
 Oy 241 TTACTGAACCTGTGAGAGATTAAGAGCCAGTTTGAAGCTTGTGTGAAGATATATGTTA 300
 Db 286 TTACTGAACCTGTGAGAGATTAAGAGCCAGTTTGAAGCTTGTGTGAAGATATATGTTA 345
 Oy 301 AACAAAG 360
 Db 346 AACAAAG 405
 Oy 361 CAAATTTGGGGCAGATGATCATATGAGGCGAGAGTAAACAAACATCTGTGTATCATGTG 420
 Db 406 CAAATTTGGGGCAGATGATCATATGAGGCGAGAGTAAACAAACATCTGTGTATCATGTG 465
 Oy 421 GCTGAAAAAGATATCTACACCATGAGCAACATTTGTAAACCTGTGAAATGAGAAACAG 480
 Db 466 GCTGAAAAAGATATCTACACCATGAGCAACATTTGTAAACCTGTGAAATGAGAAACAG 525
 Oy 481 CTGACCGTTTAAAGACAGAGACTATATATATATATATATATATATATATATATATATAT 540
 Db 526 CTGACCGTTTAAAGACAGAGACTATATATATATATATATATATATATATATATATATAT 585
 Oy 541 CGGAAAGCTTGAAGTCAAGCTCATTTATATAGCCAGCTCTGCTTAAAGTCCCGGTAGA 600
 Db 586 CGGAAAGCTTGAAGTCAAGCTCATTTATATAGCCAGCTCTGCTTAAAGTCCCGGTAGA 645
 Oy 601 TTGAGAGATCTTATCTCAGAGCTGCAATATCCAGAGTTCCGCGCAACCTTGGGGCAAA 660
 Db 646 TTGAGAGATCTTATCTCAGAGCTGCAATATCCAGAGTTCCGCGCAACCTTGGGGCAAA 705
 Oy 661 CAATTCATTCATCTGGAGAGAGATTTTGAATTTGCAACAGAGTCTTGGTGTTCAT 720
 Db 706 CAATTCATTCATCTGGAGAGAGATTTTGAATTTGCAACAGAGTCTTGGTGTTCAT 765
 Oy 721 GTGACTGATCCAGAGCAAGTGAAGCTGAGCACTGCTTCAAGCTTGGGCTTATCTCAAA 780
 Db 766 GTGACTGATCCAGAGCAAGTGAAGCTGAGCACTGCTTCAAGCTTGGGCTTATCTCAAA 825
 Oy 781 CTCTGA 786
 Db 826 CTCTGA 831

RESULT 8

AA067123 standard; DNA; 840 BP.
 ID AA067123

AC AA067123;

DT 23-MAR-1995 (first entry)

XX CD40 ligand gene.

KW Probe; primer; PCR; amplify; polymerase chain reaction; detection;

KM mutation; CD40 ligand gene; IgM; ss.

XX Synthetic.

FH Key Location/Qualifiers
 FT CDS 46..831
 FT /-tag= a
 FT /product= CD40 ligand
 XX MO9417196-A.
 XX 04-AUG-1994.
 XX
 XX 21-JAN-1994; 94MO-US00786.
 XX
 XX 22-JAN-1993; 93US-0009258.
 XX 20-JAN-1994; 94US-0184422.
 XX (IMMUNEX CORP.
 XX
 PI Armitage RJ, Davison BL, Fanslow WC, Renshaw BR;
 PI Spriggs MK, Widmer MB;
 XX WPI; 1994-264109/32.
 DR P-PSDB; AAR57469.
 XX
 PT Method for detecting mutation in CD 40 ligand gene - comprises
 PT amplification of nucleic acid, and mutational analysis
 XX
 PS Disclosure: Page 22-24; 38pp; English.
 XX
 CC This sequence represents the CD40 ligand gene. Mutations within
 CC this gene were identified by the method of the invention. The
 CC method comprises isolating DNA from an individual and selectively
 CC amplifying the isolated DNA derived from the CD40 ligand gene. The
 CC amplification product is then analysed to determine if there is a
 CC mutation present and determining if a protein expressed from the
 CC ligand gene will bind CD40. The detection of mutations in the CD40
 CC ligand gene allows subsequent treatment of a syndrome resulting in
 CC elevated levels of serum IgM and diminished levels of other Ig
 CC isotypes, due to mutation in the CD40 ligand gene. ie. X-linked
 CC hyperIgM syndrome.
 XX
 SQ Sequence 840 BP; 266 A; 185 C; 175 G; 214 T; 0 other;
 Query Match 95.9%; Score 754; DB 15; Length 840;
 Best Local Similarity 97.5%; Pred. No. 9.5e-207;
 Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
 Oy 1 ATGATAGAAACATACAGCAACCTTCCCGAGATCCGTGGCAACTGACCTTCAGCAGC 60
 Db 46 ATGATAGAAACATACAGCAACCTTCCCGAGATCCGTGGCAACTGACCTTCAGCAGC 105
 Oy 61 ATGATAGAAACATACAGCAACCTTCCCGAGATCCGTGGCAACTGACCTTCAGCAGC 120
 Db 106 ATGATAGAAACATACAGCAACCTTCCCGAGATCCGTGGCAACTGACCTTCAGCAGC 165
 Oy 121 CTTTGGCTGTGTATCTTCAATAGAGTTGCAAGATGAGTAAAGATGATCTTCAT 180
 Db 166 CTTTGGCTGTGTATCTTCAATAGAGTTGCAAGATGAGTAAAGATGATCTTCAT 225
 Oy 181 GAAGATTTTGTATTCATGAGAAACGATACAGATGACCAACAGAGAAAGATCTTATCC 240
 Db 226 GAAGATTTTGTATTCATGAGAAACGATACAGATGACCAACAGAGAAAGATCTTATCC 285
 Oy 241 TTACTGAACCTGTGAGAGATTAAGAGCCAGTTTGAAGCTTGTGTGAAGATATATGTTA 300
 Db 286 TTACTGAACCTGTGAGAGATTAAGAGCCAGTTTGAAGCTTGTGTGAAGATATATGTTA 345
 Oy 301 AACAAAG 360
 Db 346 AACAAAG 405
 Oy 361 CAAATTTGGGGCAGATGATCATATGAGGCGAGAGTAAACAAACATCTGTGTATCATGTG 420
 Db 406 CAAATTTGGGGCAGATGATCATATGAGGCGAGAGTAAACAAACATCTGTGTATCATGTG 465

QY 421 GCTGAAAAAGATACCTACCACTGAGCAACAACTTGTGTAACCTGGAATGGAAAAAG 480
 DB 466 GCTGAAAAAGATACCTACCACTGAGCAACAACTTGTGTAACCTGGAATGGAAAAAG 525
 QY 481 CTGACCGTTAAAAGACAGAGACTATTTATATCTATGCCCAGTCACTTGTTCAT 540
 DB 526 CTGACCGTTAAAAGACAGAGACTATTTATATCTATGCCCAGTCACTTGTTCAT 585
 QY 541 CGGGAAGCTTCGAGTCAAGCTTCATTTATAGCAGCTTCGCTTAAGTCCCGGTAGA 600
 DB 586 CGGGAAGCTTCGAGTCAAGCTTCATTTATAGCAGCTTCGCTTAAGTCCCGGTAGA 645
 QY 601 TTGAGAGAGATCTTATCTAGAGCTGCAAAATCCCAAGTTCGCGCAAACTTGGCGCA 660
 DB 646 TTGAGAGAGATCTTATCTAGAGCTGCAAAATCCCAAGTTCGCGCAAACTTGGCGCA 705
 QY 661 CAATTCATTCATTGGAGAGATTTGATTTGCAACAGGCTTCGCTTGTTCAT 720
 DB 706 CAATTCATTCATTGGAGAGATTTGATTTGCAACAGGCTTCGCTTGTTCAT 765
 QY 721 GTGACTGATCCAGGCAAGTGAAGCCATGCACTGCTTCAGCTTGTTCAT 780
 DB 766 GTGACTGATCCAGGCAAGTGAAGCCATGCACTGCTTCAGCTTGTTCAT 825
 QY 781 CTCTGA 786
 DB 826 CTCTGA 831

RESULT 9

ID AAT05763 standard; DNA; 840 BP.

XX AAT05763;
 DT 18-MAR-1996 (first entry)
 XX
 DE Human CD40 ligand DNA.

XX High density membrane-bound CD40 ligand; B-lymphocyte; B-cell;
 KW differentiation; proliferation; baculovirus; Spodoptera frugiperda;
 KM Sf9; insect cell culture; tumour necrosis factor receptor; ss.
 XX

OS Homo sapiens.

EH Key Location/Qualifiers
 FT CDS /*tag= a
 XX

PN WO9529935-A1.

PD 09-NOV-1995.

PF 28-APR-1995; 95WO-US05448.

PR 28-APR-1994; 94US-0234580.

PA (BOEH) BOEHRINGER INGELHEIM PHARM INC.

PI Castle BE, Kehry M;

DR WPI, 1995-393038/50.

DR P-PSDB; AAR85486.

PT High density membrane bound CD40 ligand - for stimulating the
 PT proliferation of B cells in vitro or in vivo, partic. for producing
 PT differentiated cells
 XX

PS Disclosure; Fig 1; 74pp; English.

CC The nucleotide sequence given in AAT05763 encodes a human high-density,
 CC membrane-bound (hmb) CD40 ligand (AAR85486) that induces long-term
 CC proliferation of B-cells in culture. These proliferating B-cells

CC can be induced to differentiate into antibody-prod. cells. The
 CC nucleotide sequence is incorporated into a baculovirus vector that
 CC is used to transfect Sf9 insect cells for prodn. of recombinant
 CC hmbCD40.

XX Sequence 840 BP; 263 A; 182 C; 181 G; 214 T; 0 other;

Query Match 95.9%; Score 754; DB 16; Length 840;

Best Local Similarity 97.5%; Pred. No. 9.5e-207; Mismatches 20; Indels 0; Gaps 0;

Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
 QY 1 ATGATGAAACATACGCAACCTCCCGAGATCGGTGGCAACTGGAACTTCGAGGAG 60
 DB 22 ATGATGAAACATACGCAACCTTCCTCCGATCTCGGACATCGCATGCCATAGC 81
 QY 61 ATGAGATTTTATGATATTACTCTGTTTCTTATCCCAACCAATGATGATGCTG 120
 DB 82 ATGAAATTTTATGATATTACTCTGTTTCTTATCCCAACCAATGATGATGCTG 141
 QY 121 CTTTGGCTGATCTTCATAGAGTTGCAAGATGAGATGAGATGAGATGAGATCTT 180
 DB 142 CTTTGGCTGATCTTCATAGAGTTGCAAGATGAGATGAGATGAGATGAGATCTT 201
 QY 181 GAGATTTTATGATATTATGAAACGATACAGATGCAACAGAGAAAGATCTTATCC 240
 DB 202 GAGATTTTATGATATTATGAAACGATACAGATGCAACAGAGAAAGATCTTATCC 261
 QY 241 TTACTGATCTGAGGAGATTTAAAGCCGTTGAAGCTTGTGAGATATATGTTA 300
 DB 262 TTACTGATCTGAGGAGATTTAAAGCCGTTGAAGCTTGTGAGATATATGTTA 321
 QY 301 AACAAAGAGAGACGAAAGAAAGAAACAGCTTTGAATGCAAAAGGTGATCAGATCT 360
 DB 322 AACAAAGAGAGACGAAAGAAAGAAACAGCTTTGAATGCAAAAGGTGATCAGATCT 381
 QY 361 CAATTTGGGCAATGATCATATGAGGCGAGCACTGTAACCAATCTGTGTACAGTGC 420
 DB 382 CAATTTGGGCAATGATCATATGAGGCGAGCACTGTAACCAATCTGTGTACAGTGC 441
 QY 421 GCTGAAAAAGATACCTACCACTGAGCAACAACTTGTGTAACCTGGAATGGAAAAAG 480
 DB 442 GCTGAAAAAGATACCTACCACTGAGCAACAACTTGTGTAACCTGGAATGGAAAAAG 501
 QY 481 CTGACCGTTAAAAGACAGAGACTATTTATATCTATGCCCAGTCACTTGTTCAT 540
 DB 502 CTGACCGTTAAAAGACAGAGACTATTTATATCTATGCCCAGTCACTTGTTCAT 561
 QY 541 CGGGAAGCTTCGAGTCAAGCTTCATTTATAGCAGCTTCGCTTAAGTCCCGGTAGA 600
 DB 562 CGGGAAGCTTCGAGTCAAGCTTCATTTATAGCAGCTTCGCTTAAGTCCCGGTAGA 621
 QY 601 TTGAGAGAGATCTTATCTAGAGCTGCAAAATCCCAAGTTCGCGCAAACTTGGCGCA 660
 DB 622 TTGAGAGAGATCTTATCTAGAGCTGCAAAATCCCAAGTTCGCGCAAACTTGGCGCA 681
 QY 661 CAATTCATTCATTGGAGAGATTTGATTTGCAACAGGCTTCGCTTGTTCAT 720
 DB 682 CAATTCATTCATTGGAGAGATTTGATTTGCAACAGGCTTCGCTTGTTCAT 741
 QY 721 GTGACTGATCCAGGCAAGTGAAGCCATGCACTGCTTCAGCTTGTTCAT 780
 DB 742 GTGACTGATCCAGGCAAGTGAAGCCATGCACTGCTTCAGCTTGTTCAT 801
 QY 781 CTCTGA 786
 DB 802 CTCTGA 807

RESULT 10

ID AAT93782 standard; cDNA; 840 BP.

XX AAT93782;
 AC

XX 16-FEB-1998 (first entry)
 XX CDNA of CD40L, a novel cytokine ligand for CD40.
 DE Cytokine; activated CD4+ T cell; CD40; CD40L; monoclonal antibody;
 KW neoplastic cell proliferation; B-cell lymphoma; immune deficiency; AIDS;
 KW melanoma; carcinoma; ss.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FT CDS 46..831
 FT /*tag= a
 XX US5674492-A.
 XX 07-OCT-1997.
 XX 21-DEC-1994; 94US-0360923.
 XX 23-DEC-1993; 93US-0172664.
 XX (IMMUNEX CORP.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX Armitage RJ, Fanslow WC, Longo DL, Murphy WJ;
 PI WPI; 1997-502273/46.
 DR P-PSDB; AAW34669.
 XX Treating or preventing neoplastic disease associated with
 PT CD40-expressing cells - particularly B-cell lymphoma, by
 PT administration of CD40-binding protein, preferably antibody or
 PT soluble CD40-ligand
 XX Claim 3; Columns 19-22; 21pp; English.
 XX The present sequence represents the cDNA sequence of a novel cytokine
 CC ligand for CD40 called CD40L. CD40L is a type II membrane polypeptide,
 CC which is expressed by activated CD4+ T cells, and causes B cell
 CC proliferation and induction of antibody secretion. The protein can be
 CC used to produce monoclonal antibodies, which in turn bind to its
 CC CD40-expressing cells. This inhibits binding of soluble CD40 to its
 CC ligand CD40L. The monoclonal antibody against CD40L is used to inhibit
 CC proliferation of neoplastic cells, and is particularly useful in treating
 CC B-cell lymphoma (e.g. where induced after transplants or in other cases
 CC of immune deficiency such as AIDS), and also melanoma or carcinoma. Since
 CC the monoclonal antibodies inhibit neoplastic cells directly, they may not
 CC need to be coupled to a toxin or radioisotope, avoiding toxic effects on
 CC normal B cells.
 XX Sequence 840 BP; 266 A; 185 C; 175 G; 214 T; 0 other;
 SQ
 XX Query Match 95.9%; Score 754; DB 18; Length 840;
 XX Best Local Similarity 97.5%; Pred. No. 9.5e-207;
 XX Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
 XX
 QY 1 ATGATGAACATACGACCACTCCCGAGTCCGTGGCACTGACGAGC 60
 DB 46 ATGATGAAACATACGACCACTCCCGAGTCCGTGGCACTGACGAGC 105
 QY 61 ATGAGATTTTATGATTTTACTTACTGTTTCTTATCAACCAATATGATCTGTG 120
 DB 106 ATGAAATTTTATGATTTTACTTACTGTTTCTTATCAACCAATATGATCTGTG 165
 QY 121 CTTTGGCTGTGATCTTCAATAGAGTTGCAAGATTAAGATGAAGATCTTCAT 180
 DB 166 CTTTGGCTGTGATCTTCAATAGAGTTGCAAGATTAAGATGAAGATCTTCAT 225
 QY 181 GAAGATTTTATGATGAAGATGATGACGATGACGACGAGAAAGATCTTATCC 240
 DB 226 GAAGATTTTATGATGAAGATGATGACGATGACGACGAGAAAGATCTTATCC 285

QY 241 TTACTGAACCTGTGAGAGATTTAAAGCCAGTTTGAAGCTTTGGAAGATATATGTTA 300
 DB 286 TTACTGAACCTGTGAGAGATTTAAAGCCAGTTTGAAGCTTTGGAAGATATATGTTA 345
 QY 301 AACAAAGAGAGACGAAAGAAAGAAAGAGCTTTGAAATGCAAAAGGTGATCAGATCCT 360
 DB 346 AACAAAGAGAGACGAAAGAAAGAAAGAGCTTTGAAATGCAAAAGGTGATCAGATCCT 405
 QY 361 CAAATTTGGGCACTGTCTTAAGTGAAGCCAGCAATTAATCTGTGTTACAGTGG 420
 DB 406 CAAATTTGGGCACTGTCTTAAGTGAAGCCAGCAATTAATCTGTGTTACAGTGG 465
 QY 421 GCTGAAAAAGATATACATACATGACGACCACTTGTAACTCGAAAAATGGAAAAAG 480
 DB 466 GCTGAAAAAGATATACATACATGACGACCACTTGTAACTCGAAAAATGGAAAAAG 525
 QY 481 CTGACCTTTAAAAAGCAAGAGACTTATTAATATATGCCCAGACCTTCTGTTCCAT 540
 DB 526 CTGACCTTTAAAAAGCAAGAGACTTATTAATATATGCCCAGACCTTCTGTTCCAT 585
 QY 541 CCGGAAGCTTCGAGTCAGTCAGTCATTTATAGCCAGCTCTGCTTAAAGTCCCGGTAGA 600
 DB 586 CCGGAAGCTTCGAGTCAGTCAGTCATTTATAGCCAGCTCTGCTTAAAGTCCCGGTAGA 645
 QY 601 TTGAGAGAAATTTTACTGAGAGCTGCAAAATACCAAGTCCGCAAACTTGGCGGCA 660
 DB 646 TTGAGAGAAATTTTACTGAGAGCTGCAAAATACCAAGTCCGCAAACTTGGCGGCA 705
 QY 661 CAATCATTCACTTGGAGAGATATTTGAATTGCAACAGAGTCTGATGTTGCAAT 720
 DB 706 CAATCATTCACTTGGAGAGATATTTGAATTGCAACAGAGTCTGATGTTGCAAT 765
 QY 721 GGTACTGATCCAGCAAGTGAAGCCAGTGGCAAGTCTTGGCTTACTACGAA 780
 DB 766 GGTACTGATCCAGCAAGTGAAGCCAGTGGCAAGTCTTGGCTTACTACGAA 825
 QY 781 CTCTGA 786
 DB 826 CTCTGA 831
 XX
 XX RESULT 11
 XX AAV61063
 XX ID AAV61063 standard; DNA; 840 BP.
 XX AC AAV61063;
 XX DT 08-DEC-1998 (first entry)
 XX DE Human CD40 ligand encoding DNA sequence.
 XX KW Human; CD40 ligand; TNF receptor family; activated T cell;
 XX KW type 2 membrane glycoprotein; cell proliferation; differentiation;
 XX B cell; de.
 XX OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT CDS 22..807
 FT /*tag= a
 FT /product= "CD40 ligand"
 XX
 XX US5817516-A.
 XX 06-OCT-1998.
 XX 28-APR-1995; 95US-0431055.
 XX 28-APR-1995; 95US-0431055.
 XX 28-APR-1994; 94US-0234580.
 XX (BOEHR) BOEHRINGER INGELHEIM PHARM INC.

Oy 121 CTTTGTGCTGTATCTTCAATAGAGGTTGCAAGATAGAGATGAAATCTTCAT 180
 |||||
 Db 166 CTTTGTGCTGTATCTTCAATAGAGGTTGCAAGATAGAGATGAAATCTTCAT 225
 |||||
 Oy 181 GAAGATTTTGTATTCATGAAAACGATACAGATGCAACAGAGAAAATCTTATCC 240
 |||||
 Db 226 GAAGATTTTGTATTCATGAAAACGATACAGATGCAACAGAGAAAATCTTATCC 285
 |||||
 Oy 241 TTACTGACTGTGAGAGATTAAAGCCGTTGAGGCTTTGTGAGAGATATATGTTA 300
 |||||
 Db 286 TTACTGACTGTGAGAGATTAAAGCCGTTGAGGCTTTGTGAGAGATATATGTTA 345
 |||||
 Oy 301 AACAAAGAGAGACGAAAGAAAACAGCTTTGAAAATGCAAAAAGTGATCAGATCTC 360
 |||||
 Db 346 AACAAAGAGAGACGAAAGAAAACAGCTTTGAAAATGCAAAAAGTGATCAGATCTC 405
 |||||
 Oy 361 CAATTTGCGGCACTATCATATGAGGCGAGAGTAAACAACTCTGTGTACAGTGG 420
 |||||
 Db 406 CAATTTGCGGCACTATCATATGAGGCGAGAGTAAACAACTCTGTGTACAGTGG 465
 |||||
 Oy 421 GCTGAAAAAGATATCTACCATGAGCAACATTTGTTAACTCTGAAAATGAGAAACAG 480
 |||||
 Db 466 GCTGAAAAAGATATCTACCATGAGCAACATTTGTTAACTCTGAAAATGAGAAACAG 525
 |||||
 Oy 481 CTGACCGTTTAAAAAGCAAGAGCTTATATATCTATGCCCCAGTCACTCTGTGTCCAT 540
 |||||
 Db 526 CTGACCGTTTAAAAAGCAAGAGCTTATATATCTATGCCCCAGTCACTCTGTGTCCAT 585
 |||||
 Oy 541 CGGAAAGCTTGAGTCAAGTCCATTTATATGACGCTCTGCTTAAAGTCCCCGGTAGA 600
 |||||
 Db 586 CGGAAAGCTTGAGTCAAGTCCATTTATATGACGCTCTGCTTAAAGTCCCCGGTAGA 645
 |||||
 Oy 601 TTGAGAGATCTTACTCAGAGCTGCAATATACCAAGTTCGCGCAAACTTGCGGGCAA 660
 |||||
 Db 646 TTGAGAGATCTTACTCAGAGCTGCAATATACCAAGTTCGCGCAAACTTGCGGGCAA 705
 |||||
 Oy 661 CAATCATTCACCTTGAGAGAGATTTTGAATTTGCAACAGAGTCTTCCGTGTTTTCAT 720
 |||||
 Db 706 CAATCATTCACCTTGAGAGAGATTTTGAATTTGCAACAGAGTCTTCCGTGTTTTCAT 765
 |||||
 Oy 721 GTGACTGATCCAAAGCAAGTGAAGCCATGAGCACTGGCTTCAAGCTTTGGGCTTCAAA 780
 |||||
 Db 766 GTGACTGATCCAAAGCAAGTGAAGCCATGAGCACTGGCTTCAAGCTTTGGGCTTCAAA 825
 |||||
 Oy 781 CTCTGA 786
 |||||
 Db 826 CTCTGA 831
 |||||

RESULT 13

ID AAF5539 standard; DNA; 879 BP.
 AAF5539;

29-MAY-2001 (first entry)

Nucleotide sequence of human gp39 protein, a CD40 ligand.

KW gp39; CD40 ligand; osteoblast cell death; apoptosis; bone loss;
 KW osteoporosis; osteonecrosis; inflammatory arthritis; estrogen loss;
 KW ovariectomy; histiocytosis; lupus nephritis; Takayasu's arteritis;
 KW Wegener's granulomatosis; nephritis; myositis; scleroderma;
 KW thrombocytopenia; asthma; lung disease; cancer; ss.

OS Homo sapiens.

Key Location/Qualifiers
 FH 22..807
 FT /tag= a
 FT /product= "gp39"
 XX

PN W0200116180-A2.
 XX
 PD 08-MAR-2001.
 XX
 PF 24-AUG-2000; 2000WO-US23276.
 XX
 PR 27-AUG-1999; 99US-0151250.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 PI Ahuja SS, Bonewald LP;
 XX
 DR WPI; 2001-169007/17.
 DR P-PSDB; AAB67612.
 PT CD40 agonist containing composition, used to reduce bone cell death or
 PT apoptosis associated with osteoporosis, osteonecrosis and inflammatory
 PT arthritis -
 XX
 PS Disclosure; Page 113; 118pp; English.
 XX
 CC The present sequence encodes a gp39 protein. It is a CD40 ligand.
 CC CD40 ligands are used for reducing osteoblast cell death or apoptosis,
 CC and for treating or preventing bone loss in animals, preferably humans,
 CC at risk of, or undergoing, bone loss. The bone loss is associated with
 CC osteoporosis, osteonecrosis, inflammatory arthritis, post-menopausal
 CC oestrogen loss, estrogen loss due to ovariectomy, total hysterectomy,
 CC lupus nephritis, Takayasu's arteritis, Wegener's granulomatosis,
 CC anti-glomerular basement membrane nephritis, myositis, scleroderma,
 CC idiopathic autoimmune thrombocytopenia, asthma, a chronic obstructive
 CC lung disease, nephrotic/nephritic syndrome, or cancer. They may also be
 CC used to treat or prevent bone loss in a subject undergoing, or scheduled
 CC for, an organ or bone marrow transplant.
 XX
 SQ Sequence 879 BP; 274 A; 193 C; 190 G; 222 T; 0 other;

Query Match 95.9%; Score 754; DB 22; Length 879;
 Best Local Similarity 97.5%; Pred. No. 9.7e-207;
 Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Oy 1 ATGATAGAAAATATGAGCCCACTTCCCGAGATCGGAGCACTGAGCTTCACAGAGC 60
 |||||
 Db 22 ATGATAGAAAATATGAGCCCACTTCCCGAGATCGGAGCACTGAGCTTCACAGAGC 81
 |||||
 Oy 61 ATGAAATTTTATGATTTACTTACTGTTTTCCTTATACCAATGATGATCTGTG 120
 |||||
 Db 82 ATGAAATTTTATGATTTACTTACTGTTTTCCTTATACCAATGATGATCTGTG 141
 |||||
 Oy 121 CTTTGTGCTGTATCTTCAATAGAGGTTGCAAGATAGAGATGAAATCTTCAT 180
 |||||
 Db 142 CTTTGTGCTGTATCTTCAATAGAGGTTGCAAGATAGAGATGAAATCTTCAT 201
 |||||
 Oy 181 GAAGATTTTGTATTCATGAAAACGATACAGATGCAACAGAGAAAATCTTATCC 240
 |||||
 Db 202 GAAGATTTTGTATTCATGAAAACGATACAGATGCAACAGAGAAAATCTTATCC 261
 |||||
 Oy 241 TTACTGACTGTGAGAGATTAAAGCCGTTGAGGCTTTGTGAGAGATATATGTTA 300
 |||||
 Db 262 TTACTGACTGTGAGAGATTAAAGCCGTTGAGGCTTTGTGAGAGATATATGTTA 321
 |||||
 Oy 301 AACAAAGAGAGACGAAAGAAAACAGCTTTGAAAATGCAAAAAGTGATCAGATCTC 360
 |||||
 Db 322 AACAAAGAGAGACGAAAGAAAACAGCTTTGAAAATGCAAAAAGTGATCAGATCTC 381
 |||||
 Oy 361 CAATTTGCGGCACTATCATATGAGGCGAGAGTAAACAACTCTGTGTACAGTGG 420
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 Db 382 CAATTTGCGGCACTATCATATGAGGCGAGAGTAAACAACTCTGTGTACAGTGG 441
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 Oy 421 GCTGAAAAAGATATCTACCATGAGCAACATTTGTTAACTCTGAAAATGAGAAACAG 480
 |||||
 Db 442 GCTGAAAAAGATATCTACCATGAGCAACATTTGTTAACTCTGAAAATGAGAAACAG 501
 |||||
 Oy 481 CTGACCGTTTAAAAAGCAAGAGCTTATATATCTATGCCCCAGTCACTCTGTGTCCAT 540
 |||||

Db 502 CTGACCGTTAAAGACAGACTCTATTATATCTATGCCCAGTCACTCTTCTGTTCCAAAT 561
 Qy 541 CGGGAAGCTTCGAGTCAGATCCATTTATATGAGCTCTCCCTTAAGTCCCGGTGA 600
 Db 562 CGGGAAGCTTCGAGTCAGATCCATTTATATGAGCTCTCCCTTAAGTCCCGGTGA 621
 Qy 601 TTGAGAGAACTTTACTGAGAGTCGCAAAATCCACAGTTCGCGCAAACTTCGCGGCA 660
 Db 622 TTGAGAGAACTTTACTGAGAGTCGCAAAATCCACAGTTCGCGCAAACTTCGCGGCA 681
 Qy 661 CAATCCATTCAGCTTGGAGAGATTTGATGCAACAGAGTTCGCTGCTGCTTGTCAAT 720
 Db 682 CAATCCATTCAGCTTGGAGAGATTTGATGCAACAGAGTTCGCTGCTGCTTGTCAAT 741
 Qy 721 GTGACTGATCCAGCCAGAGTCCAGTCCAGTTCAGTCTTGGCTTACTCAAA 780
 Db 742 GTGACTGATCCAGCCAGAGTCCAGTCCAGTTCAGTCTTGGCTTACTCAAA 801
 Qy 781 CTCTGA 786
 Db 802 CTCTGA 807
 RESULT 14
 ID AA51745
 AA51745 standard; cDNA, 1816 BP.
 AC AA51745;
 XX 31-OCT-2000 (first entry)
 DT Human CD40 ligand cDNA.
 DE
 XX CD40 ligand; CD40; T cell; T cell receptor; rearrangement; maturation;
 KM cell death inhibition; stress-induced; immunosuppressive; anti-thyroid;
 KM anti-inflammatory; anti-diabetic; anti-rheumatic; anti-anemic;
 KM ophthalmological; anti-psoriatic; nephrotrophic; hepatotropic; virucide;
 KM dermatological; cytostatic; ss.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH 40..825
 FT /tag= a
 FT /product= Human_CD40_ligand
 PT WO20039283-A1.
 XX
 XX PD 06-JUL-2000.
 XX PF 22-DEC-1999; 99WO-US0930.
 XX PR 29-DEC-1998; 98US-0114106.
 XX PA (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.
 XX PI Newell MK, Wagner D, Newell E;
 DR WPI: 2000-452387/39.
 DR P-PSDB; AAY6993.
 XX
 PT Inducing T cell receptor gene rearrangement for treating autoimmune
 PT diseases comprises contacting T cells with a CD40-binding agent
 XX
 XX Disclosure: Page 46; 50pp; English.
 XX CD40 engagement on T cells can be used to induce T cell receptor
 CC rearrangement and enhance T cell affinity for a particular antigen. CD40
 CC engagement can be bought about by contacting CD40 with a CD40-binding
 CC agent, e.g. human CD40 ligand. The CD40-binding agents can also be used
 CC in methods for promoting T cell maturation, inhibiting T cell receptor
 CC rearrangement, inhibiting environmental stress-induced cell death,

CC altering the specificity of a T cell towards an antigen, inducing T cell
 CC reactivity towards an antigen or enhancing environmental stress-induced
 CC cell death (all claimed). T cell affinity maturation towards a specific
 CC antigen can be inhibited, especially for a self-antigen in an autoimmune
 CC disease, which includes rheumatoid arthritis, uveitis, insulin-dependent
 CC diabetes mellitus, haemolytic anaemias, rheumatic fever, Crohn's disease,
 CC Guillain-Barre syndrome, psoriasis, thyroiditis, Grave's disease,
 CC myasthenia gravis, glomerulonephritis, autoimmune hepatitis or systemic
 CC lupus erythematosus, inducing environmental stress-induced T cell death
 CC is carried out in a cancerous T cell or a self-reactive T cell where the
 CC environmental stress is a chemotherapeutic agent (claimed).
 XX
 SQ Sequence 1816 BP; 520 A; 461 C; 343 G; 492 T; 0 other;
 Query Match 95.9%; Score 754; DB 21; Length 1816;
 Best Local Similarity 97.5%; Pred. No. 1.3e-206;
 Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
 Qy 1 ATGATGAAACATACAGCCCAACCTTCCCGAGATCCGTGGCACTTGCAAGCAGC 60
 Db 40 ATGATGAAACATACAGCCCAACCTTCCCGAGATCCGTGGCACTTGCAAGCAGC 99
 Qy 61 ATGAAATTTTATGATATTTACTTACTGTTTCTTATCCCAATGATGATCTTGG 120
 Db 100 ATGAAATTTTATGATATTTACTTACTGTTTCTTATCCCAATGATGATCTTGG 159
 Qy 121 CTTTGTGCTGTATCTTATAGAGTTGGCAAGATAGAGATGAAAGATCTTCAT 180
 Db 160 CTTTGTGCTGTATCTTATAGAGTTGGCAAGATAGAGATGAAAGATCTTCAT 219
 Qy 181 GAAGATTTTGTATATGAAACAGATACAGATGCAACAGAGAAAGATCTTATCC 240
 Db 220 GAAGATTTTGTATATGAAACAGATACAGATGCAACAGAGAAAGATCTTATCC 279
 Qy 241 TTACTGACTGTGAGAGATTTAAACCCAGTTTGAAGCTTTGTGAAGATATATGT 300
 Db 280 TTACTGACTGTGAGAGATTTAAACCCAGTTTGAAGCTTTGTGAAGATATATGT 339
 Qy 301 AACAAAGAGAACCAAGAAAGAAACAGCTTGAATGCAAAAGATGATCAATCC 360
 Db 340 AACAAAGAGAACCAAGAAAGAAACAGCTTGAATGCAAAAGATGATCAATCC 399
 Qy 361 CAATTTGCGGCATGTCATTAAGTGGCCAGCAGTAAACCAATCTGTGTTCAT 420
 Db 400 CAATTTGCGGCATGTCATTAAGTGGCCAGCAGTAAACCAATCTGTGTTCAT 459
 Qy 421 GCTGAAAAGATTAATACATGAGCAACATCTGTAACTCTGGAATATGGGAAACAG 480
 Db 460 GCTGAAAAGATTAATACATGAGCAACATCTGTAACTCTGGAATATGGGAAACAG 519
 Qy 481 CTGACGTTTAAAGACAGACTCTATTATATCTATGCCAAGTCACTTGTTCAT 540
 Db 520 CTGACGTTTAAAGACAGACTCTATTATATCTATGCCAAGTCACTTGTTCAT 579
 Qy 541 CGGGAAGCTTCGAGTCAGATCCATTTATATGAGCTCTCCCTTAAGTCCCGGTGA 600
 Db 580 CGGGAAGCTTCGAGTCAGATCCATTTATATGAGCTCTCCCTTAAGTCCCGGTGA 639
 Qy 601 TTGAGAGAACTTTACTGAGAGTCGCAAAATCCACAGTTCGCGCAAACTTCGCGGCA 660
 Db 640 TTGAGAGAACTTTACTGAGAGTCGCAAAATCCACAGTTCGCGCAAACTTCGCGGCA 699
 Qy 661 CAATCCATTCAGCTTGGAGAGATTTGATGCAACAGAGTTCGCTGCTGCTTGTCAAT 720
 Db 700 CAATCCATTCAGCTTGGAGAGATTTGATGCAACAGAGTTCGCTGCTGCTTGTCAAT 759
 Qy 721 GTGACTGATCCAGCCAGAGTCCAGTCCAGTTCAGTCTTGGCTTACTCAAA 780
 Db 760 GTGACTGATCCAGCCAGAGTCCAGTCCAGTTCAGTCTTGGCTTACTCAAA 819
 Qy 781 CTCTGA 786
 Db 820 CTCTGA 825

RESULT 15

AA86571
ID AA86571 standard; cDNA, 1816 BP.

AC AA86571;

DT 13-FEB-2002 (first entry)

DE DNA encoding novel human diagnostic protein #22375.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder; ss.

OS Homo sapiens.

PN M0200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US08631.

PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

PA (HYSE-) HYSEQ INC.

PI Dmanac RT, Liu C, Tang YT;

DR WPI; 2001-639362/73.

DR P-PSDB; ABG22384.

XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensic, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity

PS Claim 1; SEQ ID No 22375; 103bp; English.

XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridization probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (II) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensic, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AA64197-AA64564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 1816 BP; 520 A; 461 C; 343 G; 492 T; 0 other;

Query Match 95.9%; Score 754; DB 23; Length 1816;

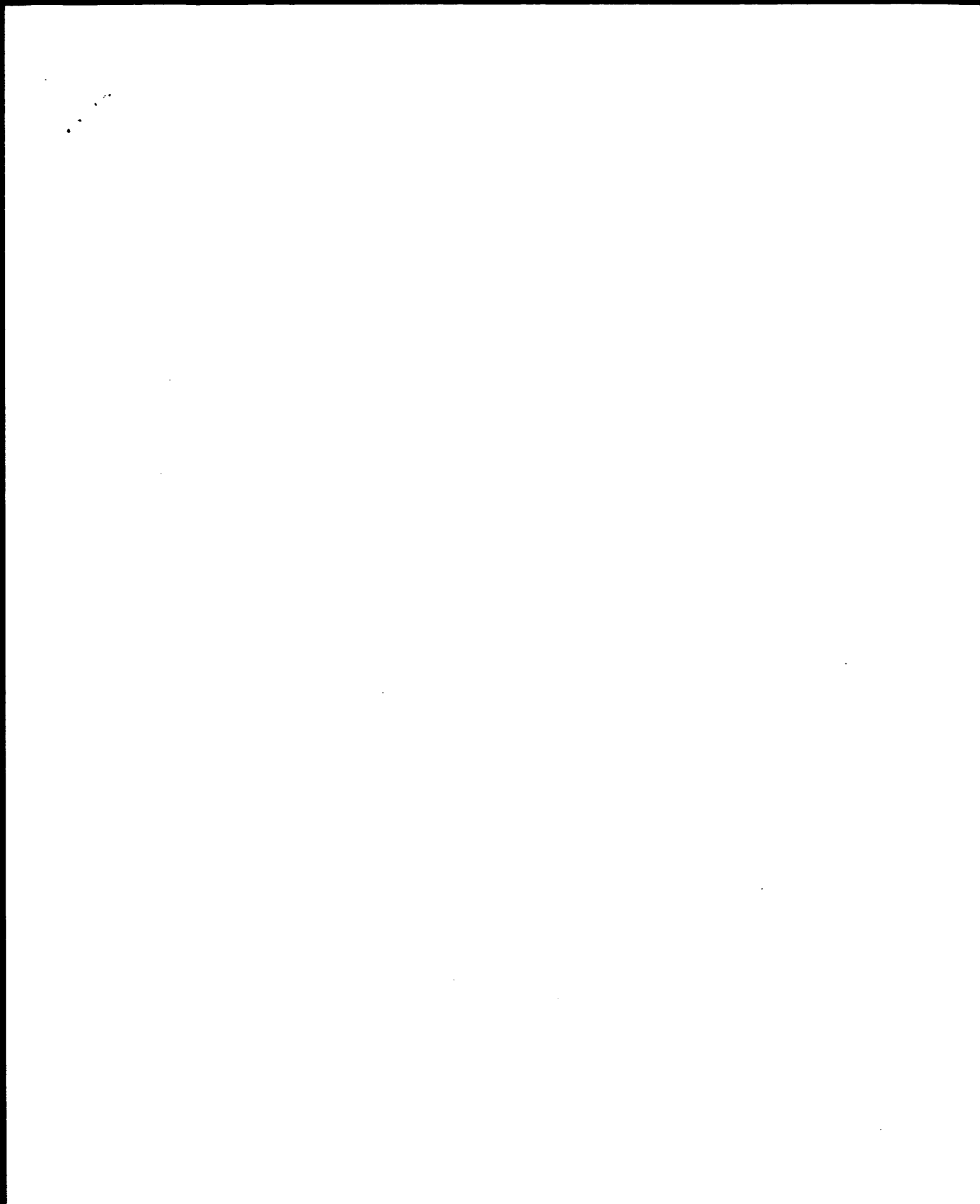
Best Local Similarity 97.5%; Pred. No. 1.3e-206;

Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ATGATGAAACATACAGCCAGCTTCCCGATCGGTGGCAACTGACCTTCCAGGAGC 60
Db 40 ATGATCGAAACATACAGCAAACTTCTCCGATCTCGGCACTGAGACTGCCATCAGC 99
Qy 61 ATGAAAGTTTATGATTTACTTACTGTTTCTTATGACCAACCAAGATTGATCTGTG 120

Db 100 ATGAAATTTTATGATTTACTTACTGTTTCTTATGACCAACCAAGATTGATCTGTG 159
Qy 121 CTTTTCGTGTATCTTATGAGAGTTGACCAAGATTGAGAGAGATCTTCAT 180
Db 160 CTTTTCGTGTATCTTATGAGAGTTGACCAAGATTGAGAGAGATCTTCAT 219
Qy 181 GAAGATTTTATGATTTACTTACTGTTTCTTATGACCAACCAAGATTGATCTGTG 240
Db 220 GAAGATTTTATGATTTACTTACTGTTTCTTATGACCAACCAAGATTGATCTGTG 279
Qy 241 TTACTGAACTGTGAGAGATTAAAGCACTTGAAGGCTTGAAGATTAATGTTA 300
Db 280 TTACTGAACTGTGAGAGATTAAAGCACTTGAAGGCTTGAAGATTAATGTTA 339
Qy 301 AACCAAG 360
Db 340 AACCAAG 399
Qy 361 CAAATTTGGGCAATGTCTAATGAGGCGCAGCAATAAACATCTGTGTTACGTG 420
Db 400 CAAATTTGGGCAATGTCTAATGAGGCGCAGCAATAAACATCTGTGTTACGTG 459
Qy 421 GCTGAAAAGGATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Db 460 GCTGAAAAGGATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 519
Qy 481 CTGACCGTTAAAG 540
Db 520 CTGACCGTTAAAG 579
Qy 541 CGGAGAGGTTGAGTCAAGCTCCATTTATGAGGAGGCTTGAAGTCCCGGTGA 600
Db 580 CGGAGAGGTTGAGTCAAGCTCCATTTATGAGGAGGCTTGAAGTCCCGGTGA 639
Qy 601 TTGAGAGAGATTTACTGAGAGCTGCAATTAACCAAGTTCGCAAACTTGGGCA 660
Db 640 TTGAGAGAGATTTACTGAGAGCTGCAATTAACCAAGTTCGCAAACTTGGGCA 699
Qy 661 CAATCATTCATCTTGGAGAGATTTGATTTGCAACCAAGGTTGGGTTTGTCAAT 720
Db 700 CAATCATTCATCTTGGAGAGATTTGATTTGCAACCAAGGTTGGGTTTGTCAAT 759
Qy 721 GTGACTGATCAAGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
Db 760 GTGACTGATCAAGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 819
Qy 781 CTCTGA 786
Db 820 CTCTGA 825

Search completed: March 8, 2003, 22:12:55
Job time: 167.215 secs



GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: March 9, 2003, 02:11:48 ; Search time 54.2612 Seconds
(without alignments)
9675.146 Million cell updates/sec

Title: US-08-982-272-7

Perfect score: 786

Sequence: 1 ATGATGAAACATACAGCA.....TTGGCTTACTCAACTCTGA 786

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 478924 seqs, 33395956 residues

Total number of hits satisfying chosen parameters: 957848

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: Published Applications NA:*

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12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	592.4	75.4	1250	9 US-10-182-093-1	Sequence 1, Appli
2	125.4	16.0	2395	9 US-09-875-453-9	Sequence 9, Appli
3	40.2	5.1	424	10 US-09-960-352-11218	Sequence 11218, A
4	37.6	4.8	418	10 US-09-960-352-22222	Sequence 2222, Ap
5	37.6	4.8	1352	9 US-09-938-842A-3149	Sequence 3149, Ap
6	37.6	4.8	1352	9 US-09-938-842A-5264	Sequence 5264, Ap
7	37.6	4.8	2000	9 US-09-938-842A-3756	Sequence 3756, Ap
8	37.4	4.8	640681	10 US-09-790-988-1	Sequence 1, Appli
9	35.8	4.6	10351	10 US-09-874-470-5	Sequence 5, Appli
10	35.4	4.5	525	9 US-10-079-754A-6	Sequence 6, Appli
11	34	4.3	1073	9 US-09-960-352-10262	Sequence 10262, A
12	34	4.3	1073	9 US-10-063-547-95	Sequence 95, Appl
13	34	4.3	1073	9 US-10-174-590-305	Sequence 305, App
14	34	4.3	1073	9 US-10-176-758-305	Sequence 305, App
15	34	4.3	1073	9 US-10-063-616-95	Sequence 95, Appl
16	34	4.3	1073	9 US-10-175-737-305	Sequence 305, App
17	34	4.3	1073	9 US-10-063-502-95	Sequence 95, Appl
18	34	4.3	1073	9 US-10-173-706-305	Sequence 305, App
19	34	4.3	1073	9 US-10-175-738-305	Sequence 305, App

20	34	4.3	1073	9 US-10-175-752-305	Sequence 305, App
21	34	4.3	1073	9 US-10-176-482-305	Sequence 305, App
22	34	4.3	1073	9 US-10-176-757-305	Sequence 305, App
23	34	4.3	1073	9 US-10-176-913-305	Sequence 305, App
24	34	4.3	1073	9 US-10-180-552-305	Sequence 305, App
25	34	4.3	1073	9 US-10-180-552-305	Sequence 305, App
26	34	4.3	1073	9 US-10-173-700-305	Sequence 305, App
27	34	4.3	1073	9 US-10-174-572-305	Sequence 305, App
28	34	4.3	1073	9 US-10-174-572-305	Sequence 305, App
29	34	4.3	1073	9 US-10-174-582-305	Sequence 305, App
30	34	4.3	1073	9 US-10-174-588-305	Sequence 305, App
31	34	4.3	1073	9 US-10-175-733-305	Sequence 305, App
32	34	4.3	1073	9 US-10-175-740-305	Sequence 305, App
33	34	4.3	1073	9 US-10-175-743-305	Sequence 305, App
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35	34	4.3	1073	9 US-10-176-488-305	Sequence 305, App
36	34	4.3	1073	9 US-10-176-747-305	Sequence 305, App
37	34	4.3	1073	9 US-10-176-750-305	Sequence 305, App
38	34	4.3	1073	9 US-10-176-985-305	Sequence 305, App
39	34	4.3	1073	9 US-10-176-987-305	Sequence 305, App
40	34	4.3	1073	9 US-10-176-991-305	Sequence 305, App
41	34	4.3	1073	9 US-10-176-992-305	Sequence 305, App
42	34	4.3	1073	9 US-10-176-993-305	Sequence 305, App
43	34	4.3	1073	9 US-10-184-658-305	Sequence 305, App
44	34	4.3	1073	9 US-10-227-884-99	Sequence 99, Appl
45	34	4.3	1073	9 US-10-173-695-305	Sequence 305, App

ALIGNMENTS

RESULT 1
US-10-182-093-1
Sequence 1, Application US/10182093
Publication No. US00030021808A1
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as represented by the Secretary, Department of Health and Human Services,
c/o Center for Disease Control and Prevention
APPLICANT: Tripp, Ralph
APPLICANT: Jones, Les
APPLICANT: Anderson, Larry
TITLE OF INVENTION: CD40 Ligand Adjuvant for Respiratory
FILE OF INVENTION: Syncytial Virus
CURRENT APPLICATION NUMBER: US/10/182,093
CURRENT FILING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: 60/179,905
PRIOR FILING DATE: 2000-02-02
NUMBER OF SEQ ID NOS: 1
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1250
TYPE: DNA
ORGANISM: Murine
Query Match 75.4%; Score 592.4; DB 9; Length 1250;
Best Local Similarity 85.5%; Pred. No. 1.3e-153;
Matches 672; Conservative 0; Mismatches 11; Indels 3; Gaps 1;
QY 1 ATGATGAAACATACAGCACTTCCCGGAGTGGCACTGACTTCAGAGC 60
DB 13 ATGATGAAACATACAGCACTTCCCGGAGTGGCACTGACTTCAGAGC 72
QY 61 ATGATGAAACATACAGCACTTCCCGGAGTGGCACTGACTTCAGAGC 120
DB 73 ATGATGAAACATACAGCACTTCCCGGAGTGGCACTGACTTCAGAGC 132
QY 121 CTTTTCGCTGATCTTCATGAAAGTTGGACAGATGAAAGATGAAAGATTTCTAT 180
DB 133 CTTTTCGCTGATCTTCATGAAAGTTGGACAGATGAAAGATGAAAGATTTCTAT 192

Db 330 ATT 332

RESULT 4
US-09-960-352-2222

; Sequence 2222, Application US/09960352

; Patent No. US20020137139A1

; GENERAL INFORMATION:

; APPLICANT: Warren, Wesley C.

; APPLICANT: Tao, Nenping

; APPLICANT: Byatt, John C.

; APPLICANT: Mathiasen, Negeppan

; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND

; FILE REFERENCE: 16511.006/31-21(10298)C

; CURRENT APPLICATION NUMBER: US/09/960,352

; CURRENT FILING DATE: 2001-09-24

; NUMBER OF SEQ ID NOS: 15112

; SEQ ID NO 2222

; LENGTH: 418

; TYPE: DNA

; ORGANISM: Bos taurus

; OTHER INFORMATION: Clone ID: 10-LIB3058-040-Q1-K1-CS

US-09-960-352-2222

Query Match 4.8%; Score 37.6; DB 10; Length 418;

Best Local Similarity 47.5%; Pred. No. 0.79;

Matches 112; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

Qy 238 TCCTTACTGAGTGTGAGAGATTAAAGCCAGTTGAGGCTTTGTGAGGATTTATG 237

Db 6 TCTATCTTACGATGCTGTGATTAATAAATTGGATGAGTGGGTTCCAGAAAGCAGATA 65

Qy 298 TTAAACAAAGAGAGACGAGAAAGAAACAGCTTGAATGCAAAAGATGATCAGAT 357

Db 66 CTCAGATATGTGATTCACATTTTCAGAAACAGAGAACTTCAGAAAGCAGATCAGAG 125

Qy 358 CCTCAATTTGCGGACATGATTAAGTGAAGCCAGCAGTAAACATCTGTGTTACG 417

Db 126 CAGTATGCAAGAGGAGAGATCGAGGGGCTGCCCCCTGAAAGAAATCTGCTGGCTGAG 185

Qy 418 TGGGCTGAAAGAAAGATACTACACCATGAGCAACAATTGTGTAACCTGTGAATG 473

Db 186 CAGAAATCTTGACGTGAACACAAAGAAACAAACAGAAACACCTGGAAATG 241

RESULT 5
US-09-938-842A-3149/C

; Sequence 3149, Application US/09938842A

; Patent No. US20020160378A1

; GENERAL INFORMATION:

; APPLICANT: Harper, Jeff

; APPLICANT: Kreps, Joel

; APPLICANT: Wang, Xun

; APPLICANT: Zhu, Tong

; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

; FILE REFERENCE: SRIPI300-3

; CURRENT APPLICATION NUMBER: US/09/938,842A

; CURRENT FILING DATE: 2001-08-24

; PRIOR APPLICATION NUMBER: US 60/227,866

; PRIOR FILING DATE: 2000-08-24

; PRIOR APPLICATION NUMBER: US 60/264,647

; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: US 60/300,111

; PRIOR FILING DATE: 2001-06-22

; NUMBER OF SEQ ID NOS: 5379

; SEQ ID NO 3149

; LENGTH: 1352

; TYPE: DNA

; ORGANISM: Arabidopsis thaliana

; Patent No. US20020160378A1

Query Match 4.8%; Score 37.6; DB 9; Length 1352;

Best Local Similarity 50.0%; Pred. No. 1.4;

Matches 94; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

Qy 64 AAGATTTTATGATTTACTACTGTTTCTTATCACCCAAAGATGGATCTGCTT 123

Db 379 ACAGCATTTATTTGTCATTTCTTGTGTATTAATAGCCATTTATTTGATCAGAC 320

Qy 124 TTTGCTGTATCTTCATTAAGAGTTGACAAATGAAATGAAGATCTTCATGAA 183

Db 319 ACTTATGCTAATTAAGAAACAGGTTCTACACCTGAAACAAAATAACGCAAAA 260

Qy 184 GATTTGATTCATGAAGAAAGATGACAGATGACAGACAGAGAAATCTTATCTTA 243

Db 259 GATTTAGCAAGTAAGCATTTATTTGATCATATTAAGAAAGAAAGATATCTTA 200

Qy 244 CTGAACCTG 251

Db 199 TTGACAG 192

RESULT 6
US-09-938-842A-5264

; Sequence 5264, Application US/09938842A

; Patent No. US20020160378A1

; GENERAL INFORMATION:

; APPLICANT: Harper, Jeff

; APPLICANT: Kreps, Joel

; APPLICANT: Wang, Xun

; APPLICANT: Zhu, Tong

; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

; FILE REFERENCE: SRIPI300-3

; CURRENT APPLICATION NUMBER: US/09/938,842A

; CURRENT FILING DATE: 2001-08-24

; PRIOR APPLICATION NUMBER: US 60/227,866

; PRIOR FILING DATE: 2000-08-24

; PRIOR APPLICATION NUMBER: US 60/264,647

; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: US 60/300,111

; PRIOR FILING DATE: 2001-06-22

; NUMBER OF SEQ ID NOS: 5379

; SEQ ID NO 5264

; LENGTH: 1352

; TYPE: DNA

; ORGANISM: Arabidopsis thaliana

; Patent No. US20020160378A1

US-09-938-842A-5264

Query Match 4.8%; Score 37.6; DB 9; Length 1352;

Best Local Similarity 50.0%; Pred. No. 1.4;

Matches 94; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

Qy 64 AAGATTTTATGATTTACTACTGTTTCTTATCACCCAAATGATGGATCTGCTT 123

Db 974 ACAGCATTTATTTGTCATTTCTTGTGTATTAATAGCCATTTATTTGATCAGAC 1033

Qy 124 TTTGCTGTATCTTCATTAAGAGTTGACAAATGAAATGAAGATCTTCATGAA 183

Db 1034 ACTTATGCTAATTAAGAAACAGGTTCTACACCTGAAACAAAATAACGCAAAA 1093

Qy 184 GATTTGATTCATGAAGAAAGATGACAGATGACAGACAGAGAAATCTTATCTTA 243

Db 1094 GATTTAGCAAGTAAGCATTTATTTGATCATATTAAGAAAGAAAGATATCTTA 1153

Qy 244 CTGAACCTG 251

Db 1154 TTGACAG 1161

RESULT 7
US-09-938-842A-3756

; Sequence 3756, Application US/09938842A

; Patent No. US20020160378A1

GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Kun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
FILE REFERENCE: SAME, AND METHODS OF USE
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 3756
LENGTH: 2000
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-3756

Query Match 4.8%; Score 37.6; DB 9; Length 2000;
Best Local Similarity 49.5%; Pred. No. 1.6;
Matches 97; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

Qy 67 ATTTTATGTAATTAATCTTACTGTTTCTTCTTATCAACCAATGATGATCTGCTTTT 126
Db 818 ATCTGTGAGTGAGTGTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 877
Qy 127 GCTGTATCTTCTTATGAGAGTTGACAGATAGAGATGAGATCTTCTTATGAGAT 186
Db 878 CTTCATATAGTCATATATGTATGATGATGATGATGATGATGATGATGATGATGAT 937
Qy 187 TTGTATGATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 246
Db 938 TAAATTATGATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 997
Qy 247 AACTGTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 262
Db 998 AATTTAGCTTTATTA 1013

RESULT 8
US-09-790-988-1/c
Sequence 1, Application US/09790988
Patent No. US20020127687A1
GENERAL INFORMATION:
APPLICANT: SHIGENOBU, SHUJI
APPLICANT: MATSUNABE, HIDEKI
APPLICANT: HATTORI, MASAHIRA
APPLICANT: SAKAKI, YOSHIYUKI
TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
FILE REFERENCE: 081356/0159
CURRENT APPLICATION NUMBER: US/09/790,988
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: JP2000-107160
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 640681
TYPE: DNA
ORGANISM: Buchnera sp.
US-09-790-988-1

Query Match 4.8%; Score 37.4; DB 10; Length 640681;
Best Local Similarity 52.2%; Pred. No. 25;
Matches 83; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

Qy 64 AAGATTTTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 123

Db 574504 AATATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 574445
Qy 124 TTTCGTGTATCTTCTTATGAGAGTTGACAGATGAGATGAGATGAGATGAGATGAG 183
Db 574444 TTTCAGAGTGTGTATGATGATGATGATGATGATGATGATGATGATGATGATG 574385
Qy 184 GATTTGATGATGAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 222
Db 574384 ATTAATCTTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 574346

RESULT 9
US-09-874-470-5/c
Sequence 5, Application US/09874470
Patent No. US20020071842A1
GENERAL INFORMATION:
APPLICANT: Gumpertz, Jenny E
APPLICANT: Brenner, Michael B
APPLICANT: Behar, Samuel M
TITLE OF INVENTION: Soluble CDI Compositions and Uses Thereof
FILE REFERENCE: B00801/70212
CURRENT APPLICATION NUMBER: US/09/874,470
CURRENT FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/209,416
PRIOR FILING DATE: 2000-06-05
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5
LENGTH: 10351
TYPE: DNA
ORGANISM: Homo sapiens
US-09-874-470-5

Query Match 4.6%; Score 35.8; DB 10; Length 10351;
Best Local Similarity 47.5%; Pred. No. 11;
Matches 106; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

Qy 164 ATGAAAGATCTTCTTATGAGATGATGATGATGATGATGATGATGATGATGATGAT 223
Db 6762 ATGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6703
Qy 224 GAGAAAGATCTTCTTATGAGATGATGATGATGATGATGATGATGATGATGATGAT 283
Db 6702 GAAAAATTTCTGGAATCATATGATGATGATGATGATGATGATGATGATGATGAT 6643
Qy 284 TGAAGATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 343
Db 6642 TGAGGAAGAAATTTGAGATATTAAGATCTTGAATTAATGATGATGATGATGAT 6583
Qy 344 AAGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 386
Db 6582 GATGGAGAGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6540

RESULT 10
US-10-079-754A-6
Sequence 6, Application US/10079754A
Patent No. US20020164625A1
GENERAL INFORMATION:
APPLICANT: Glenn, Matthew
APPLICANT: Gligor, Murray R.
APPLICANT: Molenaar, Adrian J.
APPLICANT: Davis, Stephen R.
TITLE OF INVENTION: Compositions Isolated from Bovine
FILE REFERENCE: 11000,1068
CURRENT APPLICATION NUMBER: US/10/079,754A
CURRENT FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: US 09/699,146
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60,162,701
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: US 09/644,190

Matches 67; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 224 GAGAAAGATCCTTATCTTAACTGAGAGATTAAGCCAGTTGGAAGCTTTG 283
DB 939 GAAATATATACATTATGCTGCTGAGATGATGATATTAACATATTTGGAAGCTGGA 998
QY 284 TGAAGATATATATGTTAAACAAAGAGAGAGAAAGAAACGCTTGAATGCAAA 343
DB 999 AA 1058
QY 344 AA 345
DB 1059 AA 1060

RESULT 14

US-10-176-758-305
Sequence 305, Application US/10176758
Publication No. US2003008353A1
GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jilan
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zhenlin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C104
CURRENT FILING DATE: 2002-06-21
CURRENT APPLICATION NUMBER: US/10/176,758
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 305
LENGTH: 1073
TYPE: DNA
ORGANISM: Homo Sapien
US-10-176-758-305

Query Match

Best Local Similarity 54.9%; Score 34; DB 9; Length 1073;

Matches 67; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 224 GAGAAAGATCCTTATCTTAACTGAGAGATTAAGCCAGTTGGAAGCTTTG 283
DB 939 GAAATATATACATTATGCTGCTGAGATGATGATATTAACATATTTGGAAGCTGGA 998
QY 284 TGAAGATATATATGTTAAACAAAGAGAGAGAAAGAAACGCTTGAATGCAAA 343
DB 999 AA 1058
QY 344 AA 345
DB 1059 AA 1060

RESULT 15

US-10-063-616-95
Sequence 95, Application US/10063616
Publication No. US2003013855A1
GENERAL INFORMATION:

APPLICANT: Eaton, Dan L.
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.

APPLICANT: Watanabe, Colin K.

APPLICANT: Wood, William I.

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P3430R1C1

CURRENT FILING DATE: 2002-05-03

Prior Application removed - See File Wrapper or Palm

NUMBER OF SEQ ID NOS: 170

SEQ ID NO 95

LENGTH: 1073

TYPE: DNA

ORGANISM: Homo Sapien

US-10-063-616-95

Query Match

Best Local Similarity 54.9%; Score 34; DB 9; Length 1073;

Matches 67; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 224 GAGAAAGATCCTTATCTTAACTGAGAGATTAAGCCAGTTGGAAGCTTTG 283
DB 939 GAAATATATACATTATGCTGCTGAGATGATGATATTAACATATTTGGAAGCTGGA 998
QY 284 TGAAGATATATATGTTAAACAAAGAGAGAGAAAGAAACGCTTGAATGCAAA 343
DB 999 AA 1058
QY 344 AA 345
DB 1059 AA 1060

Search completed: March 9, 2003, 09:54:15

Job time: 210.261 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using SW model

Run on: March 8, 2003, 21:49:58 ; Search time 33.6448 Seconds
(without alignments)
7164.491 Million cell updates/sec

Title: US-08-982-272-7

Perfect score: 786
Sequence: 1 ATGATGAAACATACAGCCA.....TTGGCTTACTCAAACTCTGA 786

Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents NA:
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2: /cgn2_6/prodata/2/ina/5B_COMB.seq:*
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5: /cgn2_6/prodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/prodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	754	95.9	786	1	US-08-446-922-3
2	754	95.9	786	5	PCT-US93-1003-3
3	754	95.9	840	1	US-07-940-605A-1
4	754	95.9	840	1	US-08-184-422-7
5	754	95.9	840	1	US-08-360-923A-1
6	754	95.9	840	1	US-08-431-055-3
7	754	95.9	840	2	US-08-630-096-1
8	754	95.9	840	2	US-08-249-189-11
9	754	95.9	840	2	US-08-484-624A-11
10	754	95.9	840	2	US-08-477-733B-11
11	754	95.9	840	3	US-08-763-995-1
12	754	95.9	840	3	US-09-088-913A-11
13	754	95.9	840	3	US-08-589-771B-7
14	754	95.9	840	4	US-08-769-819-11
15	754	95.9	840	4	US-08-770-974-11
16	754	95.9	840	4	US-08-858-197-3
17	754	95.9	840	4	US-08-770-981-11
18	754	95.9	840	4	US-09-399-106-11
19	638.2	81.2	1425	2	US-08-249-189-15
20	638.2	81.2	1425	2	US-08-484-624A-15
21	638.2	81.2	1425	2	US-08-477-733B-15
22	638.2	81.2	1425	3	US-09-088-913A-15
23	638.2	81.2	1425	4	US-08-769-819-15
24	638.2	81.2	1425	4	US-08-770-974-15
25	638.2	81.2	1425	4	US-08-770-981-15
26	638.2	81.2	1425	4	US-09-399-106-15
27	637.2	81.1	929	1	US-08-446-922-10

ALIGNMENTS

28	637.2	81.1	929	2	US-08-249-189-20	Sequence 20, Appl
29	637.2	81.1	929	2	US-08-484-624A-20	Sequence 20, Appl
30	637.2	81.1	929	2	US-08-477-733B-20	Sequence 20, Appl
31	637.2	81.1	929	3	US-09-088-913A-20	Sequence 20, Appl
32	637.2	81.1	929	4	US-08-769-819-20	Sequence 20, Appl
33	637.2	81.1	929	4	US-08-770-981-20	Sequence 20, Appl
34	637.2	81.1	929	4	US-08-770-981-20	Sequence 20, Appl
35	637.2	81.1	929	4	US-09-399-106-20	Sequence 20, Appl
36	594	75.6	783	1	US-08-446-922-5	Sequence 5, Appl
37	594	75.6	783	2	US-08-249-189-1	Sequence 1, Appl
38	594	75.6	783	2	US-08-484-624A-1	Sequence 1, Appl
39	594	75.6	783	3	US-08-477-733B-1	Sequence 1, Appl
40	594	75.6	783	3	US-09-088-913A-1	Sequence 1, Appl
41	594	75.6	783	4	US-08-769-819-1	Sequence 1, Appl
42	594	75.6	783	4	US-08-770-974-1	Sequence 1, Appl
43	594	75.6	783	4	US-08-770-981-1	Sequence 1, Appl
44	594	75.6	783	4	US-09-399-106-1	Sequence 1, Appl
45	594	75.6	783	5	PCT-US93-1003A-5	Sequence 5, Appl

RESULT 1
US-08-446-922-3
Sequence 3, Application US/08446922
Patent No. 5716805
GENERAL INFORMATION:
APPLICANT: Spriggs, Melanite
APPLICANT: Srinivasan, Subhashini
TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSER: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.1
SOFTWARE: Microsoft Word for Apple, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,922
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/107,353
FILING DATE: 08-13-93
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 1003-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 786 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: linear
TOPOLOGY: linear
HYPOTHETICAL: NO
MOL. TYPE: CDNA to mRNA
AMT-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Human
STRAIN: CD40-L
FEATURE:

NAME/KEY: CDS
LOCATION: 1..783
US-08-446-922-3

Query Match 95.9%; Score 754; DB 1; Length 786;
Best Local Similarity 97.5%; Pred. No. 5.1e-209;
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ATGATAGAAACATACAGCAACCTTCCCGAGATCCGAGCACTGGACCTCCAGCAGC 60
DB 1 ATGATAGAAACATACAGCAACCTTCCCGAGATCCGAGCACTGGACCTCCAGCAGC 60
QY 61 ATGAGATTTTATGATTTTACTTACTTCTTCTTATCACCAGATGATGATCTGTG 120
DB 61 ATGAGATTTTATGATTTTACTTACTTCTTCTTATCACCAGATGATGATCTGTG 120
QY 121 CTTTTCCTGTATCTTCTATGAAAGTTGGAACAATGAAAGATCTTCTAT 180
DB 121 CTTTTCCTGTATCTTCTATGAAAGTTGGAACAATGAAAGATCTTCTAT 180
QY 181 GAGATTTTGTATTCATGAAACCATACAGATGCAACAGAGAAAGATCTTATCC 240
DB 181 GAGATTTTGTATTCATGAAACCATACAGATGCAACAGAGAAAGATCTTATCC 240
QY 241 TTAAGTAACTGTAGAGAGATTAAGGCACTTGAAGCTTGTGAAGTATTAATGTTA 300
DB 241 TTAAGTAACTGTAGAGAGATTAAGGCACTTGAAGCTTGTGAAGTATTAATGTTA 300
QY 301 AACAAAG 360
DB 301 AACAAAG 360
QY 361 CAAATTCGCGACATGTCATTAAGTGAAGCCAGATTAAGACATCTGTATCACTG 420
DB 361 CAAATTCGCGACATGTCATTAAGTGAAGCCAGATTAAGACATCTGTATCACTG 420
QY 421 GCTGAAAAAGATATCAACCATGAGCAACATTTGTATCCCTGAGAAATGGAGAA 480
DB 421 GCTGAAAAAGATATCAACCATGAGCAACATTTGTATCCCTGAGAAATGGAGAA 480
QY 481 CTGACCGTTAAAG 540
DB 481 CTGACCGTTAAAG 540
QY 541 CGGAGAGCTTCAGTCAAGCTTCATTTATGAGAGAGAGAGAGAGAGAGAGAGAG 600
DB 541 CGGAGAGCTTCAGTCAAGCTTCATTTATGAGAGAGAGAGAGAGAGAGAGAGAG 600
QY 601 TTGAGAGAGATCTTACTCAGAGCTGCAAAATACCAAGTCCGAGAGAGAGAGAG 660
DB 601 TTGAGAGAGATCTTACTCAGAGCTGCAAAATACCAAGTCCGAGAGAGAGAGAG 660
QY 661 CAATTCATCTGAGAGAGAGAGATTTGAATTCGAACAGAGAGAGAGAGAGAGAG 720
DB 661 CAATTCATCTGAGAGAGAGAGATTTGAATTCGAACAGAGAGAGAGAGAGAGAG 720
QY 721 GTGATGATCAAG 780
DB 721 GTGATGATCAAG 780
QY 781 CTCTGA 786
DB 781 CTCTGA 786

RESULT 2
PCT-US93-10034-3

Sequence 3, Application PC/TUS9310034

GENERAL INFORMATION:

APPLICANT: Spriggs, Melanie
APPLICANT: Strinivasan, Subhashini
TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric
Proteins

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/10034

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia A

REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 1003

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 587-0430

TELEFAX: (206) 233-0644

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 786 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Human

STRAIN: CD40-L

FEATURE:

NAME/KEY: CDS

LOCATION: 1..783

PCT-US93-10034-3

Query Match 95.9%; Score 754; DB 5; Length 786;

Best Local Similarity 97.5%; Pred. No. 5.1e-209;

Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ATGATAGAAACATACAGCAACCTTCCCGAGATCCGAGCACTGGACCTCCAGCAGC 60
DB 1 ATGATAGAAACATACAGCAACCTTCCCGAGATCCGAGCACTGGACCTCCAGCAGC 60
QY 61 ATGAGATTTTATGATTTTACTTACTTCTTCTTATCACCAGATGATGATCTGTG 120
DB 61 ATGAGATTTTATGATTTTACTTACTTCTTCTTATCACCAGATGATGATCTGTG 120
QY 121 CTTTTCCTGTATCTTCTATGAAAGTTGGAACAATGAAAGATCTTCTAT 180
DB 121 CTTTTCCTGTATCTTCTATGAAAGTTGGAACAATGAAAGATCTTCTAT 180
QY 181 GAGATTTTGTATTCATGAAACCATACAGATGCAACAGAGAAAGATCTTATCC 240
DB 181 GAGATTTTGTATTCATGAAACCATACAGATGCAACAGAGAAAGATCTTATCC 240
QY 241 TTAAGTAACTGTAGAGAGATTAAGGCACTTGAAGCTTGTGAAGTATTAATGTTA 300
DB 241 TTAAGTAACTGTAGAGAGATTAAGGCACTTGAAGCTTGTGAAGTATTAATGTTA 300
QY 301 AACAAAG 360
DB 301 AACAAAG 360
QY 361 CAAATTCGCGACATGTCATTAAGTGAAGCCAGATTAAGACATCTGTATCACTG 420
DB 361 CAAATTCGCGACATGTCATTAAGTGAAGCCAGATTAAGACATCTGTATCACTG 420

APPLICANT: MIDMER, MICHAEL
TITLE OF INVENTION: DETECTION AND TREATMENT OF MUTATIONS
IN A CD40 LIGAND GENE
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.1
SOFTWARE: MS Word for Apple 5.1, Version a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/184,422
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/009,258
FILING DATE: 01/22/93
ATTORNEY/AGENT INFORMATION:
NAME: PERKINS, PATRICIA ANNE
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2810-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46..831
US-08-184-422-7
Query Match 95.9%; Score 754; DB 1; Length 840;
Best Local Similarity 97.5%; Pred. No. 5.3e-209;
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Db 346 AACAAAGAGAGACGAAAGAAAGAAAGCTTTGAATGAAAAAGAGATCAAAATCCT 405
Qy 361 CAATTGGCGCATGTCATTAAGTGGCCGACGATTAACAAATCTGTGTACAGTG 420
Db 406 CAATTGGCGCATGTCATTAAGTGGCCGACGATTAACAAATCTGTGTACAGTG 465
Qy 421 GCTGAAAAAGATCTACACCATAGCAACAACTTGTAACTCGTGAATAATGGAACAG 480
Db 466 GCTGAAAAAGATCTACACCATAGCAACAACTTGTAACTCGTGAATAATGGAACAG 525
Qy 481 CTGACCTTTAAAGACAGACCTCTTATATATATATATATATATATATATATATAT 540
Db 526 CTGACCTTTAAAGACAGACCTCTTATATATATATATATATATATATATATATAT 585
Qy 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGTCTAAAGTCCCGGTAG 600
Db 586 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGTCTAAAGTCCCGGTAG 645
Qy 601 TTGAGAGATCTTATCTCAGAGCTGGAATATCCAGTTCCGCAAACTTTGGGGCAA 660
Db 646 TTGAGAGATCTTATCTCAGAGCTGGAATATCCAGTTCCGCAAACTTTGGGGCAA 705
Qy 661 CAATTCATTCATTTGGAGAGATTTGAAATTTGCAACAGGTGCTTGGTGTTCAT 720
Db 706 CAATTCATTCATTTGGAGAGATTTGAAATTTGCAACAGGTGCTTGGTGTTCAT 765
Qy 721 GTACAGATCCCAAGCAAGTGAACCACTGCGCTTCAAGCTTGGTGTTCAT 780
Db 766 GTACAGATCCCAAGCAAGTGAACCACTGCGCTTCAAGCTTGGTGTTCAT 825
Qy 781 CTCTGA 786
Db 826 CTCTGA 831
RESULT 5
US-08-360-923A-1
Sequence 1, Application US/08360923A
Patent No. 5674492
GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: FANSLAW, WILLIAM
APPLICANT: LONGO, DAN L.
APPLICANT: MURPHY, WILLIAM
TITLE OF INVENTION: METHOD OF PREVENTING OR TREATING
DISEASE CHARACTERIZED BY NEOPLASTIC CELLS
TITLE OF INVENTION: EXPRESSING CD40
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: Apple Macintosh System 7.1
SOFTWARE: Microsoft Word for Macintosh, Version #5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,923A
FILING DATE: December 21, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/172,664
FILING DATE: December 23, 1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2818-A

```

1 TELECOMMUNICATION INFORMATION
2 TELEPHONE: (206)587-0430
3 TELEFAX: (206)233-0644
4 INFORMATION FOR SEQ ID NO.: 1:
5 SEQUENCE CHARACTERISTICS:
6 LENGTH: 840 base pairs
7 TYPE: nucleic acid
8 STRANDEDNESS: single
9 TOPOLOGY: linear
10 MOLECULE TYPE: cDNA
11 HYPOTHEetical: NO
12 ANTI-SENSE: NO
13 ORIGINAL SOURCE:
14 ORGANISM: Homo sapiens
15 IMMEDIATE SOURCE:
16 CLONE: CD40-L
17 FEATURE:
18 NAME/KEY: CDS
19 LOCATION: 46..831
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Query Match	95.9%	Score 754;	DB 1;	Length 840;
Best Local Similarity	97.5%;	Pred. No. 5.3e-209;		
Matches 766; Conservative	0;	Mismatches 20;	Indels 0;	Gaps 0;

Qy	1	AAATAGAAACATACAGCCAACTTCCCCAGAAACGATGCGAAACCTTGACGAGC	60
Db	46	ATGATCGAAGACATACACCAAACTTCCCGCATCTGCGGCACTGACCTGCCATCAGC	105
Qy	61	ATGAAGATTTTATATGATATTTACTACTGTCTTCCCTATCACCCAAATGATGGATCTGTG	120
Db	106	ATGAAGATTTTATATGATATTTACTACTGTCTTCTTATCACCCAGATGATTTGGTACACA	165
Qy	121	CTTTTGTGCTGTATCTTATCAGAAAGTTGGACAAGATGAAAGATCTTGAT	180
Db	166	CTTTTGTGCTGTATCTTCTTGAAAGTTGGACAAGATGAAAGATCTTGAT	225
Qy	181	GAAAGATTTTGATTCATGAAAGACGATACAGATGACACAGAGAAAGATCTTATCC	240
Db	226	GAAAGATTTTGATTCATGAAAGACGATACAGATGACACAGAGAAAGATCTTATCC	285
Qy	241	TTACTGAACCTGTGAGAGATTTAAAGCCAGTTGAAGCTTTGTGAAGATATATGTGA	300
Db	286	TTACTGAACCTGTGAGAGATTTAAAGCCAGTTGAAGCTTTGTGAAGATATATGTGA	345
Qy	301	AACAAAGAGAGACGAAAGAAAGAAACAGCTTTGAATCAGAAAAGGTATGCAATCCT	360
Db	346	AACAAAGAGAGACGAAAGAAAGAAACAGCTTTGAATCAGAAAAGGTATGCAATCCT	405
Qy	361	CAAAATGGCGACACTGTCATTAAGTGAAGCCAGACAGTAAACAAACATCTGTGTTCACGTGG	420
Db	406	CAAAATGGCGACACTGTCATTAAGTGAAGCCAGACAGTAAACAAACATCTGTGTTCACGTGG	465
Qy	421	GCTGAAAAGAGATCTACACATCAGTAGCAACACTGTGTAACTCGTGAAGATGGAACAG	480
Db	466	GCTGAAAAGAGATCTACACATCAGTAGCAACACTGTGTAACTCGTGAAGATGGAACAG	525
Qy	481	GTGACCGTTAATAACAAGACACTGATTAATATCTGAAGCCCAAGTCACTTGTGTCCAAAT	540
Db	526	GTGACCGTTAATAACAAGACACTGATTAATATCTGAAGCCCAAGTCACTTGTGTCCAAAT	585
Qy	541	CGGGAAGCTTGAGTCAAGCTCCATTTATAGCCAGCTCTGTGCTTAAAGTCCCGCGTAGA	600
Db	586	CGGGAAGCTTGAGTCAAGCTCCATTTATAGCCAGCTCTGTGCTTAAAGTCCCGCGTAGA	645
Qy	601	TTGCGAAGATCTTACTCAGAGCTGCAAAATCCACAGTTCGCGCAAAACCTTGCGGGACA	660
Db	646	TTGCGAAGATCTTACTCAGAGCTGCAAAATCCACAGTTCGCGCAAAACCTTGCGGGACA	705
Qy	661	CAATCATTCACCTTGGAGAGATATTTGAATGCAACAGAGTCTTGGGTGTTCAT	720
Db	706	CAATCATTCACCTTGGAGAGATATTTGAATGCAACAGAGTCTTGGGTGTTCAT	765

Qy	721	722	766	Db	Qy	781	826	Db
	GGAGATGATTCAGACCAAGTGAAGCATGGACATTCAGATCTTGGCTTACTCAA	780				CTCTGA	831	
	GGAGATGATTCAGACCAAGTGAAGCATGGACATTCAGATCTTGGCTTACTCAA	825				CTCTGA	831	

RESULT 6

US-08-431-055-3
Sequence 3, Application US/08431055
Patent No. 5817516
GENERAL INFORMATION:
APPLICANT: KEHRY, MERILYN R
APPLICANT: CASTLE, BRIAN E
TITLE OF INVENTION: METHODS FOR PROLIFERATING AND
NUMBER OF INVENTION: DIFFERENTIATING B CELLS, AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
STREET: 100 NEW YORK AVE. N.W. SUITE 600
CITY: WASHINGTON
STATE: D.C.

COMPUTER READABLE FORM;

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

```

; SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

```

APPLICATION NUMBER: US

FILING DATE: 28-APR-1995

CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE: 28-APR-1994

NAME: MILLMAN, ROBERT A

REGISTRATION NUMBER: 36,

REFERENCE/DOCKET NUMBER:

TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540

```

; INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:

```

LENGTH: 840 base pairs

TYPE: nucleic acid

STRADEDNESS: both
TOPOLOGY: linear

MOLECULE TYPE: DNA

FEATURE:

NAME/KEY: CDS
LOCATION: 22..807

US-08-431-055-3

Answer Match: 06 08

Best Local Similarity	97.58%
Query match	99.98%

Matches 766; Conservative

ATGATGAGAGAGTACAGAGAG

100

Db 22 ATGATCGAACAATACCAACCAA

Query Match	55.94%	Score 754	DB 1	Length 840
Best Local Similarity	97.5%	Pred. No. 5,3e-209		
Matches 766	Conservative 0	Mismatches 20	Indels 0	Gaps 0

Qy	1	ATGATAGAAACATACAGCCACCTTCCCGCAGATCCGTCGCACTGCACTTCACGAGC	60
Db	22	ATGATCGAAACATACACCAACTTCTCCCGATCTGCGGCACATGCACTGCCATCAGC	81

Qy	61	ATGAAGATTTTATATATTTACTTACTGTTTTCTTATACCCCAATGATGTGATCTGTG	120
Db	82	ATGAAGATTTTATATATTTACTTACTGTTTTCTTATACCCCAATGATGTGATCTGTG	141

Qy	121	CTTTTCTGCTGATCTTCATATAGAGGTGGACAAGATGGAAGATGAAGAAATCTTCAT	180
Db	142	CTTTTCTGCTGATCTTCATATAGAGGTGGACAAGATGGAAGATGAAGAAATCTTCAT	201

Qy	181	GAGATTTTGATTCATGAGAAACGATACAGAGATGCACACGAGAGAAATCTTTATCC	240
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Db 202 GAGATTTTGTATTCATGAAACGATCAAGATGGAACAAGGAAAGATCTTATCC 261
Qy 241 TTAAGTAACTGTGAGAGATTTAAAGCACTTTGAAGCTTTGAAAGATATATGTA 300
Db 262 TTAAGTAACTGTGAGAGATTTAAAGCACTTTGAAGCTTTGAAAGATATATGTA 321
Qy 301 AACAAAG 360
Db 322 AACAAAG 381
Qy 361 CAAATTCGGGAGATCTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Db 382 CAAATTCGGGAGATCTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 441
Qy 421 GCTGAAAAAGATCTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Db 442 GCTGAAAAAGATCTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 501
Qy 481 CTGACCGTTAAAG 540
Db 502 CTGACCGTTAAAG 561
Qy 541 CGGAGAGCTTGAAGTCAAGCTTCAATTTATAGCAGGCTTCTGCTTAAAGTCCCGGTAGA 600
Db 562 CGGAGAGCTTGAAGTCAAGCTTCAATTTATAGCAGGCTTCTGCTTAAAGTCCCGGTAGA 621
Qy 601 TTGAGAGAGATCTTCAAGAGCTGCAAAATACCAAGTCCGCAAACTTGGGGGAA 660
Db 622 TTGAGAGAGATCTTCAAGAGCTGCAAAATACCAAGTCCGCAAACTTGGGGGAA 681
Qy 661 CAATTCATCTTGGAGAGAGATTTGAATTTGCAACAGAGTGGCTTGGTGTTCAT 720
Db 682 CAATTCATCTTGGAGAGAGATTTGAATTTGCAACAGAGTGGCTTGGTGTTCAT 741
Qy 721 GTGACTGATCAAG 780
Db 742 GTGACTGATCAAG 801
Qy 781 CTCTGA 786
Db 802 CTCTGA 807

RESULT 7
US-08-690-096-1
Sequence 1, Application US/08690096
Patent No. 5945513
GENERAL INFORMATION:
APPLICANT: ARUPPO, ALEJANDRO
APPLICANT: HOLLENBAUGH, DIANE
APPLICANT: LEDBETTER, JEFFREY A.
TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/690,096
FILING DATE: 31-JUL-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/940,605
FILING DATE: 04-SEP-1992

ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-184
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 22..807
US-08-690-096-1

Query Match 95.9%; Score 754; DB 2; Length 840;
Best Local Similarity 97.5%; Pred. No. 5.3e-209;
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

1 ATGATGAAACATACAGCCAACTTCCCGAGATCCGTGCAACTGCACTTCAGCGAGC 60
22 ATGATGAAACATACAGCCAACTTCCCGAGATCCGTGCAACTGCACTTCAGCGAGC 81
Qy 61 ATGATGAACTTTATGATTTTATCTGTTTCTTATGACCCCAATGATGATCTGTC 120
Db 82 ATGATGAACTTTATGATTTTATCTGTTTCTTATGACCCCAATGATGATCTGTC 141
Qy 121 CTTTTCCTGTATCTTCAATGAGAGTTGCAAGATGAGATGAAAGAACTTTCAT 180
Db 142 CTTTTCCTGTATCTTCAATGAGAGTTGCAAGATGAGATGAAAGAACTTTCAT 201
Qy 181 GAAGATTTGTATCAAGAAACGATACAGAGATGCAACACGAGAGAAAGTCTTATCC 240
Db 202 GAAGATTTGTATCAAGAAACGATACAGAGATGCAACACGAGAGAAAGTCTTATCC 261
Qy 241 TTAAGTAACTGTGAGAGATTTAAAGCACTTTGAAGCTTTGAAAGATATATGTA 300
Db 262 TTAAGTAACTGTGAGAGATTTAAAGCACTTTGAAGCTTTGAAAGATATATGTA 321
Qy 301 AACAAAG 360
Db 322 AACAAAG 381
Qy 361 CAAATTCGGGAGATCTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Db 382 CAAATTCGGGAGATCTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 441
Qy 421 GCTGAAAAAGATCTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Db 442 GCTGAAAAAGATCTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 501
Qy 481 CTGACCGTTAAAG 540
Db 502 CTGACCGTTAAAG 561
Qy 541 CGGAGAGCTTGAAGTCAAGCTTCAATTTATAGCAGGCTTCTGCTTAAAGTCCCGGTAGA 600
Db 562 CGGAGAGCTTGAAGTCAAGCTTCAATTTATAGCAGGCTTCTGCTTAAAGTCCCGGTAGA 621
Qy 601 TTGAGAGAGATCTTCAAGAGCTGCAAAATACCAAGTCCGCAAACTTGGGGGAA 660
Db 622 TTGAGAGAGATCTTCAAGAGCTGCAAAATACCAAGTCCGCAAACTTGGGGGAA 681
Qy 661 CAATTCATCTTGGAGAGAGATTTGAATTTGCAACAGAGTGGCTTGGTGTTCAT 720
Db 682 CAATTCATCTTGGAGAGAGATTTGAATTTGCAACAGAGTGGCTTGGTGTTCAT 741
Qy 721 GTGACTGATCAAG 780

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Db 742 GTGACTGATCCAAAGCAAGTGAAGCCATGCGCTTACGCTCTTGCGCTTACTCAAA 801
Qy 781 CTCCTGA 786
Db 802 CTCCTGA 807

RESULT 8

US-08-249-189-11
; Sequence 11, Application US/08249189
; Patent No. 5961974

GENERAL INFORMATION:

APPLICANT: ARMITAGE, RICHARD
APPLICANT: FANSLAW, WILLIAM
APPLICANT: SPRIGGS, MELANIE
APPLICANT: SRINIVASAN, SUBHASHINI
APPLICANT: GIBSON, MARYLOU
TITLE OF INVENTION: NOVEL CYTOKINE
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESSES:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.1
SOFTWARE: Microsoft Word for Apple, version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/249,189
FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/969,703
FILING DATE: October 23, 1992

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/805,723
FILING DATE: December 5, 1991

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/783,707
FILING DATE: October 25, 1991

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 840 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

IMMEDIATE SOURCE:

CLONE: CD40-L

FEATURE: CDS

NAME/KEY: 46..831

US-08-249-189-11

Query Match 95.9%; Score 754; DB 2; Length 840;
Best Local Similarity 97.5%; Pred. No. 5,3e-209;
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ATGATAGAAAATATACAGCCAACTTCCCGCAAGTCCGTGGCACTGCACTTCACAGCAGC 60
Db 46 ATGATAGAAAATATACAGCCAACTTCCCGCAAGTCCGTGGCACTGCACTTCACAGC 105
Qy 61 ATGAAAGATTTTATGATTTTATCTTACAGTTTCTTATCACCAGAAATGATGATCTG 120
Db 106 ATGAAAGATTTTATGATTTTATCTTACAGTTTCTTATCACCAGAAATGATGATCTG 165
Qy 121 CTTTTCCTGTGATCTTATGAGAGTTTGAACAAGATAGAAATGAAAGATCTTCAT 180
Db 166 CTTTTCCTGTGATCTTATGAGAGTTTGAACAAGATAGAAATGAAAGATCTTCAT 225
Qy 181 GAAGATTTTGTATATGAAAAGATACAGAGATGCAACAGAGAAAGATCCATTATCC 240
Db 226 GAAGATTTTGTATATGAAAAGATACAGAGATGCAACAGAGAAAGATCCATTATCC 285
Qy 241 TTACTGAATCTGTAGAGAGATTTAAAGCCAGTTTGAAGCTTTGAAAGATTAATGTTA 300
Db 286 TTACTGAATCTGTAGAGAGATTTAAAGCCAGTTTGAAGCTTTGAAAGATTAATGTTA 345
Qy 301 AACAAAGAGAGACGAAGAAAGAAAGAGCTTTGAAATGCAAAAGGTATAGAAATCT 360
Db 346 AACAAAGAGAGACGAAGAAAGAAAGAGCTTTGAAATGCAAAAGGTATAGAAATCT 405
Qy 361 CAATTCGCGCAATGTCTAATAGTGAAGCCAGAGTAAACAAATCTGTGTTACAGTG 420
Db 406 CAATTCGCGCAATGTCTAATAGTGAAGCCAGAGTAAACAAATCTGTGTTACAGTG 465
Qy 421 GGTGAAAAGATATATGACCAATGAGCAACATCTGTAAACCTGGAAGAAATGGAAAG 480
Db 466 GGTGAAAAGATATATGACCAATGAGCAACATCTGTAAACCTGGAAGAAATGGAAAG 525
Qy 481 CTGACCGTTAAAGACAGAGACTGATATATATCTATGCCCAGATCATCTTGTTCAT 540
Db 526 CTGACCGTTAAAGACAGAGACTGATATATATCTATGCCCAGATCATCTTGTTCAT 585
Qy 541 CGGGAGACTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGGTGA 600
Db 586 CGGGAGACTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGGTGA 645
Qy 601 TTGAGAGAAATCTTATCTGAGAGCTGCAAAATACCAAGTTCCGCAAACTTTCGAG 660
Db 646 TTGAGAGAAATCTTATCTGAGAGCTGCAAAATACCAAGTTCCGCAAACTTTCGAG 705
Qy 661 CAATTCATTCATCTGGAGAGATTTTGAATTTGCAACAGAGTCTTCGATTTGTCAT 720
Db 706 CAATTCATTCATCTGGAGAGATTTTGAATTTGCAACAGAGTCTTCGATTTGTCAT 765
Qy 721 GTGACTGATCAAGCCAAAGTGAAGCCATGAGCATGAGCTTCAAGTCTTGGCTTACTCAA 780
Db 766 GTGACTGATCAAGCCAAAGTGAAGCCATGAGCATGAGCTTCAAGTCTTGGCTTACTCAA 825
Qy 781 CTCCTGA 786
Db 826 CTCCTGA 831

RESULT 9

US-08-484-624A-11
; Sequence 11, Application US/08484624A
; Patent No. 5962406

GENERAL INFORMATION:

APPLICANT: ARMITAGE, RICHARD
APPLICANT: FANSLAW, WILLIAM
APPLICANT: SPRIGGS, MELANIE
APPLICANT: SRINIVASAN, SUBHASHINI
APPLICANT: GIBSON, MARYLOU
APPLICANT: MORRIS, ARVIA B.
APPLICANT: MCGREW, JEFFERY

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,733B
FILING DATE: June 07, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,189
FILING DATE: May 24, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,703
FILING DATE: October 23, 1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/805,723
FILING DATE: December 5, 1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/783,707
FILING DATE: October 25, 1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46..831
US-08-477-733B-11

Query Match 95.9%; Score 754; DB 2; Length 840;
Best Local Similarity 97.5%; Pred. No. 5.3e-209;
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ATGATGAAACATACACCACTTCCCGCATCCGTGCAACTGACTTCCAGGAGC 60
DB 46 ATGATGAAACATACACCACTTCCCGCATCCGTGCAACTGACTTCCAGGAGC 105
QY 61 ATGAGATTTTATGATTTTACTTCTTCTTATCACTCCAAATGATGATCTG 120
DB 106 ATGAAATTTTATGATTTTACTTCTTCTTATCACTCCAAATGATGATCTG 165
QY 121 CTTTTCGTGTATCTTCTTATGAGGTGCAAGATGAGATGAAAGATCTTCA 180
DB 166 CTTTTCGTGTATCTTCTTATGAGGTGCAAGATGAGATGAAAGATCTTCA 225
QY 181 GAAGATTTGATTCATGAAACGATACAGATGCAACACGAGAAATCTTATCC 240
DB 226 GAAGATTTGATTCATGAAACGATACAGATGCAACACGAGAAATCTTATCC 285
QY 241 TTAAGAACTGTGAGAGATTTAAAGCACTTGAAGCTTTGTGAAGATATATGTTA 300
DB 286 TTAAGAACTGTGAGAGATTTAAAGCACTTGAAGCTTTGTGAAGATATATGTTA 345
QY 301 AACAAAG 360
DB 346 AACAAAG 405

QY 361 CAATTGGCGACATGTCTAATAGAGCGCAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 406 CAATTGGCGACATGTCTAATAGAGCGCAGAGAGAGAGAGAGAGAGAGAGAG 465
QY 421 GCTGAAAAAGATATACACATGAGAGCAACCTTGTAACCTGGAAAAAGAGAG 480
DB 466 GCTGAAAAAGATATACACATGAGAGCAACCTTGTAACCTGGAAAAAGAGAG 525
QY 481 CTGACCTTTAAAG 540
DB 526 CTGACCTTTAAAG 585
QY 541 CGGAGAGCTTGAGAGTCAAGCTCATTATAGCCAGCTTGCTTAAAGTCCCGGTAGA 600
DB 586 CGGAGAGCTTGAGAGTCAAGCTCATTATAGCCAGCTTGCTTAAAGTCCCGGTAGA 645
QY 601 TTGAGAGAGATTTTACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
DB 646 TTGAGAGAGATTTTACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 705
QY 661 CAATCATTCATCTTGGAGAGAGATTTGAATTGCAACAGAGTCTTGCTTGTCAAT 720
DB 706 CAATCATTCATCTTGGAGAGAGATTTGAATTGCAACAGAGTCTTGCTTGTCAAT 765
QY 721 GTGAGTATCCAGAGCAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
DB 766 GTGAGTATCCAGAGCAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 825
QY 781 CTCTGA 786
DB 826 CTCTGA 831

RESULT 11
US-08-763-995-1
Sequence 1, Application US/08763995
Patent No. 601/527
GENERAL INFORMATION:
APPLICANT: MARASOVSKY, EUGENE
TITLE OF INVENTION: METHOD OF ACTIVATING DENDRITIC CELLS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Power Macintosh 7200/90
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Macintosh, Version #6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/763,995
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USN 08/677,762
FILING DATE: 10 JUL 1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2845-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHEITICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46..831
US-08-763-995-1

Query Match 95.9%; Score 754; DB 3; Length 840;
Best Local Similarity 97.5%; Pred. No. 5.3e-209;
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ATGATAGAAATACATACAGCACTTCCCGATCCGAGGCACTGAGCTTCAGGAGC 60
DB 46 ATGATCGAAACATACACCAACTTCCCGATCCGAGGCACTGAGCTTCAGGAGC 105
QY 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATCCCAATGATGATCTGTG 120
DB 106 ATGAAATTTTATGATTTACTTACTGTTTCTTATCCCAATGATGATCTGTG 165
QY 121 CTTTGTGCTGATCTTATGAAAGTTGGAAGATGAAAGATGAAAGATCTTCAT 180
DB 166 CTTTGTGCTGATCTTATGAAAGTTGGAAGATGAAAGATGAAAGATCTTCAT 225
QY 181 GAAGATTTTATGATTTACTTACTGTTTCTTATCCCAATGATGATCTGTG 240
DB 226 GAAGATTTTATGATTTACTTACTGTTTCTTATCCCAATGATGATCTGTG 285
QY 241 TTAAGATCTGAGGAGATTTAAAGCAGTTTGAAGCTTTGAAGATTAATGTTA 300
DB 286 TTAAGATCTGAGGAGATTTAAAGCAGTTTGAAGCTTTGAAGATTAATGTTA 345
QY 301 AACAAAG 360
DB 346 AACAAAG 405
QY 361 CAATTTGCGGACATGTCATTAAGTGGGCGAGAGTAAACAACTGTTACAGTGG 420
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QY 421 GGTGAAAAAGATCTACCACTGAGCACACTTGTAACTCTGAAAAATGGAAAAAG 480
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QY 481 CTGACCGTTTAAAG 540
DB 526 CTGACCGTTTAAAG 585
QY 541 CGGGAAGCTTGGAGTCAAGCTTCAATTAAGCAAGCTTGGCTTAAGAGTCCCGG 600
DB 586 CGGGAAGCTTGGAGTCAAGCTTCAATTAAGCAAGCTTGGCTTAAGAGTCCCGG 645
QY 601 TTGAGAGAACTTACTGAGAGCTGCAAAATCCACAGTTTCGCGCAAACTTGG 660
DB 646 TTGAGAGAACTTACTGAGAGCTGCAAAATCCACAGTTTCGCGCAAACTTGG 705
QY 661 CAATTCATTCCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
DB 706 CAATTCATTCCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 765
QY 721 GTGACTGATCCAG 780
DB 766 GTGACTGATCCAG 825
QY 781 CTCTGA 786
DB 826 CTCTGA 831

RESULT 12
US-09-088-913A-11
Sequence 11, Application US/09088913A
Patent No. 6087329
GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: FANSLAW, WILLIAM
APPLICANT: SPRIGGS, MELANIE
APPLICANT: SRINIVASAN, SUBHASHINI
APPLICANT: GIBSON, MARYLOU
APPLICANT: MORRIS, ARVIA E.
APPLICANT: MCGREM, JEFFERY
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSER: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/088,913A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484,624
FILING DATE:
APPLICATION NUMBER: 08/477,733
FILING DATE: June 07, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,703
FILING DATE: October 23, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/805,723
FILING DATE: December 5, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/783,707
FILING DATE: October 25, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEO ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHEITICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46..831
US-09-088-913A-11
Query Match 95.9%; Score 754; DB 3; Length 840;
Best Local Similarity 97.5%; Pred. No. 5.3e-209;
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ATGATGAAACATACAGCAACCTTCCCGAGATCCGTCGCACTTCCAGGAGC 60
 DB 46 ATGATGAAACATACAGCAACCTTCCCGAGATCCGTCGCACTTCCAGGAGC 105
 QY 61 ATGAAATTTTATGATTTTACTTACTGTTTTCTTTATCCAGCCAAATGATGATCTGTG 120
 DB 106 ATGAAATTTTATGATTTTACTTACTGTTTTCTTTATCCAGCCAGATGATGATGATGAGCA 165
 QY 121 CTTTGTGCTGTATCTCATAGAGTTGAGCAAGATGATGATGATGATGATGATGATGATGATGAT 180
 DB 166 CTTTGTGCTGTATCTCATAGAGTTGAGCAAGATGATGATGATGATGATGATGATGATGATGAT 225
 QY 181 GAAGATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
 DB 226 GAAGATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 285
 QY 241 TTACTGATCTGTAGAGATTTAAAGCCAGTTTGAAGGCTTTGATGATGATGATGATGATGATGAT 300
 DB 286 TTACTGATCTGTAGAGATTTAAAGCCAGTTTGAAGGCTTTGATGATGATGATGATGATGATGAT 345
 QY 301 AACAAAGAGAGACGAG 360
 DB 346 AACAAAGAGAGACGAG 405
 QY 361 CAAATTTGCGGACATGTCATAGTGAAGGCGAGAGTAAACATCTGTGTTCACTG 420
 DB 406 CAAATTTGCGGACATGTCATAGTGAAGGCGAGAGTAAACATCTGTGTTCACTG 465
 QY 421 GCTGAAAGAGATCTACCATGAGCAACATTTGTAACCTTGAGAAATGAGAAACAG 480
 DB 466 GCTGAAAGAGATCTACCATGAGCAACATTTGTAACCTTGAGAAATGAGAAACAG 525
 QY 481 CTGACCGTTTAAAGCAAGGACTCTATTAATCTATGCGCAAGTCACTCTGTGTTCAAT 540
 DB 526 CTGACCGTTTAAAGCAAGGACTCTATTAATCTATGCGCAAGTCACTCTGTGTTCAAT 585
 QY 541 CGGAAAGCTTGAAGTCAAGCTCAATTAATGAGCGCTCTGCTTAAAGTCCCGGATGA 600
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 QY 601 TTGAGAGAGATCTTACATGAGCTGCAAAATACCAAGTTCCGCGCAAACTTGCGGAGCA 660
 DB 646 TTGAGAGAGATCTTACATGAGCTGCAAAATACCAAGTTCCGCGCAAACTTGCGGAGCA 705
 QY 661 CAATTCATCTACTTGGAGAGATTAATGATGCAACCAAGTCTTCCGTTGTTGTCAT 720
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 QY 721 GTGACTGATCCAAAGCAAGTGAAGCACTGAGCTTCAAGTCTTGGCTTACTCAAA 780
 DB 766 GTGACTGATCCAAAGCAAGTGAAGCACTGAGCTTCAAGTCTTGGCTTACTCAAA 825
 QY 781 CTCTGA 786
 DB 826 CTCTGA 831

ADDRESS: IMMUNEX CORPORATION
 STREET: 51 UNIVERSITY STREET
 CITY: SEATTLE
 STATE: WASHINGTON
 COUNTRY: USA
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: MS-DOS/Windows 95
 SOFTWARE: Word for Windows 95, 7.0a
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/589, 771B
 FILING DATE: January 22, 1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/009, 258
 FILING DATE: 01/22/93
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: HENRY, JANIS C.
 REGISTRATION NUMBER: 34,347
 REFERENCE/DOCKET NUMBER: 2810-C
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 2065870430
 TELEFAX: 2065870606
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 840 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHEICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 IMMEDIATE SOURCE:
 CLONE: CD40-L
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 46..831
 US-08-589-771B-7

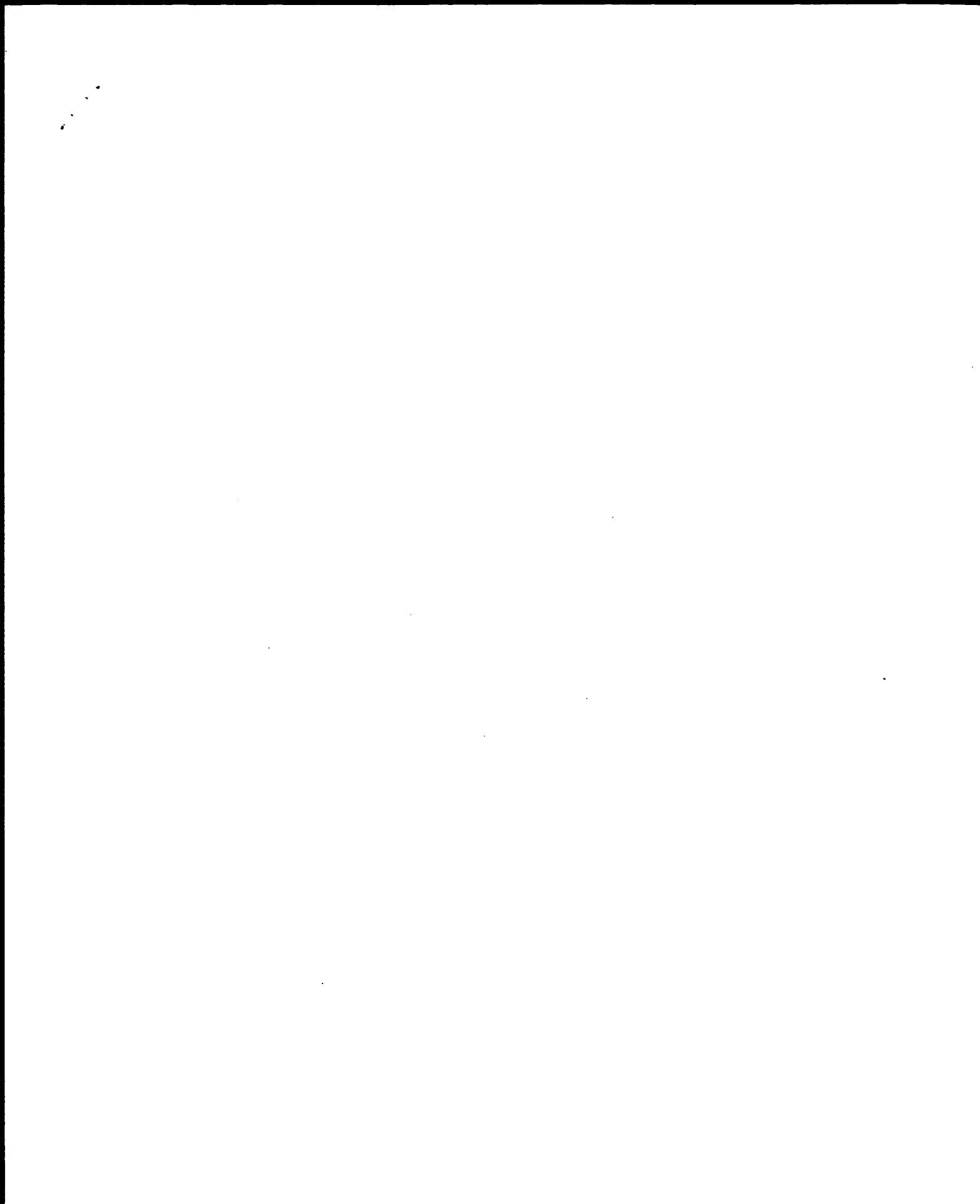
Query Match 95.9%; Score 754; DB 3; Length 840;
 Best Local Similarity 97.5%; Pred. No. 5,3e-209;
 Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ATGATGAAACATACAGCAACCTTCCCGAGATCCGTCGCACTTCCAGGAGC 60
 DB 46 ATGATGAAACATACAGCAACCTTCCCGAGATCCGTCGCACTTCCAGGAGC 105
 QY 61 ATGAAATTTTATGATTTTACTTACTGTTTTCTTTATCCAGCCAAATGATGATCTGTG 120
 DB 106 ATGAAATTTTATGATTTTACTTACTGTTTTCTTTATCCAGCCAGATGATGATGATGATGATGATGATGAT 165
 QY 121 CTTTGTGCTGTATCTCATAGAGTTGAGCAAGATGATGATGATGATGATGATGATGATGATGAT 180
 DB 166 CTTTGTGCTGTATCTCATAGAGTTGAGCAAGATGATGATGATGATGATGATGATGATGATGAT 225
 QY 181 GAAGATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
 DB 226 GAAGATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 285
 QY 241 TTACTGATCTGTAGAGATTTAAAGCCAGTTTGAAGGCTTTGATGATGATGATGATGATGATGAT 300
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 QY 301 AACAAAGAGAGACGAG 360
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 QY 361 CAAATTTGCGGACATGTCATAGTGAAGGCGAGAGTAAACATCTGTGTTCACTG 420

ORIGINAL SOURCE:

Job time : 36.6448 secs

Search completed: March 9, 2003, 04:46:20
Job time : 36.6448 secs



GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: March 8, 2003, 18:35:23 ; Search time 2040.79 Seconds

(without alignments)
11166.008 Million cell updates/sec

Title: US-08-982-272-20

Perfect score: 783

Sequence: 1 ATGATGAAACATCAACCA.....TTGGCTTACTCAAACTCTGA 783

Scoring table:

IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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13: gb_un: *
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score greater than or equal to the score being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	726.8	92.8	840	6	AR044779
3	726.8	92.8	840	6	AR076926
4	726.8	92.8	840	6	AR078316
5	726.8	92.8	840	6	AR085419
6	726.8	92.8	840	6	AR103375
7	726.8	92.8	840	6	AR106246
8	726.8	92.8	840	6	AR169232
9	726.8	92.8	840	6	AR171647
10	726.8	92.8	840	6	123893
11	726.8	92.8	840	6	127345
12	726.8	92.8	840	6	167828
13	726.8	92.8	879	6	AX090039
14	726.8	92.8	879	9	HSGP39MR
15	726.8	92.8	1803	9	HSCD40
16	726.8	92.8	1816	9	HUMCD40L
17	725.2	92.6	1822	9	HSTRAPA
18	712.4	91.0	1058	9	AF344841
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36	603.8	77.1	788	4	AF079105
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ALIGNMENTS

RESULT 1
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LOCUS 187864
DEFINITION Sequence 3 from patent US 5716805.
ACCESSION 187864
VERSION 187864.1 GI:3407804
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 786)
AUTHORS Srinivasan,S. and Spriggs,M.K.
TITLE Methods of preparing soluble, oligomeric proteins
JOURNAL Patent: US 5716805-A 3 10-FEB-1998;
FEATURES Location/Qualifiers

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ORIGIN

Query Match 92.8%; Score 726.8; DB 6; Length 786;
Best Local Similarity 96.2%; Pred. No. 4.9e-171;
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

QY 1 ATGATCGAAACATACACAACTTCTCCCGATCGGGGCACTGGACCTGCCATCAGC 60
DB 1 ATGATCGAAACATACACAACTTCTCCCGATCGGGGCACTGGACCTGCCATCAGC 60
QY 61 ATGAAATTTTATGATTTACTTACTGTTTTCTTATCCAGATGATGGGTACCA 120
DB 61 ATGAAATTTTATGATTTACTTACTGTTTTCTTATCCAGATGATGGGTACCA 120
QY 121 CTTTTGCTGTATCTTATGATGAAAGTGGATGAGTGAAGAGTAAAGTTCAT 180
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DB 781 CTCTGA 786

RESULT 2
AR044779 840 bp DNA linear PAT 29-SEP-1999
LOCUS AR044779
DEFINITION Sequence 3 from patent US 5817516.
ACCESSION AR044779
VERSION AR044779.1 GI:5966244
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 840)
AUTHORS Kenry, W. and Castle, B.
TITLE Methods for proliferating and differentiating B cells with high density membrane CD40 ligand
JOURNAL Patent: US 5817516-A 3 06-OCT-1998;
FEATURES
source 1. .840
/organism="unknown"
BASE COUNT 263 a 182 c 181 g 214 t
ORIGIN

Query Match 92.8%; Score 726.8; DB 6; Length 840;
Best Local Similarity 96.2%; Pred. No. 4.9e-171;
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

QY 1 ATGATGAAACATACACAACTTCTCCCGATCGGGGCACTGGACCTGCCATCAGC 60
DB 22 ATGATGAAACATACACAACTTCTCCCGATCGGGGCACTGGACCTGCCATCAGC 81
QY 61 ATGAAATTTTATGATTTACTTACTGTTTTCTTATCCAGATGATGGGTACCA 120
DB 82 ATGAAATTTTATGATTTACTTACTGTTTTCTTATCCAGATGATGGGTACCA 141
QY 121 CTTTTGCTGTATCTTATGATGAAAGTGGATGAGTGAAGAGTAAAGTTCAT 180
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QY 181 GAAGATTTTATTCATTAATAAAGCTAAAGATGCAACAAAGAGAGATCTTATCC 240
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QY 241 TTGCTGAACGTGAGAGATGAAAGCAATTTGAAGCCTTGTCAAGATATTAAGTTA 300
DB 262 TTGCTGAACGTGAGAGATGAAAGCAATTTGAAGCCTTGTCAAGATATTAAGTTA 321
QY 301 AACAAAGAGA--GAAAAAGAAAAGCTTTGAATGCAAAAAGGTGATCAGATCT 357
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QY 478 CTGACCGTTAAAGACAAAGACTCTATATATCTATGCGCAAGTCACTTGTTCAT 537
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DB 622 TTGAGAGAAATCTTACTCAGAGCTGCAAAATACCAAGTTCGCGCAAACTTGGCGCA 681
QY 658 CAATTCATTCATTTGGAGAGATTTGAAATTCGAAACCAAGTCTTGGTTTGTCAAT 717
DB 682 CAATTCATTCATTTGGAGAGATTTGAAATTCGAAACCAAGTCTTGGTTTGTCAAT 741
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DB 742 GTGACTGATCAGAGCAAGTGAAGCAATGCACTGCTTCAAGTCTTGGCTTAAGTCAAA 801
QY 778 CTCTGA 783
DB 802 CTCTGA 807

RESULT 3
 LOCUS AR076926 840 bp DNA linear PAT 31-AUG-2000
 DEFINITION Sequence 11 from patent US 5961974.
 ACCESSION AR076926
 VERSION AR076926.1 GI:10003672
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 840)
 AUTHORS Armitage, R.J., Fanslow, W.C. and Spriggs, M.K.
 TITLE Monoclonal antibodies to CD40 ligand, pharmaceutical composition comprising the same and hybridomas producing the same
 JOURNAL Patent: US 5961974-A 11 05-OCT-1999;
 FEATURES Location/Qualifiers
 source 1..840
 /organism="unknown"

BASE COUNT 266 a 185 c 175 g 214 t
 ORIGIN

Query Match 92.8%; Score 726.8; DB 6; Length 840;
 Best Local Similarity 96.2%; Pred. No. 4.9e-171;
 Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

Qy 1 ATGATCGAAACATACACCAACTTCTCCCGATCTGCGGCACTGAGTCCCATCAGC 60
 Db 46 ATGATCGAAACATACACCAACTTCTCCCGATCTGCGGCACTGAGTCCCATCAGC 105
 Qy 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCAGATGTTGGTGAGCA 120
 Db 106 ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCAGATGTTGGTGAGCA 165
 Qy 121 CTTTTCCTGCTGCTTCTTCTTGAAGATTGATGAGTGAAGAGATTAACCTTCT 180
 Db 166 CTTTTCCTGCTGCTTCTTCTTGAAGATTGATGAGTGAAGAGATTAACCTTCT 225
 Qy 181 GAAGATTTTGTATTCATTAAGAGTGAAGATGCAACAAAGAGATCTTATCC 240
 Db 226 GAAGATTTTGTATTCATTAAGAGTGAAGATGCAACAAAGAGATCTTATCC 285
 Qy 241 TTGCTGAACCTGAG 300
 Db 286 TTACTGAACCTGAG 345
 Qy 301 AACAAAGAGA---GAAAAAGAAAAAGCTTGAATGCAAAAAGTGAATCAAAATCCT 357
 Db 346 AACAAAG 405
 Qy 358 CAAATTTGGGCACTGATCAATAGAGGCGAGAGAGAGAGAGAGAGAGAGAGAGAG 417
 Db 406 CAAATTTGGGCACTGATCAATAGAGGCGAGAGAGAGAGAGAGAGAGAGAGAGAG 465
 Qy 418 GCTGAAAAAGATCTACACATGAGCAACACTTGTAACTCTGAAAAATGGAAAAAG 477
 Db 466 GCTGAAAAAGATCTACACATGAGCAACACTTGTAACTCTGAAAAATGGAAAAAG 525
 Qy 478 CTGACCGTTAAAAAG 537
 Db 526 CTGACCGTTAAAAAG 585
 Qy 538 CCGGAAGCTTGAAGTCAAGCTCATTTATAGCCAGCTCTGCTAAAGTCCCGGTAGA 597
 Db 586 CCGGAAGCTTGAAGTCAAGCTCATTTATAGCCAGCTCTGCTAAAGTCCCGGTAGA 645
 Qy 598 TTGAGAGAGATCTTACTCAGAGCTGAAGTCAAGAGTTCGCGCAAGCTTGGGGGCA 657
 Db 646 TTGAGAGAGATCTTACTCAGAGCTGAAGTCAAGAGTTCGCGCAAGCTTGGGGGCA 705
 Qy 658 CAATCCATTCACTTGGAGAGAGATTTGAATTGCAACAGGTCTTGGTGTTCAT 717

Db 706 CAATCCATTCACTTGGAGAGAGATTTGAATTGCAACAGGTCTTGGTGTTCAT 765
 Qy 718 GTGACTGATCCAAAGCCAAAGTGAAGCCATGAGCTTCAAGTCTTTGGCTTACTCAA 777
 Db 766 GTGACTGATCCAAAGCCAAAGTGAAGCCATGAGCTTCAAGTCTTTGGCTTACTCAA 825
 Qy 778 CTCTGA 783
 Db 826 CTCTGA 831

RESULT 4
 LOCUS AR078316 840 bp DNA linear PAT 31-AUG-2000
 DEFINITION Sequence 11 from patent US 5962406.
 ACCESSION AR078316
 VERSION AR078316.1 GI:10005062
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 840)
 AUTHORS Armitage, R.J., Fanslow, W.C., Spriggs, M.K., Srinivasan, S.,
 Gibson, M.G., Morris, A.E. and McGrew, J.T.
 TITLE Recombinant soluble CD40 ligand polypeptide and pharmaceutical composition containing the same
 JOURNAL Patent: US 5962406-A 11 05-OCT-1999;
 FEATURES Location/Qualifiers
 source 1..840
 /organism="unknown"

BASE COUNT 266 a 185 c 175 g 214 t
 ORIGIN

Query Match 92.8%; Score 726.8; DB 6; Length 840;
 Best Local Similarity 96.2%; Pred. No. 4.9e-171;
 Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

Qy 1 ATGATCGAAACATACACCAACTTCTCCCGATCTGCGGCACTGAGTCCCATCAGC 60
 Db 46 ATGATCGAAACATACACCAACTTCTCCCGATCTGCGGCACTGAGTCCCATCAGC 105
 Qy 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCAGATGTTGGTGAGCA 120
 Db 106 ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCAGATGTTGGTGAGCA 165
 Qy 121 CTTTTCCTGCTGCTTCTTCTTGAAGATTGATGAGTGAAGAGATTAACCTTCT 180
 Db 166 CTTTTCCTGCTGCTTCTTCTTGAAGATTGATGAGTGAAGAGATTAACCTTCT 225
 Qy 181 GAAGATTTTGTATTCATTAAGAGTGAAGATGCAACAAAGAGATCTTATCC 240
 Db 226 GAAGATTTTGTATTCATTAAGAGTGAAGATGCAACAAAGAGATCTTATCC 285
 Qy 241 TTGCTGAACCTGAG 300
 Db 286 TTACTGAACCTGAG 345
 Qy 301 AACAAAGAGA---GAAAAAGAAAAAGCTTGAATGCAAAAAGTGAATCAAAATCCT 357
 Db 346 AACAAAG 405
 Qy 358 CAAATTTGGGCACTGATCAATAGAGGCGAGAGAGAGAGAGAGAGAGAGAGAGAG 417
 Db 406 CAAATTTGGGCACTGATCAATAGAGGCGAGAGAGAGAGAGAGAGAGAGAGAGAG 465
 Qy 418 GCTGAAAAAGATCTACACATGAGCAACACTTGTAACTCTGAAAAATGGAAAAAG 477
 Db 466 GCTGAAAAAGATCTACACATGAGCAACACTTGTAACTCTGAAAAATGGAAAAAG 525
 Qy 478 CTGACCGTTAAAAAG 537
 Db 526 CTGACCGTTAAAAAG 585

Qy	538	CGGGAAGCTTCAGATCAAGCTCCATTATTAAGCAAGCTCTGCTAAAGTCCCGGGATGA	597
Db	586	CGGGAAGCTTCAGATCAAGCTCCATTATTAAGCAAGCTCTGCTAAATCCCGCGGTGA	645
Qy	598	TTGAGAGAAATCTTACTAGAGCTGCGCAATTAACCAAGTTCCGCCAACCCTGCGGGACA	657
Db	646	TTGAGAGAAATCTTACTAGAGCTGCGCAATTAACCAAGTTCCGCCAACCCTGCGGGACA	705
Qy	658	CAATCAATTAAGCTGGGAGAGAGATTTGAAATTGGCAACAAGTGTCTGGATTTGTCAAT	717
Db	706	CAATCAATTAAGCTGGGAGAGAGATTTGAAATTGGCAACAAGTGTCTGGATTTGTCAAT	765
Qy	718	GTGAATGATCAAGCCCAAGTACGCAATGGCACTGGCTCAACGTCCTTTGGCTTAACGAA	777
Db	766	GTGAATGATCAAGCCCAAGTACGCAATGGCACTGGCTTAACGTCCTTTGGCTTAACGAA	825
Qy	778	CTCTCTGA 783	
Db	826	CTCTCTGA 831	

RESULT	5			PAT 01-SEP-2006
LOCUS	AR085419	840 bp	DNA linear	
DEFINITION	Sequence from patent US 5981724.			
ACCESSION	AR085419			
VERSION	AR085419.1	GI:10012188		
KEYWORDS				
SOURCE	Unknown.			

ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 840)
TITLE	Armitage,R.J., Fanslow,W.C., Spriggs,M.K., Srinivasan,S., Gibson,M.G., Morris,A.E. and McGrew,J.T. DNA encoding CD40 ligand, a cytokine that binds CD40
JOURNAL	Patent: US 5981724 A 11/09-NOV-1999;
FEATURES	Location/Qualifiers
source	1..840

	/organism="unknown"			
BASE COUNT	266 a	185 c	175 g	214 t
ORIGIN				

Query Match	92.8%	Score 726.8	DB 6	Length 840
Best Local Similarity	96.2%	Pred. No. 4,9e-771		
Matches 756; Conservative	0	Mismatches 27	Indels 3	Gaps 1

Dy 1 ATGATCGGAACATACACCAAACTTCTCCCGCATCTGGGCCATGAGCTGCCCATCAGC 60
Db 46 ATGATCGGAACATACACCAAACTTCTCCCGCATCTGGGCCATGAGCTGCCCATCAGC 105	

Qy 61 ATGAATAATTTATGATTTACTACGTTTTCTTATCAACCAATGATGGGTACGA 120
|||||
Db 106 ATGAATAATTTATGATTTACTACGTTTTCTTATCAACCAATGATGGGTACGA 165
|||||

Qy 121 CTTTTCGTGTGATCTTCATAGAAAGTTGSA.TAAGTCGAAGAGAAATTAACCTTCAT 180
|||||
Dp 166 CTTTTCGTGTGATCTTCATAGAAAGTTGSA.CAAGTAAAGATGAAAGGAATCTTCAT 225
|||||

Qy 181 GAAGTTTGTATTCATAAAAAGCTAAAGAGATGCACAAGAGAGTCTTATTC 240
|||||
Dy 226 GAAGTTTGTATTCATGAAACGATACAGAGATGCACAAGAGAAAGCTTATTC 285
|||||

Qy 241 TTGCTGAACGTGTAGAGATGAGAGGCAATTGTAGAACCCTTGTCAAGATATATACGTTA 300
Db 286 TTACTGAACGTGTAGAGATTAAGGACGATTGTAGAGCTTTGTAGAGATATATATGTTA 345

Qy 301 AACAAAGAGT---GAAAAAGAAAACAGCTTTGAAATGCAAAAAGTGATCGAACTCT 357
Db 346 AACAAAGGAGAGCGAAGAAAGAAAACAGCTTTGAAATGCAAAAAGTGATCGAACTCT 405

Dy 358 CAAATTTGGGCACATCTCTAATAGTGAAGCGCCACGACTAAAAACAATCTGTGTTAACAGTG 417
Dz 406 CAAATTGGGGACATCTCTAATAGTAGAGGCCACGACTAAAACAATCTGTGTTAACAGTG 465			

Oy	418	GCTGAAAAGGATCTAACCATGAGCAAACTCTGGTAACTCGGAAAAATGGGAAACAG	477
Db	466	GCTGAAAAGGATCTAACCATGAGCAAACTCTGGTAACTCGGAAAAATGGGAAACAG	525
Oy	478	CTGACCGTTAAAGCAGGACGCTTTATATCTAAGGCCAAGACGCTCTGTTCGAA	537
Db	526	CTGACCGTTAAAGCAGGACGCTTTATATCTAAGGCCAAGACGCTCTGTTCGAA	585
Oy	538	CGGGAAGCTTCGAGTCAGAGCTCAATTATATAGCCAGGCTCTGCTPAAAGTCCCCGGGTAGA	597
Db	586	CGGGAAGCTTCGAGTCAGAGCTCAATTATATAGCCAGGCTCTGCTPAAAGTCCCCGGGTAGA	645
Oy	598	TTGCGAGGAACTCTATCTCAGAGCTGCAAATACCAACGTTTCGGCGCAAACTTTCGGGGCAA	657
Db	646	TTGCGAGGAACTCTATCTCAGAGCTGCAAATACCAACGTTTCGGCGCAAACTTTCGGGGCAA	705
Oy	658	CAATTCATTCATCTTGGGAGAGATTTGAAATTGCAACAGAGTGCTTCCGAGTTTGTCAAT	717
Db	706	CAATTCATTCATCTTGGGAGAGATTTGAAATTGCAACAGAGTGCTTCCGAGTTTGTCAAT	765
Oy	718	GTGACTATCAAGCCAAAGTAGACCCATGGCACTGGCTTACAGTCTCTTTGGCTTACTCAAA	777
Db	766	GTGACTATCAAGCCAAAGTAGACCCATGGCACTGGCTTACAGTCTCTTTGGCTTACTCAAA	825
Oy	778	CTCTGGA 783	
Db	826	CTCTGGA 831	

RESULT 6			
AR103375			
LOCUS	AR103375	840 bp	DNA
DEFINITION	Sequence 11 from patent US 6087329.	linear	PAT 14-FEB-2001

ACCESSION	ARKU33/5	GI:12814963
VERSION	AR103375.1	
KEYWORDS		
SOURCE	Unknown.	
ORGANISM	Unknown.	
	Unclassified.	

REFERENCE	1 (pages 1 to 840)
AUTHORS	Armitage, R. J., Fanslow, W. C. and Spriggs, M. K.
TITLE	CD40 ligand polypeptide
JOURNAL	Patent: US 6087329-A 11 11-JUL-2000;
FEATURES	Location/Qualifiers
source	1..840

/organism="unknown"				
BASE COUNT	266 a	185 c	175 g	214 t
ORIGIN				

Query Match	92.84	Score 726.8	DB 6	Length 840
Best Local Similarity	96.25	Pred. No. 4.9e-17		
Matches 756; Conservative	0	Mismatches 27	Indels 3	Gaps 1

Oy 1 ATGATCGAAACATAACAACAACTTCTCCGGATCTGCGGCCCATGTGAATTGCCATCAGC 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 46 ATGATCGAAACATAACAACAACTTCTCCGGATCTGCGGCCCATGTGAATTGCCATCAGC 105

Oy 61 ATGAAATTTTATGTATTACTTACTGTTTTTTTATACCCAGATGATGGGTACGA 120
| | | | | | | | | | | | | | | | | | | | | |
Db 106 ATGAAAATTTTATGTATTACTTACTGTTTTTTTATACCCAGATGATGGGTACGA 165

Oy 121 CTTTTCGCTGTGATCTTCATAGAGATTGGATAGGTGAAAGAGAACTTCAT 180
 |||||
 Dd 166 CTTTTCGCTGTGATCTTCATAGAGATTGGACAAAGTAGAAGATGAAAGAACTTCAT 225
 |||||

OY 181 GAAGTTTGTATCATAAAAAGCTAAGAGATGCACAAAGAAGATCTTTATCC 240
DB 226 GAAAGTTTTGTTATTCATGAAGAACGATACAGAGATGCACAACGAGAAAATCTCTTATCC 285

OY		241 TTGCGAATCTGTAGAGATGAGAAGCAATTTAAGACCTGTCAAGTATAAACGTTA 300
Dd	286 TTAGTGAACTGTAGAGATTAAAAACCAGTTTAAGCCTTCGTGAAGATATAAATGTTA 345	

OY	301	AACTAAAGAG---	GAATAAAAGAAACAGCTTTGAATGCAAAAAAGTGATCGAATCTT	357
Db	346	AACTAAAGAGAGAG	GAAGAAAGAAACAGCTTTGAATGCAAAAAAGTGATCGAATCTT	405
OY	358	CAAAATGGGGGACATG	CAATTAAGTAGGGCCAGAGTAAACAACTGTTGTTACATGG	417
Db	406	CAAAATGGGGGACATG	CAATTAAGTAGGGCCAGAGTAAACAACTGTTGTTACATGG	465
OY	418	GCTGAAAAAGAGATCT	CACTACATGAGCAACACTTGTAACCTGGAAAAATGGGAAACAG	477
Db	466	GCTGAAAAAGAGATCT	CACTACATGAGCAACACTTGTAACCTGGAAAAATGGGAAACAG	525
OY	478	CTGACCGTTAAAAACA	CAAGGACTATTAATATCTATGCCAAGTCACTTGTTCCAAAT	537
Db	526	CTGACCGTTAAAAACA	CAAGGACTATTAATATCTATGCCAAGTCACTTGTTCCAAAT	585
OY	538	CGGGAAGCTTGAGATCA	AGCTCATTTATAGCAGGCTGTGCTTAAAGTCCCGGGTGA	597
Db	586	CGGGAAGCTTGAGATCA	AGCTCATTTATAGCAGGCTGTGCTTAAAGTCCCGGGTGA	645
OY	598	TTTGAGAGATCTTACT	CAAGCTGCAATATCCCAAGTTCCGCAAACTTTCGCGGCAA	657
Db	646	TTTGAGAGATCTTACT	CAAGCTGCAATATCCCAAGTTCCGCAAACTTTCGCGGCAA	705
OY	658	CAATCATTTCACTTGG	AGAGATTTTGAATATGCAACAGAGTCTTGCGTGTGTCAAAT	717
Db	706	CAATCATTTCACTTGG	AGAGATTTTGAATATGCAACAGAGTCTTGCGTGTGTCAAAT	765
OY	718	GTACAGATTCGAACCA	CAAGTAGGCAATGGCACTGTGCTTACGCTTTGGCTTACGAAA	777
Db	766	GTACAGATTCGAACCA	CAAGTAGGCAATGGCACTGTGCTTACGCTTTGGCTTACGAAA	825
OY	778	CTCTGA	783	
Db	826	CTCTGA	831	

RESULT	7			PAT 14-FEB-2001
LOCUS	ARI06246			
DEFINITION	Sequence 7 from patent US 6106832.	840 bp	DNA	linear
ACCESSION	ARI06246			
VERSION	ARI06246.1	GI:12820776		
KEYWORDS	.			
SOURCE	unknown.			
ORGANISM	unclassified.			
REFERENCE	1 (bases 1 to 840)			
AUTHORS	Spijgsma,M.K., Amelunge,R.J., Fanslow,W.C. III and Widmer,M.B.			
TITLE	Treatment of immunites exhibiting defective CD40L			
JOURNAL	Patent: US 6106832-A 7 22-Aug-2000;			
FEATURES	Location/Qualifiers			
source	1..840			
	/organism="unknown"			
BASE COUNT	266 a 185 c 175 g 214 t			
ORIGIN				

Query Match	92.8%	Score 726.8;	DB 6;	Length 840;
Best Local Similarity	96.2%;	Pred. No. 4.9e-17;		
Matches 756;	Conservative	0;	Mismatches 27;	Indels 3;
				Gaps 1;

Qy	1	ATATGAAACATCAACCAAACTTCTCCGCACTGAGGCACTGGACATGAC	60
Db	46	ATGATGAAACATCAACCAAACTTCTCCGCACTGAGGCACTGGACATGAC	1050
Qy	61	ATGAAAAATTTTATGATTTACTCTGTTTTCTATACACCGAAGATGTGGTCA	1200
Db	106	ATGAAAAATTTTATGATTTACTCTGTTTTCTATACACCGAAGATGTGGTCA	1650
Qy	121	CTTTTGGCTGCTATCTTACATGAAGATTGGATTAAGCTCGAAGAGAACTTCTAT	1800
Db	166	CTTTTGGCTGCTATCTTACATGAAGATTGGATTAAGCTCGAAGAGAACTTCTAT	2250

Qy	181	GAAGATTTTGTATTCATTTAAAAAGCTTAAAGAGATGACAATAAGGAGAAAGATCTTTATCC	240
Db	226	GAAGATTTTGTATTCATTTAAAAAGATACAGAGATGCACACAGAGAAAAGATCTTTATCC	285
Qy	241	TTTGCTGAACCTGGAGAGATGAGAAAGCAATTTGAAAGACTTTGCAAGATTTAAAGTTAA	300
Db	286	TTTACTGAACCTGGAGAGATTTAAAGCCAGTTTGAAGGCTTTGGAAGGATTTAATGTAT	345
Qy	301	AACAAAGAGA---GAAATAAGAAAAACAGCTTTGAAATGCAAAAAGGTATCAGAACTCT	357
Db	346	AACAAAGAGGAGAGAAAGAAAAACAAGCTTTGAAATGCAAAAAGGTATCAGAACTCT	405
Qy	358	CAAAATTCGGGCACATGTCATTAAGTAGGCCACGACGTAAAAACAATCTGTGTACTAGTGG	417
Db	406	CAAAATTCGGGCACATGTCATTAAGTAGGCCACGACGTAAAAACAATCTGTGTACTAGTGG	465
Qy	418	GCTGAAAAAGGATCTACACCAAGAGCAACACTTGGTAACTCTGAAAAATGGGAAACAG	477
Db	466	GCTGAAAAAGGATCTACACCAATGAGCAACACTTGGTAACTCTGAAAAATGGGAAACAG	525
Qy	478	CTGACGCTTTAAAGACAAAGACCTTATATTCATAGCCCAAGACACTCTTGTTCCAAAT	537
Db	526	CTGACGCTTTAAAGACAAAGACCTTATATTCATAGCCCAAGACACTCTTGTTCCAAAT	585
Qy	538	CGGGAAGCTTGCAGTCAAGCTCCATTTATTAAGCCAGGCTCTCCCTAAAGTCCCCCGGTAGA	597
Db	586	CGGGAAGCTTGCAGTCAAGCTCCATTTATTAAGCCAGGCTCTCCCTAAAGTCCCCCGGTAGA	645
Qy	598	TTTCGAGAGATCTTATCTCAGAGCTGCAATACCAAGTTCGGGCAAACTTTGGGGGGCAAA	657
Db	646	TTTCGAGAGATCTTATCTCAGAGCTGCAATACCAAGTTCGGGCAAACTTTGGGGGGCAAA	705
Qy	658	CAATTCATTCACCTTGGAGAGATTTGAATTGCAACAGGCTTCGGTGGTTGTCAAT	717
Db	706	CAATTCATTCACCTTGGAGAGATTTGAATTGCAACAGGCTTCGGTGGTTGTCAAT	765
Qy	718	GTGACATGATCAAGCAAGAGACCATGGCACTGAGCTTCAAGTCTTTGGCTTACTCAAA	777
Db	766	GTGACATGATCAAGCAAGAGACCATGGCACTGAGCTTCAAGTCTTTGGCTTACTCAAA	825
Qy	778	CTCTGA 783	
Db	826	CTCTGA 831	

RESULT	8			
LOCUS	AR169232			
DEFINITION	AR169232	840 bp	DNA	linear
ACCESSION	Sequence	11	from patent US 6290972.	PAT 17-DEC-2001
VERSION	AR169232			
KEYWORDS	AR169232.1	GI:17907047		
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	Unclassified.			
	1	(bases 1 to 840)		

TITLE	Gibson, M.G.	Method of augmenting a vaccine response by administering CD40 ligand
JOURNAL	Patent: US 6290972-A	11 18-SEP-2001;
FEATURES	Location/Qualifiers	
source	1. .840	
	/organism="unknown"	
BASE COUNT	266 a 185 c 175 g	214 t
ORIGIN		
Query Match	92.8%;	Score 726.8; DB 6;
Best Local Similarity	96.2%;	Pred. No. 4.9e-171;
Matches 756; Conservative	0;	Mismatches 27; Indels 3; Gaps 1;
1 ATGATCGAACAATCAACCAAACTTCTCCCGATCTGCGGCGCACTGAGCTGCCCATCAGC	60	

Db	Accession	Gene	Protein	Length	Start	Stop	Strand	Source
Db	46	ARGANCGAAGAACATACACCAACCACTCTCCCGAATCTGCGGCCACTGCACTGCCCATCAGC	105	1	105	105	+	GenBank
Qy	61	ATGAAAAATTTTATATGTAATTTACTACTGTTTTTTCTTATCAACCAGATGATGGGTCA	120	1	120	120	+	GenBank
Db	106	ATGAAAAATTTTATGTAATTTACTACTGTTTTTTCTTATCAACCAGATGATGGGTCA	165	1	165	165	+	GenBank
Qy	121	CTTTTTCGTGTATCTTCATAGAAATGGATTAAGTGTGAGAGAGAAATGTAACCTTCAT	180	1	180	180	+	GenBank
Db	166	CTTTTTCGTGTATCTTCATAGAAATGGATTAAGTGTGAGAGAGAAATGTAACCTTCAT	225	1	225	225	+	GenBank
Qy	181	GAAAGATTTTGTATCTTAAAAAGCTTAAAGATGCAACAAAGAGAGAAATGTTTATCC	240	1	240	240	+	GenBank
Db	226	GAAAGATTTTGTATCTTAAAAAGCTTAAAGATGCAACAAAGAGAGAAATGTTTATCC	285	1	285	285	+	GenBank
Qy	241	TTGCTGAATCTGTAGAGAGATGAGAAAGCAATTTGAACCTTGTCAGAGATATTAACCTTA	300	1	300	300	+	GenBank
Db	286	TTACTGAATCTGTAGAGAGATTTAAAGCAAGTTTGAAGGCTTTGTGAAGATTAATGTTA	345	1	345	345	+	GenBank
Qy	301	AACCAAGAA--GAAAAAGAAACAGCTTTGAATGCAAAAAGGTGATCAAGATCTT	357	1	357	357	+	GenBank
Db	346	AACCAAG	405	1	405	405	+	GenBank
Qy	358	CAAAATGGCGACATGTCTATAGTGAAGGCGACAGTAAACAAACATCTGTGTACAGTGG	417	1	417	417	+	GenBank
Db	406	CAAAATGGCGACATGTCTATAGTGAAGGCGACAGTAAACAAACATCTGTGTACAGTGG	465	1	465	465	+	GenBank
Qy	418	GCTGAAAAAGATATCAACATGAGACAAACCTTGGTAACTCCCTGAAAAATGGAAAAAG	477	1	477	477	+	GenBank
Db	466	GCTGAAAAAGATATCAACATGAGACAAACCTTGGTAACTCCCTGAAAAATGGAAAAAG	525	1	525	525	+	GenBank
Qy	478	CTGACCGTTTAAAGACAGAGACTTATATATCTATGCTCCCAAGTCACTTCTGTTCAT	537	1	537	537	+	GenBank
Db	526	CTGACCGTTTAAAGACAGAGACTTATATATCTATGCTCCCAAGTCACTTCTGTTCAT	585	1	585	585	+	GenBank
Qy	538	CGGGAAGCTTGGAGTCAAGCTCCATTTATAGCAAGCTGCTGCTTAAAGTCCCGGTGA	597	1	597	597	+	GenBank
Db	586	CGGGAAGCTTGGAGTCAAGCTCCATTTATAGCAAGCTGCTGCTTAAAGTCCCGGTGA	645	1	645	645	+	GenBank
Qy	598	TTGAGAGAAATCTTACTCAGAGCTGCAAAATCCCAAGTTCCGCCAAACCTTGCGGGCA	657	1	657	657	+	GenBank
Db	646	TTGAGAGAAATCTTACTCAGAGCTGCAAAATCCCAAGTTCCGCCAAACCTTGCGGGCA	705	1	705	705	+	GenBank
Qy	658	CAATCATCTCACTGGGAGAGATTTTGAATTTGCAACAGAGTGCCTGGGTGTATGCAAT	717	1	717	717	+	GenBank
Db	706	CAATCATCTCACTGGGAGAGATTTTGAATTTGCAACAGAGTGCCTGGGTGTATGCAAT	765	1	765	765	+	GenBank
Qy	718	GTCATGATCCAAAGCCAAAGTGAAGCCATGCGCTTCAACGTCTTTGGCTTACTCAA	777	1	777	777	+	GenBank
Db	766	GTCATGATCCAAAGCCAAAGTGAAGCCATGCGCTTCAACGTCTTTGGCTTACTCAA	825	1	825	825	+	GenBank
Qy	778	CTCTGA 783					+	GenBank
Db	826	CTCTGA 831					+	GenBank
RESULT 9	AR171647	840 bp	DNA	linear	PAT 17-DEC-2001			
LOCUS	AR171647							
DEFINITION	Sequence 3 from patent US 6297052.							
ACCESSION	AR171647							
VERSION	AR171647.1	GI:17910597						
KEYWORDS								
SOURCE	Unknown.							
ORGANISM	Unknown.							
REFERENCE	1 (bases 1 to 840)							
AUTHORS	Kehry, M. and Castle, B.							
TITLE	B cell culture system comprising high density membrane bound CD40							
JOURNAL	Patent: US 6297052-A 3 02-OCT-2001;							
FEATURES	Location/Qualifiers							
source	1..840							

BASE COUNT	263	a	182	c	181	g	214	t
ORIGIN	/organism="unknown"							
Query Match	92.8%	Score	726.8;	DB	6;	Length	840;	
Best Local Similarity	96.2%;	Pred.	No. 4.9e-171;					
Matches	756;	Conservative	0;	Mismatches	27;	Indels	3;	Gaps
OY	1	ATATGAAACATTCACAACCAACTTCTCCCGCATCTGGGCAGCTGACCTGCCATCAGC	60					
Dd	22	ATATGTGAACATTCACAACCAACTTCTCCCGCATCTGGGCAGCTGACCTGCCATCAGC	81					
OY	61	ATGAAAATTTTATTGTAATTTACTTACTCTGTTTTTTCTTATCACCCAATGATTTGGGTACAGA	120					
Dd	82	ATGAAAATTTTATTGTAATTTACTTACTCTGTTTTTTCTTATCACCCAATGATTTGGGTACAGA	141					
OY	121	CTTTTGCTGTGATCTCTTCATGAAAGATTGGATGAGTAGAAGAGAAAGTAACTTTCAT	180					
Dd	142	CTTTTGCTGTGATCTCTTCATGAAAGATTGGATGAGTAGAAGTAGAAGTAGAAGAAATCTTCAT	201					
OY	181	GAGATTTTGTAATTCATAAAAAAGCTAAAGATGCAACAAAGAGAAAGATCTTTATCC	240					
Dd	202	GAGATTTTGTAATTCATAAAAAAGCTAAAGATGCAACAAAGAGAAAGATCTTTATCC	261					
OY	241	TTCGTGAAGCTGTGAGAGATGAGAAAGCAATTTGAAAGCTTGTCAAGATATACGTTA	300					
Dd	262	TTCGTGAAGCTGTGAGAGATGAGAAAGCAATTTGAAAGCTTGTGTGAAGATATATGTTA	321					
OY	301	AACAAAGAGA--GAAAAAGAAAACGCTTTGAAATGCAAAAAGTGATCAGATCCT	357					
Dd	322	AACAAAGAGAGACGAAAGAAAGAAACGCTTTGAAATGCAAAAAGTGATCAGATCCT	381					
OY	358	CAATATGGCGACATGTCATAGTAGAGCCAGCAGTAAACAAATCTGTGTTACAGTGG	417					
Dd	382	CAATATGGCGACATGTCATAGTAGAGCCAGCAGTAAACAAATCTGTGTTACAGTGG	441					
OY	418	GCTGAAAAAGATCTACACCATGAGCAACACTGGTAAACCCTGSAATAAGSAAACAG	477					
Dd	442	GCTGAAAAAGATCTACACCATGAGCAACAACCTGGTAAACCCTGSAATAAGSAAACAG	501					
OY	478	CTGACCGCTTAAAGAACAGGACTCTATTATATCTGATGCCAAGTCACTCTGTCCAAAT	537					
Dd	502	CTGACCGCTTAAAGAACAGGACTCTATTATATCTGATGCCAAGTCACTCTGTCCAAAT	561					
OY	538	CGGGAAGCTGTGAGTCAAGTCCATTATPACCGAGCTCTGAGCTAAATGCCCGGGTAA	597					
Dd	562	CGGGAAGCTGTGAGTCAAGTCCATTATPACCGAGCTCTGAGCTAAATGCCCGGGTAA	621					
OY	598	TTGAGAGATCTTACTCAGAGCTGCAAAATCCACAGTTCCGCAAACTTTGGGGCAA	657					
Dd	622	TTGAGAGATCTTACTCAGAGCTGCAAAATCCACAGTTCCGCAAACTTTGGGGCAA	681					
OY	658	CAATCCATTCCTGGGAGAGATTTGAATTGCAACGAGGCTTGGGATTTGTCAAT	717					
Dd	682	CAATCCATTCCTGGGAGAGATTTGAATTGCAACGAGGCTTGGGATTTGTCAAT	741					
OY	718	GTCAGTATCCAAAGCAGTAGACGANTGGCACTGGCTTCAAGTCTTTGGCTTAACTCAA	777					
Dd	742	GTCAGTATCCAAAGCAGTAGAGCAGTGGCACTGGCTTCAAGTCTTTGGCTTAACTCAA	801					
OY	778	CTCTGA 783						
Dd	802	CTCTGA 807						
RESULT	10							
LOCUS	123893		840 bp	DNA	linear	PAT	07-OCT-1996	
DEFINITION	Sequence 1 from patent US 5540926.							
ACCESSION	U23893							
VERSION	U23893.1		GI:1603763					
KEYWORDS	Unknown.							
SOURCE								

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 840)

AUTHORS Aniffo, A., Hollenbaugh, D. and Ledbetter, J. A.

TITLE Soluble and its use in B cell stimulation

JOURNAL Patent: US 5540926-A 1 30-JUL-1996;

FEATURES Location/Qualifiers

source 1..840 /organism="unknown"

BASE COUNT 263 a 182 c 181 g 214 t

Query Match 92.8%; Score 726.8; DB 6; Length 840;

Best Local Similarity 96.2%; Pred. No. 4.9e-171;

Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

Qy 1 ATGATCGAAACATACACCAAACTTCTCCCGCATCTGCGGCACTGAGACTGCCATCAGC 60
 Db 22 ATGATCGAAACATACACCAAACTTCTCCCGCATCTGCGGCACTGAGACTGCCATCAGC 81

Qy 61 ATGAAATTTTATGATTTTACTTACTCTGTTTCTTATCACCAGATGATTGGGTACGA 120
 Db 82 ATGAAATTTTATGATTTTACTTACTCTGTTTCTTATCACCAGATGATTGGGTACGA 141

Qy 121 CTTTGTGCTGTATCTTATGATGATTTGATTAAGGTGAGAGAGATTAACCTTCAT 180
 Db 142 CTTTGTGCTGTATCTTATGATGATTTGATTAAGGTGAGAGATTAACCTTCAT 201

Qy 181 GAAGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATG 240
 Db 202 GAAGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATG 261

Qy 241 TTGCTGAACCTGTAGAGAGATGAGAGAGATTTGAAGACTTGTCAAGATATTAAGCTTA 300
 Db 262 TTACTGAACCTGTAGAGAGATTTGAAGACTTGTCAAGATATTAAGCTTA 321

Qy 301 AACAAAGAGA--GAAAAAGAAAAAGCTTTGAAATGCAAAAAGTGATCGAATCTT 357
 Db 322 AACAAAGAGAAG 381

Qy 358 CAAATTTGCGGACATGCTATAGTAGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 417
 Db 382 CAAATTTGCGGACATGCTATAGTAGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 441

Qy 418 GCTGAAAAAGATCTACCATGAGCAAACTTGGTAACTCTGAAATGAGAAACAG 477
 Db 442 GCTGAAAAAGATCTACCATGAGCAAACTTGGTAACTCTGAAATGAGAAACAG 501

Qy 478 CTGACCGTTTAAAG 537
 Db 502 CTGACCGTTTAAAG 561

Qy 538 CCGGAAAGCTTGAAGTCAAGCTCATTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 597
 Db 562 CCGGAAAGCTTGAAGTCAAGCTCATTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 621

Qy 598 TTGAGAGAGATCTTACTCAGAGGTCGAAATACCAAGTTCCGCAAACTTGGGGGCA 657
 Db 622 TTGAGAGAGATCTTACTCAGAGGTCGAAATACCAAGTTCCGCAAACTTGGGGGCA 681

Qy 658 CAATCATTTCACTTGGAGAGATTTGATTTGCAACAGAGTCTTGGGTGTCAT 717
 Db 682 CAATCATTTCACTTGGAGAGATTTGATTTGCAACAGAGTCTTGGGTGTCAT 741

Qy 718 GTGACTGATCCAGAGCAAGTGAGGATGAGCACTGGCTTCAAGCTTGTGGCTTAACCA 777
 Db 742 GTGACTGATCCAGAGCAAGTGAGGATGAGCACTGGCTTCAAGCTTGTGGCTTAACCA 801

Qy 778 CTCTGA 783
 Db 802 CTCTGA 807

RESULT 11

LOCUS 127345

DEFINITION Sequence 7 from patent US 5565321.

ACCESSION 127345

VERSION 127345.1 GI:1818121

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source 1..840 /organism="unknown"

BASE COUNT 266 a 185 c 175 g 214 t

Query Match 92.8%; Score 726.8; DB 6; Length 840;

Best Local Similarity 96.2%; Pred. No. 4.9e-171;

Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

Qy 1 ATGATCGAAACATACACCAAACTTCTCCCGCATCTGCGGCACTGAGACTGCCATCAGC 60
 Db 46 ATGATCGAAACATACACCAAACTTCTCCCGCATCTGCGGCACTGAGACTGCCATCAGC 105

Qy 61 ATGAAATTTTATGATTTTACTTACTCTGTTTCTTATCACCAGATGATTGGGTACGA 120
 Db 106 ATGAAATTTTATGATTTTACTTACTCTGTTTCTTATCACCAGATGATTGGGTACGA 165

Qy 121 CTTTGTGCTGTATCTTATGATGATTTGATTAAGGTGAGAGAGATTAACCTTCAT 180
 Db 166 CTTTGTGCTGTATCTTATGATGATTTGATTAAGGTGAGAGAGATTAACCTTCAT 225

Qy 181 GAAGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATG 240
 Db 226 GAAGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATG 285

Qy 241 TTGCTGAACCTGTAGAGAGATGAGAGAGATTTGAAGACTTGTCAAGATATTAAGCTTA 300
 Db 286 TTACTGAACCTGTAGAGAGATTTGAAGACTTGTGTGAGATATTAAGCTTA 345

Qy 301 AACAAAGAGA--GAAAAAGAAAAAGCTTTGAAATGCAAAAAGTGATCGAATCTT 357
 Db 346 AACAAAG 405

Qy 358 CAAATTTGCGGACATGCTATAGTAGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 417
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Qy 418 GCTGAAAAAGATCTACCATGAGCAAACTTGGTAACTCTGAAATGAGAAACAG 477
 Db 466 GCTGAAAAAGATCTACCATGAGCAAACTTGGTAACTCTGAAATGAGAAACAG 525

Qy 478 CTGACCGTTTAAAG 537
 Db 526 CTGACCGTTTAAAG 585

Qy 538 CCGGAAAGCTTGAAGTCAAGCTCATTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 597
 Db 586 CCGGAAAGCTTGAAGTCAAGCTCATTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 645

Qy 598 TTGAGAGAGATCTTACTCAGAGGTCGAAATACCAAGTTCCGCAAACTTGGGGGCA 657
 Db 646 TTGAGAGAGATCTTACTCAGAGGTCGAAATACCAAGTTCCGCAAACTTGGGGGCA 705

Qy 658 CAATCATTTCACTTGGAGAGATTTGATTTGCAACAGAGTCTTGGGTGTCAT 717
 Db 706 CAATCATTTCACTTGGAGAGATTTGATTTGCAACAGAGTCTTGGGTGTCAT 765

Qy 718 GTGACTGATCCAGAGCAAGTGAGGATGAGCACTGGCTTCAAGCTTGTGGCTTAACCA 777

Db 766 GTGATGATCCAGCCAGTACGACCTGCTTCACTTGGCTTACTCAAA 825
 Qy 778 CTCTGA 783
 Db 826 CTCTGA 831

RESULT 12

167828

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

92.8%; Score 726.8; DB 6; Length 840;

96.2%; Pred. No. 4.9e-171;

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Qy 598 TTGAGAGATCTTACTCAGAGCTGCAATATCCAGATTCCGCGCAAACTTTGGGGCAA 657
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 Qy 658 CAATTCATCTTGGAGAGATTTGATTTGCAACAGAGTCTTGGTGTTCAT 717
 Db 706 CAATTCATCTTGGAGAGATTTGATTTGCAACAGAGTCTTGGTGTTCAT 765
 Qy 718 GTGATGATCCAGCCAGTACGACCTGCTTCACTTGGCTTACTCAAA 777
 Db 766 GTGATGATCCAGCCAGTACGACCTGCTTCACTTGGCTTACTCAAA 825
 Qy 778 CTCTGA 783
 Db 826 CTCTGA 831

RESULT 13

AX090039

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

92.8%; Score 726.8; DB 6; Length 879;

96.2%; Pred. No. 4.9e-171;

0; Mismatches 27; Indels 3; Gaps 1;

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Db	502	CTGACCGCTTTAAAGACAAAGACTGTATTATCTATTCCTCCAGTACCTCTCTTCAT	561
Oy	538	CGGGAAGCTTCGAGTCAGCTCATTATTAAGCCAGCTCTGCCTTAAGTCCCAGGTAGA	597
Db	562	CGGGAAGCTTCGAGTCAGCTCATTATTAAGCCAGCTCTGCCTTAAGTCCCAGGTAGA	621
Oy	598	TTCGAGAACATCTTACTCGAGAGCTGGCAATAFACCAGAGTTCCGCCAAAACCTTSCGAGCAA	657
Db	622	TTCGAGAACATCTTACTCGAGAGCTGGCAATAFACCAGAGTTCCGCCAAAACCTTSCGAGCAA	681
Oy	658	CAATCATCTTACCTGGAGAGAGATTTTGATTTGCAACAGAGTGCTTCGGTGTGTTCAT	717
Db	682	CAATCATCTTACCTGGAGAGAGATTTTGATTTGCAACAGAGTGCTTCGGTGTGTTCAT	741
Oy	718	GTGACGTGATCCAGCCAGTAGAGCATGTGACCTGAGCTTCACGCTCTTGACTTACTCAAA	777
Db	742	GTGACGTGATCCAGCCAGTAGAGCATGTGACCTGAGCTTCACGCTCTTGACTTACTCAAA	801
Oy	778	CTCTCA 783	
Db	802	CTCTCA 807	
RESULT 14			
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LOCUS			
DEFINITION	H.sapiens mRNA for glycoprotein 39 (gp39).		
ACCESSION	Z15017 S49392		
VERSION	Z15017.1 GI:38483		
KEYWORDS	glycoprotein 39.		
SOURCE	Homo sapiens.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
	1 (bases 1 to 879)		
	Hollenbaugh,D., Grosmaire,L.S., Kullas,C.D., Chalupny,N.J.,		
	Braesch-Anderson,S., Noelle,R.U., Stamenkovic,I., Ledbetter,J.A.		
	and Anuff,A.		
	The human T cell antigen gp39, a member of the TNF gene family, is		
	a ligand for the CD40 receptor: expression of a soluble form of		
	gp39 with B cell co-stimulatory activity		
	EMBO J. 11 (12), 4313-4321 (1992)		
TITLE			
JOURNAL			
AUTHORS			
TITLE			
JOURNAL			
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AUTHORS			
TITLE			
JOURNAL			
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Mismatches	27							
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DB	82	ATGAAATTTTATGTATTTACTTAACTGTCTTTTCTTATCAACCCAGATGATGGGTCA	141					
OR	121	CTTTTCTCTGTATCTTCAATAGAAATTTGATGAAAGAGAAAGTAAACCTTCAT	180					
DB	142	CTTTTCTCTGTATCTTCAATAGAGTTTGAACAAATGAAAGTAAAGAAATTTTCAT	201					
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DB	322	AACAAAGAAACAAAGCTTTGAAATGCAAAAGGTGATCAAGATCT	381					
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DB	382	CAATTCGCGCACTGTCTATTAAGTAGGCGCAGTAACAAACATCTGTTCACATGG	441					
OR	418	GCTGAAAGATTAATCAACATGAGCAACAACTGTGAACCTGGAATTTGGAAACAG	477					
DB	442	GCTGAAAGATTAATCAACATGAGCAACAACTGTGAACCTGGAATTTGGAAACAG	501					
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OR	538	CGGGAAGCTTCAGATCAAGCTTCATTTATACCAAGCTCTGCTTAAGTCCCCCGTAGA	597					
DB	562	CGGGAAGCTTCAGATCAAGCTTCATTTATACCAAGCTCTGCTTAAGTCCCCCGTAGA	621					
OR	598	TTTCAGAGGATCTTCACTCAGAGTGAATAACCAAGTCCGCGCAACCTTGGCGGCA	657					
DB	622	TTTCAGAGGATCTTCACTCAGAGTGAATAACCAAGTCCGCGCAACCTTGGCGGCA	681					
OR	658	CAATTCATTCATCTTGGAGAGATTTGAATTGAATTCACCAAGTCTTGGTGTTCAT	717					
DB	682	CAATTCATTCATCTTGGAGAGATTTGAATTGAATTCACCAAGTCTTGGTGTTCAT	741					
OR	718	GTGACATATCAAGCAAGTGAACCATGGAATCTTCAAGTCTTGGCTTATCTCAAA	777					
DB	742	GTGACATATCAAGCAAGTGAACCATGGAATCTTGGCTTATCTCAAA	801					
OR	778	CTTCGA	793					
DB	802	CTTCGA	807					
RESULT 15								
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LOCUS	HSCD40	1803 bp	mrna	linear	PRI 06-JUN-1997			
DEFINITION	H.sapiens mRNA for CD40 ligand.							
ACCESSION	X67878	S05086						
VERSION	X67878.1	GI:38411						

KEYWORDS glycoprotein.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS Spriggs, M.
TITLE Direct Submersion
JOURNAL Submitted (28-JUN-1992) M. Spriggs, Immunex Res & Development
Corporation, 51 University Street, Seattle WA 98101, USA
2 (bases 1 to 1803)
AUTHORS Spriggs, M.K., Armitage, R.J., Strockbine, L., Clifford, K.N.,
Macduff, B.W., Sato, T.A., Maliszewski, C.R., and Fanslow, W.C.
TITLE Recombinant human CD40 ligand stimulates B cell proliferation and
immunoglobulin E secretion
JOURNAL J. Exp. Med. 176 (6), 1543-1550 (1992)
MEDLINE 93094757
PubMed 1281209

FEATURES
source Location/Qualifiers
1..1803
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/db_xref="taxon:9606"
/cell_type="peripheral blood T-cell"
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/db_xref="UniProt: P29965"
/translation="MIEYNTSPSPSAATGLPSMKIEMYLITVPLITOMIGSALPAV
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112..183
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BASE COUNT 510 a 456 c 344 g 493 t
ORIGIN

Query Match 92.8%; Score 726.8; DB 9; Length 1803;
Best Local Similarity 96.2%; Pred. No. 4.7e-171;
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

QY 1 ATGATCGAAACATACACAACTTCCCGATCGGCGCCACTGAGATCGCCCATCAGC 60
DB 46 ATGATCGAAACATACACAACTTCCCGATCGGCGCCACTGAGATCGCCCATCAGC 105
QY 61 ATGAAATTTTATGATTACTTACTGTTTCTTATCACCAGATGATGGGTACGA 120
DB 106 ATGAAATTTTATGATTACTTACTGTTTCTTATCACCAGATGATGGGTACGA 165
QY 121 CTTTGTGCTGATCTTATGATGAAGATGATGAAGTGAAGAGAAATTAACCTCAT 180
DB 166 CTTTGTGCTGATCTTATGATGAAGATGATGAAGTGAAGAGAAATTAACCTCAT 225
QY 181 GAAGATTTTGTATCTATTAAGAAAGCTAAGATGCAACAAAGAGAGATCTTATCC 240
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QY 241 TTGCTGAACGTGAGAGATGAGAAAGCAATTTGAAGACTTGTCAAGGATATTAAGTTA 300
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QY 301 AACAAAG 357
DB 346 AACAAAG 405
QY 358 CAAATGGGCAATGATCATAGTAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 417
DB 406 CAAATGGGCAATGATCATAGTAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 465
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DB 466 GCTGAAAAGAGATCTACACATGAGCAACACTTGTAACTTGAAATGGGAAACAG 525
QY 478 CTGACCGTTAAAG 537
DB 526 CTGACCGTTAAAG 585
QY 538 CGGAAAGCTTGCAGTCAAGCTCCATTATATAGCCAGCTTGCCTTAAGTCCCGGTAGA 597
DB 586 CGGAAAGCTTGCAGTCAAGCTCCATTATATAGCCAGCTTGCCTTAAGTCCCGGTAGA 645
QY 598 TTGAGAGATCTTACTCAGAGTGAATATCCAGAGTTCGCGCAAACTTGAGGAGCA 657
DB 646 TTGAGAGATCTTACTCAGAGTGAATATCCAGAGTTCGCGCAAACTTGAGGAGCA 705
QY 658 CAATCCATTCACCTTGGAGAGAGATTTGAATTGCAACCAAGTGTCTTGCTTTGTCAAT 717
DB 706 CAATCCATTCACCTTGGAGAGAGATTTGAATTGCAACCAAGTGTCTTGCTTTGTCAAT 765
QY 718 GTGACTGATCCAGAGCAAGTGAAGCACTGAGCTTCAAGTCTTGGCTTACTCAAA 777
DB 766 GTGACTGATCCAGAGCAAGTGAAGCACTGAGCTTCAAGTCTTGGCTTACTCAAA 825
QY 778 CTCTGA 783
DB 826 CTCTGA 831

Search completed: March 9, 2003, 02:11:41
Job time: 2043.79 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 8, 2003, 21:32:03 ; Search time 1286.6 Seconds
(without alignments)
9856.249 Million cell updates/sec

Title: US-08-982-272-20
Perfect score: 783
Sequence: 1 ATGATGAACATCAACCA.....TTGGCTTACTCAACTCTGA 783

Scoring table: IDENTITY NUC
Gapop 10_0, Gapext 1_0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST.*
1: em_estda.*
2: em_esthnm.*
3: em_estin.*
4: em_estnu.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_hic.*
9: gb_est1.*
10: gb_est2.*
11: gb_hic.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estom.*
16: em_estom.*
17: gb_gss.*
18: em_gss_hum.*
19: em_gss_inv.*
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21: em_gss_vit.*
22: em_gss_fun.*
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25: em_gss_other.*
26: em_gss_pro.*
27: em_gss_rod.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	256.4	32.7	398	10	AM486605 75217 MAR
3	69.6	8.9	638	9	AI982044 pat.p007
4	54	6.9	797	9	AL534423 AL534423
5	52	6.6	1101	17	CNS0039G
6	51.4	6.6	1043	17	CNS0145P

Result No.	Score	Match	Length	ID	Description
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9	47.8	6.1	807	17	CNS0119V
10	47.4	6.1	799	17	CNS011SA
11	46.8	6.0	458	9	AL514085
12	46.4	5.9	1064	17	CNS015HX
13	46.2	5.9	858	17	CNS0127J
14	46	5.9	1101	17	CNS0181N
15	45.8	5.8	329	9	AL513719
16	45.8	5.8	529	9	AL514657
17	45.8	5.8	597	9	AL514721
18	45.6	5.8	974	17	CNS001TT
19	45.4	5.8	1084	17	CNS021NO
20	45.2	5.8	458	9	AL514085
21	45.2	5.8	559	17	AQ373239
22	45.2	5.7	633	9	AL513979
23	45	5.7	878	17	CNS0187R
24	44.6	5.7	534	17	CNS030HB
25	44.4	5.7	814	17	AZ203738
26	44.4	5.7	828	17	CNS011TX
27	44.2	5.6	805	9	AL557564
28	44.2	5.6	959	17	CNS00655
29	44	5.6	802	17	CNS0383B
30	43.8	5.6	330	9	AL513817
31	43.8	5.6	901	17	CNS020N3
32	43.8	5.6	1099	17	CNS06PYL
33	43.6	5.6	588	17	AQ515757
34	43.6	5.6	629	17	CNS048YV
35	43.6	5.6	920	17	AZ691914
36	43.6	5.6	926	17	CNS006YV
37	43.4	5.5	542	17	AZ045586
38	43.4	5.5	596	13	B158745
39	43.4	5.5	625	17	CNS036A2
40	43.4	5.5	899	17	CNS0006P
41	43.4	5.5	955	17	BH136744
42	43.2	5.5	644	17	AG134982
43	43	5.5	277	17	CNS000FP
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ALIGNMENTS

RESULT 1
LOCUS BF599437 492 bp mRNA linear EST 25-APR-2001
DEFINITION 263218 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BF599437
VERSION BF599437.1 GI:11695919
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.

REFERENCE
AUTHORS Smith,T.P.L., Grose,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Caeas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,G.L., Heaton,W.F., Laegreid,W.M., Kohrer,G.A., Chitko-Wckom,C.G., Pettes,G., Holt,I., Karayancheva,S., Liang,F., Quackenbush,J. and Keefe,J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)

TITLE
JOURNAL MEDLINE
COMMENT
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

REFERENCE

AUTHORS

1 (bases 1 to 638)
Irimagaru, V.G., Sofer, L., Chi, J. and Burnside, J.

TITLE

An expressed sequence tag database of T-cell-enriched activated chicken splenocytes: sequence analysis of 5251 clones

JOURNAL

Genomics, 66 (2), 144-151 (2000)

MEDLINE

20318616

COMMENT

Contact: Joan Burnside
Molecular Endocrinology
University of Delaware
40 Townsend Hall, Newark, DE 19717, USA
Tel: 302 831-1345
Fax: 302-831-3411
Email: joan@udel.edu, www.chickest.udel.edu

FEATURES

location/Qualifiers
1..638
/organism="Gallus gallus"
/db_xref="taxon:9031"
/clone="pat:pk0072.c9.f"
/clone_1ib="chicken activated T cell cDNA"
/sex="male"
/cell_type="Con A-activated splenic T cell"
/lab_host="E.coli TOP10 F"
/note="Vector: pCDNA3"

BASE COUNT 132 a 171 c 151 g 180 t 4 others
ORIGIN

Query Match

Best Local Similarity 8.9%; Score 69.6; DB 9; Length 638;
Best Local Similarity 57.6%; Pred. No. 6.7e-05;

Matches 167; Conservative 0; Mismatches 114; Indels 9; Gaps 2;

495 AGGACCTATTATATCTATGAGCCCAAGTCACTTCTGTCACATCGGGAAGCTTCAGATCA 554
Db 2 AGGGCTTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 56
555 AGCTCATTATTAAGCCAGCTCTGCTTAAGTCCCGGAGATTCGAGAGATCTTACT 614
Db 57 -GGCCATTACACCTCTATATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 115
615 CAGAGCTGCAATATCCAGAGCTTCGCGCAACCT---TGGGGCAAGCATCATCACTT 671
Db 116 GAGGAGCTTGAACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 175
672 GGGAGAGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 731
Db 176 GGGCGGTCTTCGAGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 235
732 CCAAGTGAAGCATGAGCATGAGCTTCGCTTCTTGGCTTCACTCAACTCT 781
Db 236 AGCAGTGAACGTCACCTTGGCAACCTTCTTGGCTTCACTCAACTCT 285

RESULT 4

AL534423 797 bp mRNA linear EST 13-FEB-2001

LOCUS

AL534423 LTI_Fl013_Fbml Homo sapiens cDNA clone CS0DP004YD24 5

DEFINITION

prime, mRNA sequence.

ACCESSION

AL534423

VERSION

AL534423.1 GI:12797916

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

AUTHORS

Li, M.B., Gruber, C., Jessee, J. and Polyes, D.

TITLE

Full-length cDNA libraries and normalization

JOURNAL

Unpublished (2001)

COMMENT

Genoscope - Centre National de Sequencage

BP 191 91006 Evry cedex - France
Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES

source

1..797
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DP004YD24"
/clone_1ib="LTI_Fl013_Fbml"
/dev_stage="pooled tissue from post conception fetuses (20 week, 24 week and 26 week)"
/lab_host="DH10B"

/note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dt) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 407 a 43 c 120 g 152 t 75 others
ORIGIN

Query Match

Best Local Similarity 6.9%; Score 54; DB 9; Length 797;
Best Local Similarity 39.3%; Pred. No. 0.13;

Matches 168; Conservative 35; Mismatches 225; Indels 0; Gaps 0;

140 ATGAGATTTGATTAAGTTCGAGAGAGAGTAACTTCATGAAATTTGATTCATTA 199
Db 240 AGAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 299
200 AAAAGCTTAAGATGCAACAAGAGAGAGATCTTCTCTGTAACCTGTGAGAGA 259
Db 300 AGGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 359
260 TGAAGAGCAATTTGAGACCTCTGCAAGATTTAACTTAAACAAGAGAGAGAGAG 319
Db 360 TGTAAAG 419
320 AAAACAGCTTGAATATGCAAAAAGATGATGATGATGATGATGATGATGATGATGAT 379
Db 420 AAAAAGATTAAG 479
380 GTGAGGACGACGATTAACACATCTGTGTACAGTGGCTGAGAGAGATCTACCA 439
Db 480 AAGGATTAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 539
440 TGAGCAACAATTTGATTAACCTTGAATATGCAACAAGATGATGATGATGATGATGAT 499
Db 540 TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 599
500 TCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 559
Db 600 TTTATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 659
560 CATTTATA 567
Db 660 TTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 667

RESULT 5

CNS0039G/c 1101 bp DNA linear GSS 03-JUN-1999

LOCUS

CNS0039G Drosophila melanogaster genome survey sequence TE13 end of BAC #

DEFINITION

BACR08X10 of RPI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION

AL063921

VERSION

AL063921.1 GI:4941778

KEYWORDS

GSS.

SOURCE

Drosophila melanogaster.

ORGANISM

Drosophila melanogaster

REFERENCE

Eukaryota; Metazoa; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 889)

REFERENCE

Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

COMMENT

Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org> The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mamoser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCL-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
p1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

source
1. 889
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="BACR1409"
/clone_1b="RPCL-98"
/note="end : TET3"
BASE COUNT 307 a 36 c 68 g 252 t 226 others
ORIGIN

Query Match 6.5%; Score 50.8; DB 17; Length 889;
Best Local Similarity 33.9%; Pred. No. 0.58; Indels 1; Gaps 1;
Matches 155; Conservative 73; Mismatches 228; Indels 1; Gaps 1;

QY 68 TTTTATGTAATTAAGTCTGTTTCTTATGACCGAGATGATGGTGCACCTTTTG 127
DB 272 TTTTATGTAATTAAGTCTGTTTCTTATGACCGAGATGATGGTGCACCTTTTG 127
QY 128 CTGTGATCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 187
DB 332 WAKTKRRRDAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 391
QY 188 TTGTATTCATTAATAAGTAAAGATGACCAAGAAAGAAATCTTATCTTGTCTGA 247
DB 392 GAGGAGAAKAAWAAWTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 451
QY 248 ACTGTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 306
DB 452 GAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 511
QY 307 GAAAGAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 366
DB 512 TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 571
QY 367 GCATGATCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 426
DB 572 AACAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 631
QY 427 GGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 486
DB 632 RSRAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 691
QY 487 AAAAGCAAGACTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 523
DB 692 RASACSTWGAATAATTTTAAAGCTWGA 728

RESULT 8
CNS005TE/c 997 bp DNA linear GSS 03-JUN-1999
LOCUS

DEFINITION
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR12K22 of RPCL-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
A060767.1 GI:4943573
GSS.
Drosophila melanogaster.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE
AUTHORS
TITLES
JOURNAL
Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

COMMENT

Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org> The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mamoser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCL-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
p1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

source
1. 997
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="BACR12K22"
/clone_1b="RPCL-98"
/note="end : TET3"
BASE COUNT 89 a 99 c 13 g 258 t 538 others
ORIGIN

Query Match 6.4%; Score 50.2; DB 17; Length 997;
Best Local Similarity 18.1%; Pred. No. 0.75;
Matches 64; Conservative 133; Mismatches 156; Indels 0; Gaps 0;

QY 140 ATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 199
DB 881 ARARARRRRRAARARARRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 822
QY 200 AAAAGCTTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 259
DB 821 RAGAAARRRRRRAARARARRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 762
QY 260 TGAAGGCAATTTGAAGACCTTCTCAAGATTAAGTAAACAAATAAGAAAAAG 319
DB 761 ARARARRRRRAARARARRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 702
QY 320 AAAAGCTTTGAATGCAAAAGTGAATGCAATGCAATGCAATGCAATGCAATGCA 379
DB 701 GAGARR 642
QY 380 GTAGCCGACGATTAACCACTCTGTTTACAGTGGGTGAAAAAGATTAACCA 439
DB 641 RRARARR 582
QY 440 TGAGCAACAATCTGTAACCTGTAATGGAATGGAATGGAATGGAATGGAATGGA 492
DB 581 GAGARRRRRRRRRAARARARRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 529

RESULT 9
CNS0119V

LOCUS CNS0119V 807 bp DNA linear GSS 26-JUL-1999
 DEFINITION Drosophila melanogaster genome survey sequence T7 end of BAC
 BACN05C05 of DrosBAC library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.
 ACCESSION AL039997
 VERSION AL039997.1 GI:5611608
 KEYWORDS GSS.
 SOURCE Drosophila melanogaster.
 ORGANISM Drosophila melanogaster.
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 REFERENCE Genoscope.
 1 (bases 1 to 807)
 AUTHORS Direct Submission
 TITLE Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
 JOURNAL - Web : www.genoscope.cns.fr)
 COMMENT Determination of this BAC-end sequence was carried out as part of a
 collaboration with the European Drosophila Genome Project (EDGP) -
 http://www.edgp.ebi.ac.uk. This Drosophila melanogaster BAC
 library (Dros BAC) was made by Alain Billard at CEPH (Centre
 d'Etude du Polymorphisme Humain) with funding provided by a MRC
 project grant. The DNA was prepared from embryos by Alain Bucheton
 and Genevieve Payan. It has been constructed in the vector
 pBelobAC11.

FEATURES
 source
 1..807
 /organism="Drosophila melanogaster"
 /db_xref="taxon:7227"
 /clone_id="BACN05C05"
 /clone_1lb="DrosBAC"
 /plasmid="pBelobAC11"
 /note="end : 77"

BASE COUNT 157 a 38 c 17 g 287 t 308 others
 ORIGIN

Query Match 6.1%; Score 48; DB 17; Length 807;
 Best Local Similarity 27.1%; Pred. No. 2.3;
 Matches 117; Conservative 88; Mismatches 227; Indels 0; Gaps 0;

QY 68 TTTTATGATTTACTGATGTTTCTTATCACCAGATGATGGTCAAGCACTTTTG 127
 |||||
 Db 315 TTTTATGATTTACTGATGTTTCTTATCACCAGATGATGGTCAAGCACTTTTG 127
 |||||
 QY 128 CTGTGATCTTCATAGAAAGTTGATAGTGCAGAGAGAACTTATGATGAAATT 187
 |||||
 Db 375 NNNTNNNTTTTATTTATTTATTAAGAAACNAAGNNTGNNNTTNNNNNTNNN 434
 |||||
 QY 188 TTGTATTCATTAAGCTAAAGATGCAACAAGAGAGATCTTATCCCTGCTGA 247
 |||||
 Db 435 NTNNNTTNNNTTTTCCSCRSACACASSGMCASGCGTGVMSVAMGMSAVTAMAS 494
 |||||
 QY 248 ACTGTGAGAGATGAGCAATTTGAAGACCTTGTCAAGATTTAACTTAAACAAG 307
 |||||
 Db 495 MSARMAAIVAVARRARASAGSVSAVASVSVSSVSAASAAVAASAAASAAVA 554
 |||||
 QY 308 AAGAGAAAAAGAAAACAGCTTGAATGCAAAAAGTATGAGATCCCAATTTGCG 367
 |||||
 Db 555 AAAAAAATAAAAAAAMCMAAIVMTACMCMAACMMCVAVSAAHAAVAASASAM 614
 |||||
 QY 368 CACATGTATAGTGAAGCCAGACATTAACAATCTGTGTACAGTGGCTGAAAAAG 427
 |||||
 Db 615 AAVAVASAA 674
 |||||
 QY 428 GATACCTACCATGAGCAACAATCTGTAACCTGGAATAAGGAAACAGCTGACGTTA 487
 |||||
 Db 675 MACACVMSMCAAC 734
 |||||
 QY 488 AAGACAAAGAC 499
 |||||
 Db 735 HBMVTSMSAV 746

RESULT 10
 LOCUS CNS011SA
 DEFINITION Drosophila melanogaster genome survey sequence T7 end of BAC
 BACN06A03 of DrosBAC library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.
 ACCESSION AL100660
 VERSION AL100660.1 GI:5612271
 KEYWORDS GSS.
 SOURCE Drosophila melanogaster.
 ORGANISM Drosophila melanogaster.
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 REFERENCE Genoscope.
 1 (bases 1 to 799)
 AUTHORS Direct Submission
 TITLE Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
 JOURNAL - Web : www.genoscope.cns.fr)
 COMMENT Determination of this BAC-end sequence was carried out as part of a
 collaboration with the European Drosophila Genome Project (EDGP) -
 http://www.edgp.ebi.ac.uk. This Drosophila melanogaster BAC
 library (Dros BAC) was made by Alain Billard at CEPH (Centre
 d'Etude du Polymorphisme Humain) with funding provided by a MRC
 project grant. The DNA was prepared from embryos by Alain Bucheton
 and Genevieve Payan. It has been constructed in the vector
 pBelobAC11.

FEATURES
 source
 1..799
 /organism="Drosophila melanogaster"
 /db_xref="taxon:7227"
 /clone_id="BACN06A03"
 /clone_1lb="DrosBAC"
 /plasmid="pBelobAC11"
 /note="end : 77"

BASE COUNT 333 a 123 c 104 g 140 t 99 others
 ORIGIN

Query Match 6.1%; Score 47.4; DB 17; Length 799;
 Best Local Similarity 35.9%; Pred. No. 3.1;
 Matches 139; Conservative 48; Mismatches 200; Indels 0; Gaps 0;

QY 140 ATGAGATTTGATTAAGTTCGAGAGAGATTAACCTTCATGAGATTTTATTCATTA 199
 |||||
 Db 13 AAGAGAGAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 72
 |||||
 QY 200 AAAAGCTAAAGATGCAACAAGAGAGATCTTATCCTGCTGAACCTGTGAGAGA 259
 |||||
 Db 73 AATATMCAAMMAATMCAAMMAAATAAAGGAAAAAAMMAAATAATATATAMADA 132
 |||||
 QY 260 TGAGAGCAATTTGAGACCTTGTCAAGATTAATCACTTAACAAGAGAAAAAG 319
 |||||
 Db 133 AATATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 192
 |||||
 QY 320 AAAAGCTTGAATGCAAAAAGTATGCAAAAAGTATGCAAAAAGTATGCAAAAAG 379
 |||||
 Db 193 AAAAAAAMCAAGAAATTAATAAAGCAAAAAAATAAAGAAACAAATTAATAAATAA 252
 |||||
 QY 380 GTGAGCCAGCAGTAAAAACAATCTGTGTAACATGAGGCTGAAAAAGATCTACCA 439
 |||||
 Db 253 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 312
 |||||
 QY 440 TGAACCAACAATCTGTGTAACCTGGAATAAGGAAACAGCTGACCTTAAGAACAAGAC 499
 |||||
 Db 313 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 372
 |||||
 QY 500 TCTATTATATCTATGCCCAAGTCACT 526
 |||||
 Db 373 AAAAAAATAAACAAGGAAMCRAT 399

RESULT 11	
AL514085/c	458 bp mRNA linear EST 13-FEB-2001
LOCUS	
DEFINITION	AL514085 LTR1 NPL06_P12 Homo sapiens cDNA clone CLOBM04ZE10 3
ACCESSION	AL514085
VERSION	AL514085
KEYWORDS	AL514085.1 GI:1277579
SOURCE	EST.
ORGANISM	human.
	Homo sapiens

FEATURES	location/qualifiers
source	1. .458

BASE COUNT	186 a	13 c	3 g	207 t	49 others
ORIGIN					

RESULT 12	
CNS015HX/C	
LOCUS	
DEFINITION	CNS015HX 1064 bp DNA linear GSS 26-JUL-1999
ACCESSION	BCMN14C18 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
VERSION	AI105471.1 GI:5617485

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

GSS.
Drosophila melanogaster.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Prexygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephyroidae; Drosophilidae; Drosophila.
1 (bases 1 to 1064)
Genoscope.
Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 131 91006 EVRY cedex - FRANCE [E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
<http://www.edgp.ebi.ac.uk> -. This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billard at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
peloDBAC11.

BASE COUNT	262 a	216 c	154 g	263 t	169 others
ORIGIN					

RESULT 13	
CNS0127J	
LOCUS	CNS0127J
DEFINITION	CNS0127J 858 bp DNA linear GSS 26-JUL-1999
ACCESSION	Drosophila melanogaster genome survey sequence T7 end of BAC
VERSION	BACN0707 of DrosBAC library from Drosophila melanogaster (fruit
KEYWORDS	fly), genomic survey sequence.
SOURCE	AL101209
ORGANISM	AL101209.1 GI:56128920
REFERENCE	GSS.
AUTHORS	Drosophila melanogaster.
TITLE	Drosophila melanogaster.
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
	Ephyroidae; Drosophilidae; Drosophila.
	1 (bases 1 to 858)
	Genoscope.
	Direct Submission

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

FEATURES Email: sequef@genoscope.cns.fr, Web: www.genoscope.cns.fr.
Location/Qualifiers
source 1. .329

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CLOBA0072H01"
/clone_1ib="LTI_NPL006_PL2"
/issue_type="Placenta"
/note="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com"

BASE COUNT 186 a 13 c 3 g 60 t 67 others
ORIGIN

Query Match 5.8%; Score 45.8; DB 9; Length 329;
Best Local Similarity 36.1%; Pred. No. 9.1;
Matches 105; Conservative 44; Mismatches 142; Indels 0; Gaps 0;

```
Qy 68 TTTTATGATTACTTACTGTTTCTTATCCACCGATGATGGTCAGACCTTTTG 127
Db 9 TTTTATGATTACTTACTGTTTCTTATCCACCGATGATGGTCAGACCTTTTG 68
Qy 128 CTGTGATCTTCATAGAGATGATGATGATGATGATGATGATGATGATGATGAT 187
Db 69 WWWWWWMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMM 128
Qy 188 TTGTATTCATTAAGCTTAAGAGATGACCAAGAGAGAGATCTTATCTTGCTGA 247
Db 129 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 188
Qy 248 ACTGTGAGAGATGAGAGCAATTGAAACCTGTCAAGATATAAGTTAAACAAG 307
Db 189 MAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 248
Qy 308 AAGAGAAAAAAGAAACAGCTTGAATGCAAAAGGTGATCGAATCCTG 358
Db 249 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAMCCCC 299
```

Search completed: March 9, 2003, 04:42:33
Job time: 1292.6 secs

10

PT Vectors containing accessory molecule ligand genes - used for altering immunoreactivity of cells, particularly for treatment of neoplasia or autoimmune disorders, e.g. rheumatoid arthritis

PS Disclosure, Page 116, 167pp; English.

The present sequence represents an exemplary nucleotide sequence, where nucleotides encoding human domain III have been replaced with nucleotide encoding mouse domain III. The sequence is used to exemplify the method of the invention. The specification describes a method for altering the immunoreactivity of human cells which comprises introducing a gene encoding an accessory molecule ligand (AML) into the cells so that the AML is expressed on the surface of the cells. Vectors containing the AML genes can be used in gene therapy for treating neoplasia or autoimmune disorders such as rheumatoid arthritis. The gene can also be used for vaccination to produce immunity against a virus cell, bacteria, protein, fungus or neoplasia.

Query Match	100.0%	Score 783;	DB 19;	Length 783;
Best Local Similarity	100.0%	Pred. No. 9.2e-207;		
Matches 783; Conservative	0;	Mismatches	0;	Indels 0;
				Gaps 0

Qy	1	ATGATCGAAACATCAACAAACCTTCCCGCATCTGCGGCACTGACATCGCATACGC	60
Db	1	ATGATCGAAACATCAACAAACCTTCCCGCATCTGCGGCACTGACATCGCATACGC	60
Qy	61	ATGATAAGAAACATCAACAAACCTTCCCGCATCTGCGGCACTGACATCGCATACGC	60
Db	61	ATGATAAGAAACATCAACAAACCTTCCCGCATCTGCGGCACTGACATCGCATACGC	60
Qy	121	CTTTTTCGTGTATCTCTAATGAAAGATTGGATAGGTGAAAGAGAAATTAACCTTCAT	180
Db	121	CTTTTTCGTGTATCTCTAATGAAAGATTGGATAGGTGAAAGAGAAATTAACCTTCAT	180
Qy	181	GAAAGATTTTGATTCATATTAATAAGGATGCAACAAAGAGAAAGATCTTTATCC	240
Db	181	GAAAGATTTTGATTCATATTAATAAGGATGCAACAAAGAGAAAGATCTTTATCC	240
Qy	241	TTGCTGAACTGTGAGGAGATGGAAGGCAATTTGAAGACTTTGCAAGATATTAAGTTA	300
Db	241	TTGCTGAACTGTGAGGAGATGGAAGGCAATTTGAAGACTTTGCAAGATATTAAGTTA	300
Qy	301	AAACAAGAGAGAAAAAGAAAAACGCTTTGAAATGCAAAAAAGGTGATCAGATCCTCA	360
Db	301	AAACAAGAGAGAAAAAGAAAAACGCTTTGAAATGCAAAAAAGGTGATCAGATCCTCA	360
Qy	361	ATTGGGCGACATGTCAATAGTGGGCGAGGAGTAAACAACTGTGTACAGTGGGCT	420
Db	361	ATTGGGCGACATGTCAATAGTGGGCGAGGAGTAAACAACTGTGTACAGTGGGCT	420
Qy	421	GAAAAAGATCTACACTGAGCAACACTTGTAACCTTGAAAAATGAGAAACAAGTGG	480
Db	421	GAAAAAGATCTACACTGAGCAACACTTGTAACCTTGAAAAATGAGAAACAAGTGG	480
Qy	481	ACCGTTAAAAACAAGGACTCTAATATATCTAATGAGCCCAAGTCACTTGTTCGAATCGG	540
Db	481	ACCGTTAAAAACAAGGACTCTAATATATCTAATGAGCCCAAGTCACTTGTTCGAATCGG	540
Qy	541	GAGCTTGAGTCAAGCTCAATTAATAGCAAGCTGTGCTTAAAGTCCCGGTGATTC	600
Db	541	GAGCTTGAGTCAAGCTCAATTAATAGCAAGCTGTGCTTAAAGTCCCGGTGATTC	600
Qy	601	GAGAGAAATCTTACTCGAGACTGCAATTAACCAACAGTTCCGCGCAAACTTTGCGGGCAACA	660
Db	601	GAGAGAAATCTTACTCGAGACTGCAATTAACCAACAGTTCCGCGCAAACTTTGCGGGCAACA	660
Qy	661	TTCATTCACTTGGGAGAGATTTTGAATGCAACAAGGCTGTGGGTGTTGCAATGTG	720
Db	661	TTCATTCACTTGGGAGAGATTTTGAATGCAACAAGGCTGTGGGTGTTGCAATGTG	720
Qy	721	ACTGATCCAGCCAGTGAAGCATTGAGCTTCAAGTCTTTGCTTACTCAAACTC	780
Db	721	ACTGATCCAGCCAGTGAAGCATTGAGCTTCAAGTCTTTGCTTACTCAAACTC	780

D_b 721 ACTGATCCAGCCAGTAGCCATGGCACTGGCTTACGCTCTTGGCTTACTCAAACTC 780
Q_y 781 TGA 783	
D_b 781 TGA 783

RESULT 2
AAQ63959
ID AAQ63959 standard; cDNA to mRNA; 786 BP.

DT	11-JAN-1995 (first entry)
XX	
DE	Human CD40-L type II transmembrane protein coding sequence

KM Leucine zipper; trimerisation; trimeric CD40-L; fusion protein
KM hetero-oligomer; homo-oligomer; type II transmembrane protein;
KM soluble CD40-L; tumour necrosis factor family; ss.

OS Homo sapiens.
yy

Key	Location/Qualifiers
CD5	1..786
FT	/+tag= a
FT	/product= human CD40-L
FT	/note= "nucleotides 148-783 code for the extracellular region (amino acids 50-261) "
FT	

PN W09410308-A.
XX

PD 11-MAY-1994
XX

XX 20-001-1995; 33MC-0310034-
 EF
 XX

PR 13-AUG-1993; 93US-0107353.

PA (IMMV) IMMUNEX CORP.
XX

P1 spriggs mk, srinivasan s;
 XX

DR P-PSDB; AAR53969.

PT Prepn. of soluble oil
PT cells to express a f

PT domain and a heterol

FS Example 1: Page 44-45! copy! English.

CD40-L was ligated to a synthetic oligo-

CC (AAS33968) and the Plag (RTM) linker sequence. Cells expressing the
CC fusion constructs are grown to accumulate oligomeric, soluble Cb40-L
CC in the supernatant. The leucine zipper sequence spontaneously
CC trimerises in solution and fusion proteins comprising
CC the sequence fused to a heterologous mammalian protein also form
CC oligomers.

SQ Sequence 786 BP; 250 A; 168 C; 168 G; 200 T; 0 other;

Query Match	92.8%	Score 726.8;	DB 15;	Length 786;
Best Local Similarity	96.2%;	Pred. No. 3.4e-19;		
Matches 756; Conservative	0;	Mismatches 27;	Indels 3;	Gaps 1

Oy

1 ATGATGAACACTACAACCACCTTCTCCCGATCTGGGGCACTGAGTCGCCCATCAGC 60

Dδ

1 ATGATGGAACACTACAACCACCTTCTCCCGATCTGGGGCACTGAGTCGCCCATCAGC 60

Qy	61	ATGAAATATTTTATGATTAATTCTACGTTTTTTCTATACCCAGATGATGGTCACA	120
Db	61	ATGAAATATTTTATGATTAATTCTACGTTTTTTCTATACCCAGATGATGGTCACA	120
Qy	121	CTTTTTCCTGTCATCTCTCATGGAAGTTGGATAGCTCGAAGAGAAATCCTTCAT	180
Db	121	CTTTTTCCTGTCATCTCTCATGGAAGTTGGATAGCTCGAAGAGAAATCCTTCAT	180
Qy	181	GAAATATTTTATTCATATTAATAAGCTTAAGATGCAACAAAGAGAAAGATCTTATCC	240
Db	181	GAAATATTTTATTCATATTAATAAGCTTAAGATGCAACAAAGAGAAAGATCTTATCC	240
Qy	241	TTCCTGAACTGTGAGAGATGGAAGGCATTTGAAAGCCTTGCAAGATATACCTTA	300
Db	241	TTCCTGAACTGTGAGAGATGGAAGGCATTTGAAAGCCTTGCAAGATATATGTTA	300
Qy	301	AACAAAGAGA--GAAAAAAGAAACAGCTTTGAATGCAAAAAAGTGATGCAATCCT	357
Db	301	AACAAAGAGAGACGAAGAAAGAAACAGCTTTGAATGCAAAAAAGTGATGCAATCCT	360
Qy	358	CAATTTGGCGACATGTCATAGTGAAGCCACGACGTAAACAACTCTGTGTTACATGG	417
Db	361	CAATTTGGCGACATGTCATAGTGAAGCCACGACGTAAACAACTCTGTGTTACATGG	420
Qy	418	GCTGAAAAGAGTACTACACATGAGCAACACTTGTAACCTGGAAAAATGGAAAAAG	477
Db	421	GCTGAAAAGAGATCTACACATGAGCAACACTTGTAACCTGGAAAAATGGAAAAAG	480
Qy	478	CTGACCGTTAAAGACAGGACTCTATATATCTATGCCAAATGACCTCTGTTCAT	537
Db	481	CTGACCGTTAAAGACAGGACTCTATATATCTATGCCAAATGACCTCTGTTCAT	540
Qy	538	CGGAAAGCTTGAGTCAAGCTCATTTATAGCCAGCTCTGCTAAAGTCCCGGTTAGA	597
Db	541	CGGAAAGCTTGAGTCAAGCTCATTTATAGCCAGCTCTGCTAAAGTCCCGGTTAGA	600
Qy	598	TTTGAGAAATCTTACTCAGAGCTCAATATCCAGTTCCGCGAAACCTTGCGGGCA	657
Db	601	TTTGAGAAATCTTACTCAGAGCTCAATATCCAGTTCCGCGAAACCTTGCGGGCA	660
Qy	718	GTGACGTATCCAAAGCAGTGAAGCCATGGCATGGCTTCAAGTCTTTGGCTTACTCAA	777
Db	721	GTGACGTATCCAAAGCAGTGAAGCCATGGCATGGCTTCAAGTCTTTGGCTTACTCAA	780
Qy	778	CTCTGA 783	
Db	781	CTCTGA 786	
RESULT 3			
AAV38997			
ID AAV38997 standard; DNA; 786 BP.			
AAV38997;			
23-SEP-1998 (first entry)			
CD40 ligand gene used in the course of the invention.			
CD40 ligand; alteration; immunoreactivity; human cell;			
accessory molecule ligand; AM; gene therapy; treatment; neoplasia;			
autoimmune disorder; rheumatoid arthritis; vaccine; ss.			
Mus sp.			
M09826061-A2.			
18-JUN-1998.			

PF	08-DEC-1997;	97MO-US22740.
XX		
PR	01-DEC-1997;	97US--0982272.
PR	09-DEC-1996;	96US--0032145.
XX		
PA	(REGC) UNIV CALIFORNIA.	
XX		
PI	Cantwell M, Kipses TJ, Sharma S;	
DR	WPI; 1998-348521/30.	
XX		
PT	Vectors containing accessory molecule ligand genes - used for altering immunoreactivity of cells, particularly for treatment of neoplasia or autoimmune disorders, e.g. rheumatoid arthritis	
PS	Disclosure; Page 104; 167pp; English.	
CC	The present sequence represents the CD40 ligand gene. The sequence is used to exemplify the method of the invention. The specification describes a method for altering the immunoreactivity of human cells which comprises introducing a gene encoding an accessory molecule ligand (AML) into the cells so that the AML is expressed on the surface of the cell(s). Vectors containing the AML genes can be used in gene therapy for treating neoplasia or autoimmune disorders such as rheumatoid arthritis. They can also be used for vaccination to produce immunity against a virus cell, bacteria, protein, fungus or neoplasia.	
XX		
SO	Sequence 786 BP; 250 A; 168 C; 166 G; 200 T; 0 other:	
	Query Match	92.8%; Score 726.8; DB 19; Length 786;
	Best Local Similarity	96.2%; Pred. No. 3,4e-191;
	Matches 756; Conservative	0; Mismatches 27; Indels 3; Gaps 1
OY	1 ATGATCGAAGCATACAACTTCCTCCGCATCTGCGGCCACTGACGCCCATCAGC	60
DB	1 ATGATCGAAGCATACAACTTCCTCCGCATCTGCGGCCACTGACGCCCATCAGC	60
OY	61 ATGAAAATTTTATGTATTACTTACTTGTTTTCTTATCACCCAGATGATGGGTCA	120
DB	61 ATGAAAATTTTATGTATTACTTACTTGTTTTCTTATCACCCAGATGATGGGTCA	120
OY	61 ATGAAAATTTTATGTATTACTTACTTGTTTTCTTATCACCCAGATGATGGGTCA	120
DB	61 ATGAAAATTTTATGTATTACTTACTTGTTTTCTTATCACCCAGATGATGGGTCA	120
OY	121 CTCTTTCCTGTGATCTTCATAGAAATGGATGAAGTCGAGAAGATAAAGTTCAT	180
DB	121 CTCTTTCCTGTGATCTTCATAGAAATGGATGAAGTCGAGAAGATAAAGTTCAT	180
OY	181 GAAGATTTTGATTCATTAATAAAGCTTAAGATGCACAAGAGAGATCTTTATCC	240
DB	181 GAAGATTTTGATTCATTAATAAAGCTTAAGATGCACAAGAGAGATCTTTATCC	240
OY	181 GAAGATTTTGATTCATTAATAAAGCTTAAGATGCACAAGAGAGATCTTTATCC	240
DB	181 GAAGATTTTGATTCATTAATAAAGCTTAAGATGCACAAGAGAGATCTTTATCC	240
OY	241 TTGCTGAACGTGAGAGATAGAGAGCAATTTGAAACCTTGTCAGAGATTAACGTTA	300
DB	241 TTGCTGAACGTGAGAGATAGAGAGCAATTTGAAACCTTGTCAGAGATTAACGTTA	300
OY	301 AACAAAGAGA--GAAAAAGAAAACAGCTTTGAAATGCAAAAAGGTATCGAATCCT	357
DB	301 AACAAAGAGA--GAAAAAGAAAACAGCTTTGAAATGCAAAAAGGTATCGAATCCT	357
OY	301 AACAAAGAGA--GAAAAAGAAAACAGCTTTGAAATGCAAAAAGGTATCGAATCCT	357
DB	301 AACAAAGAGA--GAAAAAGAAAACAGCTTTGAAATGCAAAAAGGTATCGAATCCT	357
OY	358 CAATATCGGCACATGTCATATAGTAGAGCGCAGCAGTAAAAACAACATCTGTGTACAGTGG	417
DB	358 CAATATCGGCACATGTCATATAGTAGAGCGCAGCAGTAAAAACAACATCTGTGTACAGTGG	417
OY	358 CAATATCGGCACATGTCATATAGTAGAGCGCAGCAGTAAAAACAACATCTGTGTACAGTGG	417
DB	358 CAATATCGGCACATGTCATATAGTAGAGCGCAGCAGTAAAAACAACATCTGTGTACAGTGG	417
OY	418 GTGAAAAAGAGATCTACACATGAGACAACAATCTGGTAAACCTGTGAAAAATGGGAAACAG	477
DB	418 GTGAAAAAGAGATCTACACATGAGACAACAATCTGGTAAACCTGTGAAAAATGGGAAACAG	477
OY	418 GTGAAAAAGAGATCTACACATGAGACAACAATCTGGTAAACCTGTGAAAAATGGGAAACAG	477
DB	418 GTGAAAAAGAGATCTACACATGAGACAACAATCTGGTAAACCTGTGAAAAATGGGAAACAG	477
OY	478 CTGACCGTTAAAGACAAGACTCTATTATATCTATCCCAAATGACACTCTTCTTTCAT	537
DB	478 CTGACCGTTAAAGACAAGACTCTATTATATCTATCCCAAATGACACTCTTCTTTCAT	537
OY	478 CTGACCGTTAAAGACAAGACTCTATTATATCTATCCCAAATGACACTCTTCTTTCAT	537
DB	478 CTGACCGTTAAAGACAAGACTCTATTATATCTATCCCAAATGACACTCTTCTTTCAT	537
OY	538 CGGGAAGCTTCAGATCAAGCTCCATTTATAGCAGAGCTGCGCTTAAAGTCCCCGGGTAGA	597
DB	538 CGGGAAGCTTCAGATCAAGCTCCATTTATAGCAGAGCTGCGCTTAAAGTCCCCGGGTAGA	597
OY	538 CGGGAAGCTTCAGATCAAGCTCCATTTATAGCAGAGCTGCGCTTAAAGTCCCCGGGTAGA	597
DB	538 CGGGAAGCTTCAGATCAAGCTCCATTTATAGCAGAGCTGCGCTTAAAGTCCCCGGGTAGA	597

QY 598 TTGAGAGAAATCTTACTGAGAGCTGCAAAATACCCAGATTCCGCGCAAACTTGGCGGCAA 657
 DB 601 TTGAGAGAAATCTTACTGAGAGCTGCAAAATACCCAGATTCCGCGCAAACTTGGCGGCAA 660
 QY 658 CAATTCATTCATCTTGGAGAGAGATTTGAATTGCAACAGAGTCTTGGTGTTCAT 717
 DB 661 CAATTCATTCATCTTGGAGAGAGATTTGAATTGCAACAGAGTCTTGGTGTTCAT 720
 QY 718 GTGACTGATCCAGAGCAGAGTGCATGAGTCTTGGCTTGGCTTACTCAAA 777
 DB 721 GTGACTGATCCAGAGCAGAGTGCATGAGTCTTGGCTTGGCTTACTCAAA 780
 QY 778 CTCTGA 783
 DB 781 CTCTGA 786

RESULT 4
 AAV12852
 ID AAV12852 standard; cDNA to mRNA; 786 BP.

AC AAV12852;
 DT 13-MAY-1998 (first entry)
 XX
 DE CD40 ligand coding sequence.

XX Leucine zipper; fusion protein production; soluble oligomeric protein;
 KM heterologous mammalian type II transmembrane protein; activated T cell;
 KM heterologous mammalian type I transmembrane protein; antibody production;
 KM CD40-L; B-cell proliferation; CD27-L; lymphocyte antigen; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT CDS 1..786
 FT /*tag= a

PN US5716805-A.

XX 10-FEB-1998.

XX 18-MAY-1995; 95US-0446922.

XX 18-MAY-1995; 95US-0446922.

XX 25-OCT-1991; 91US-0783707.

XX 05-DEC-1991; 91US-0805723.

XX 23-OCT-1992; 92US-0965703.

XX 13-AUG-1993; 93US-0107353.

XX (IMMV) IMMUNEX CORP.

XX Spriggs MK, Srinivasan S;

XX WPI, 1998-144789/13.

XX P-PSDB; AAW41178.

XX Soluble oligomeric fusion proteins - comprising leucine zipper fused

XX to extracellular region of transmembrane protein

XX Example 1; column 19-20; 21pp; English.

XX This sequence is the coding sequence for the human CD40 ligand (CD40-L).
 CC The encoded protein can be used in a fusion protein produced using the
 CC method of the invention. The method is for preparing soluble oligomeric
 CC protein by culturing a host cell transfected with a vector for the
 CC fusion protein. The soluble oligomeric proteins comprise a leucine zipper
 CC fused to the N terminus of the extracellular region of a heterologous
 CC mammalian type II transmembrane protein or to the C terminus of the
 CC extracellular region of a heterologous mammalian type I transmembrane
 CC protein, where the leucine zipper is a peptide comprising at least part
 CC of AAW41171 or AAW41172, optionally with conservative amino acid
 CC substitutions, provided that the peptide trimers are in solution. A

CC soluble fusion protein comprising the leucine zipper of AAW41171 linked
 CC to the extracellular region of CD40-L (a type II transmembrane protein
 CC that is found on activated T cells and acts as a ligand for the B-cell).
 CC antigen (CD40) stimulates B-cell proliferation and antibody production in
 CC a similar manner to membrane-bound CD40-L. A soluble fusion protein
 CC comprising the leucine zipper of AAW41172 linked to the extracellular
 CC region of CD27-L (a type II transmembrane protein that binds to the
 CC lymphocyte antigen CD27) inhibits binding of CD27c (a fusion protein
 CC comprising the extracellular region of CD27 and a human IgG1 Fc region)
 CC to EBV-transformed B cells expressing CD27-L.

XX Sequence 786 BP; 250 A; 168 C; 168 G; 200 T; 0 other;

Query Match 92.8%; Score 726.8; DB 19; Length 786;
 Best Local Similarity 96.2%; Pred. No. 3,4e-191;
 Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

QY 1 ATGATGAAACATACACCAAACTTCCCGATCTGCGCACTGCACTGCCATCAGC 60
 DB 1 ATGATGAAACATACACCAAACTTCCCGATCTGCGCACTGCACTGCCATCAGC 60
 QY 61 ATGAAATTTTATGATATTACTTACTGTTTCTTATCCACCAATGATGGTCAACA 120
 DB 61 ATGAAATTTTATGATATTACTTACTGTTTCTTATCCACCAATGATGGTCAACA 120
 QY 121 CTTTGGCTGATCTTCTTATGAAATGATGATGATGATGATGATGATGATGATGAT 180
 DB 121 CTTTGGCTGATCTTCTTATGAAATGATGATGATGATGATGATGATGATGATGAT 180
 QY 181 GAAGATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
 DB 181 GAAGATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
 QY 241 TTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
 DB 241 TTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
 QY 301 AACAAAGAGA---GAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 357
 DB 301 AACAAAG 357
 QY 358 CAAATTCGCGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 417
 DB 358 CAAATTCGCGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 417
 QY 418 GCTGAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 477
 DB 418 GCTGAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 477
 QY 421 GCTGAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
 DB 421 GCTGAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
 QY 478 CTGACCGTTAAAG 537
 DB 478 CTGACCGTTAAAG 537
 QY 538 CCGGAGAGCTTGAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 597
 DB 538 CCGGAGAGCTTGAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 597
 QY 541 CGGAGAGCTTGAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 600
 DB 541 CGGAGAGCTTGAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 600
 QY 598 TTGAGAGAAATCTTACTGAGAGCTGCAAAATACCCAGATTCCGCGCAAACTTGGCGGCAA 657
 DB 601 TTGAGAGAAATCTTACTGAGAGCTGCAAAATACCCAGATTCCGCGCAAACTTGGCGGCAA 660
 QY 658 CAATTCATTCATCTTGGAGAGAGATTTGAATTGCAACAGAGTCTTGGTGTTCAT 717
 DB 661 CAATTCATTCATCTTGGAGAGAGATTTGAATTGCAACAGAGTCTTGGTGTTCAT 720
 QY 718 GTGACTGATCCAGAGCAGAGTGCATGAGTCTTGGCTTGGCTTACTCAAA 777
 DB 721 GTGACTGATCCAGAGCAGAGTGCATGAGTCTTGGCTTGGCTTACTCAAA 780
 QY 778 CTCTGA 783
 DB 781 CTCTGA 786

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RESULT 5
AA041506
ID AA041506 standard; DNA; 840 BP.
AC AA041506;
XX
XX 12-AUG-1993 (first entry)
XX
XX CD40-L DNA.
XX
XX Human; CD40-L; CD40; type II; membrane; polypeptide; extracellular;
XX transmembrane; region; intracellular; soluble; activity; B cell;
XX proliferation; induction; antibody; secretion; IgE; agonist;
XX antagonist; binding assay; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 46..831
XX /tag= a
XX
XX MO9308207-A.
XX
XX 29-APR-1993.
XX
XX 23-OCT-1992; 92MO-US08990.
XX
XX 25-OCT-1991; 91US-0783707.
XX
XX 05-DEC-1991; 91US-0805723.
XX
XX (IMMV ) IMMUNEX CORP.
XX
XX Armltage RJ, Fanslow WC, Spriggs MK;
XX
XX WPI: 1993-152417/18.
XX
XX P-PSDB; AAR36701.
XX
XX New cytokine CD40-L as CD40 agonist and antagonist - is used for
XX treating allergies, lupus, rheumatoid arthritis,
XX graft-versus-host disease and insulin-dependent diabetes mellitus
XX
XX Claim 1; Fig 2; 80pp; English.
XX
XX
XX This sequence encodes a human CD40-L polypeptide which binds to CD40.
XX CD40-L is a type II membrane polypeptide which has an extracellular
XX region at its C-terminus, a transmembrane region and an
XX intracellular region at its N-terminus. A soluble form of CD40-L
XX lacks the transmembrane domain. CD40-L activity is mediated by
XX binding with CD40 and induces B cell proliferation and induction of
XX antibody secretion, including IgE. Membrane bound CD40-L acts as a
XX CD40 agonist and soluble CD40-L acts as a CD40 antagonist. CD40-L
XX can be used in a binding assay to detect cells expressing CD40.
XX
XX Sequence 840 BP; 266 A; 185 C; 175 G; 214 T; 0 other;
XX
XX Query Match 92.8%; Score 726.8; DB 14; Length 840;
XX Best Local Similarity 96.2%; Pred. No. 3,5e-191;
XX Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;
XX
XX 1 ATGATGAAACATCAACCAACCTTCTCCGATCTCGGCCACTGACCTCCATGAC 60
XX |||
XX 46 ATGATGAAACATCAACCAACCTTCTCCGATCTCGGCCACTGACCTCCATGAC 105
XX |||
XX 61 ATGAAATTTTATGATTTACTACTGTTTTCTATCAACCAAGATGTTGGTGACGA 120
XX |||
XX 106 ATGAAATTTTATGATTTACTACTGTTTTCTATCAACCAAGATGTTGGTGACGA 165
XX |||
XX 121 CTTTTCGCTGCTATCTTCAAGAGATTGATGAGAGTGAAGTAACTTCTCAT 180
XX |||
XX 166 CTTTTCGCTGCTATCTTCAAGAGATTGATGAGAGTGAAGTAACTTCTCAT 225
XX |||
XX 181 GAAGATTTTGTATTCATTAAGAGCTAAAGAGATGCAACAAAGAGATCTTTATCC 240

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Db 226 GAAAGTTTGTATTCATGAAAAAGATACAGATGACCAACAGAGAAAGATCTTATCC 285
|||
Qy 241 TTGCTGAACCTGTGAGAGATGAGAGCAATTGTAAGCCTTGCAAGATTAACGTTA 300
|||
Db 286 TTACTGAACCTGTGAGAGATTAAGCAGTTTGAAGCTTTGGAAGATTAATGTTA 345
|||
Qy 301 AACAAAGNAGA--GAAAAAGAAAAACAGCTTTGAAATGCAAAAAGGTATGAGATCT 357
|||
Db 346 AACAAAGAGAGACGAGAAAGAAAAACAGCTTTGAAATGCAAAAAGGTATGAGATCT 405
|||
Qy 358 CAATTCGGGCAATGCTATTAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 417
|||
Db 406 CAATTCGGGCAATGCTATTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 465
|||
Qy 418 GCTGAAAAAGATATCAACATGAGCAACATGCTGTTAACCTGAAAAAGGAGAAACAG 477
|||
Db 466 GCTGAAAAAGATATCAACATGAGCAACATGCTGTTAACCTGAAAAAGGAGAAACAG 525
|||
Qy 478 CTGACCGTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 537
|||
Db 526 CTGACCGTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 585
|||
Qy 538 CGGAGAGCTTGAAGTCAAGCTCAATTTATGAGAGAGAGAGAGAGAGAGAGAGAG 597
|||
Db 586 CGGAGAGCTTGAAGTCAAGCTCAATTTATGAGAGAGAGAGAGAGAGAGAGAGAG 645
|||
Qy 598 TTCCGAGAGATCTTATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 657
|||
Db 646 TTCCGAGAGATCTTATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 705
|||
Qy 658 CAATCATTCACTTGGAGAGAGATTTTGAATGCAACAGAGTGTGTTGTCAAT 717
|||
Db 706 CAATCATTCACTTGGAGAGAGATTTTGAATGCAACAGAGTGTGTTGTCAAT 765
|||
Qy 718 GTGACTGATCCAGCCAAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 777
|||
Db 766 GTGACTGATCCAGCCAAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 825
|||
Qy 778 CTCTGA 783
|||
Db 826 CTCTGA 831
|||
RESULT 6
AA067123
ID AA067123 standard; DNA; 840 BP.
AC AA067123;
XX
XX 23-MAR-1995 (first entry)
XX
XX CD40 ligand gene.
XX
XX Probe; primer; PCR; amplify; polymerase chain reaction; detection;
XX mutation; CD40 ligand gene; IGM; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX CDS 46..831
XX /tag= a
XX /product= CD40 ligand
XX
XX MO9417196-A.
XX
XX 04-AUG-1994.
XX
XX 21-JAN-1994; 94MO-US00786.
XX
XX 22-JAN-1993; 93US-0009258.
XX
XX 20-JAN-1994; 94US-0184422.
XX

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PA (IMMUNEX CORP.
 XX
 PI Armitage RJ, Davison BL, Fanslow WC, Renshaw BR;
 PI Spriggs MK, Widmer MB;
 DR WPI: 1994-264109/32.
 DR P-PSDB; AAR57469.
 XX
 PT Method for detecting mutation in CD 40 ligand gene - comprises
 PT amplification of nucleic acid, and mutational analysis
 XX
 PS Disclosure; Page 22-24; 38pp; English.
 XX
 CC This sequence represents the CD40 ligand gene. Mutations within
 CC this gene were identified by the method of the invention. The
 CC method comprises isolating DNA from an individual and selectively
 CC amplifying the isolated DNA derived from the CD40 ligand gene. The
 CC amplification product is then analysed to determine if there is a
 CC mutation present and determining if a protein expressed from the
 CC ligand gene will bind CD40. The detection of mutations in the CD40
 CC ligand gene allows subsequent treatment of a syndrome resulting in
 CC elevated levels of serum IgM and diminished levels of other Ig
 CC isotypes, due to mutation in the CD40 ligand gene. ie. X-linked
 CC hyperIgM syndrome.
 XX
 SO Sequence 840 BP; 266 A; 185 C; 175 G; 214 T; 0 other;
 Query Match 92.8%; Score 726.8; DB 15; Length 840;
 Best Local Similarity 96.2%; Pred. No. 3,5e-191;
 Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;
 QY 1 ATGATCGAAACATACCAACCACTTCTCCCGATCTGCGGCACCTGAGTCCCATCAGC 60
 DB 46 ATGATCGAAACATACCAACCACTTCTCCCGATCTGCGGCACCTGAGTCCCATCAGC 105
 QY 61 ATGAAATTTTATGATTTACTTACTGTTTCTTACCCAGATGGTGGCAGCA 120
 DB 106 ATGAAATTTTATGATTTACTTACTGTTTCTTACCCAGATGGTGGCAGCA 165
 QY 121 CTTTTCCTGTGATCTTATGAAAGATTGGATAGGTGGAAGAAAGTAAACCTTCAT 180
 DB 166 CTTTTCCTGTGATCTTATGAAAGATTGGATAGGTGGAAGAAAGTAAACCTTCAT 225
 QY 181 GAGATTTTGTATTCATAAAAGCTAAAGATGCAAGAGAGAGATCTTATCC 240
 DB 226 GAGATTTTGTATTCATAAAAGCTAAAGATGCAAGAGAGAGATCTTATCC 285
 QY 241 TTGCTGAAGTGTGAGAGATGAAGCAATTTGAAGCCTTGTCAAGATTAACGTTA 300
 DB 286 TTACTGAAGTGTGAGAGATGAAGCAATTTGAAGCCTTGTCAAGATTAACGTTA 345
 QY 301 AACCAAGAGA---GAAAAAGAAAAAGCTTTGAAGTGAAGAAAGGTGATCGAATCCT 357
 DB 346 AACCAAGAGA---GAAAAAGAAAAAGCTTTGAAGTGAAGAAAGGTGATCGAATCCT 405
 QY 358 CAAATTCGGGCACATGTCATTAAGTAGGCGCAGCAATAAACATCTGTGTACAGTG 417
 DB 406 CAAATTCGGGCACATGTCATTAAGTAGGCGCAGCAATAAACATCTGTGTACAGTG 465
 QY 418 GGTGAAAAAGATACCAACCATGAGCAACATCTGTGTACAGTGGAAAAAGAG 477
 DB 466 GGTGAAAAAGATACCAACCATGAGCAACATCTGTGTACAGTGGAAAAAGAG 525
 QY 478 CTGACCGTTAAAGACAGAGCTATATATATATATGCCCAAGTCACTTGTTCAT 537
 DB 526 CTGACCGTTAAAGACAGAGCTATATATATATATGCCCAAGTCACTTGTTCAT 585
 QY 538 CGGAGAGCTTGAAGTCAAGCTCCATTTATAGCAGCTCTGCTAAAGTCCCGGTGA 597
 DB 586 CGGAGAGCTTGAAGTCAAGCTCCATTTATAGCAGCTCTGCTAAAGTCCCGGTGA 645
 QY 598 TTGAGAGAAATCTTACTGAGAGTGAAGTCAAGTCCCGCAACCTTGCAGGAGCA 657
 DB 646 TTGAGAGAAATCTTACTGAGAGTGAAGTCAAGTCCCGCAACCTTGCAGGAGCA 705
 QY 658 CAATTCATTCATCTTGGAGAGATTTGAATTTGCAACAGAGTCTTGGTGTCAAT 717
 DB 706 CAATTCATTCATCTTGGAGAGATTTGAATTTGCAACAGAGTCTTGGTGTCAAT 765
 QY 718 GTGACTGATCAAGCAGATGAGCAGTGCATGCTTCAAGTCTTGGCTTACTCAAA 777
 DB 766 GTGACTGATCAAGCAGATGAGCAGTGCATGCTTCAAGTCTTGGCTTACTCAAA 825
 QY 778 CTCTGA 783
 DB 826 CTCTGA 831
 RESULT 7
 ID AAT05763
 XX AAT05763 standard; DNA, 840 BP.
 XX
 AC AAT05763;
 XX
 DT 18-MAR-1996 (first entry)
 XX
 DE Human CD40 ligand DNA.
 XX
 KW High density membrane-bound CD40 ligand; B-lymphocyte; B-cell;
 KW differentiation; proliferation; baculovirus; Spodoptera frugiperda;
 KW Sf9; insect cell culture; tumour necrosis factor receptor; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 22..807
 FT /tag= a
 XX
 PN W09529335-A1.
 XX
 PD 09-NOV-1995.
 XX
 PF 28-APR-1995; 95WO-US05448.
 XX
 PR 28-APR-1994; 94US-0234580.
 XX
 PA (BOEH) BOEHRINGER INGELHEIM PHARM INC.
 XX
 PI Casle BE, Kehy M;
 XX
 DR WPI: 1995-393038/50.
 XX
 DR P-PSDB; AAR5486.
 XX
 PT High density membrane bound CD40 ligand - for stimulating the
 PT proliferation of B cells in vitro or in vivo, partic. for producing
 PT differentiated cells
 XX
 PS Disclosure; Fig 1; 74pp; English.
 XX
 CC The nucleotide sequence given in AAT05763 encodes a human high-density,
 CC membrane-bound (hmb) CD40 ligand (AAR5486) that induces long-term
 CC proliferation of B-cells in culture. These proliferating B-cells
 CC can be induced to differentiate into antibody-prod. cells. The
 CC nucleotide sequence is incorporated into a baculovirus vector that
 CC is used to transfect Sf9 insect cells for prodn. of recombinant
 CC hmbCD40.
 CC
 SQ Sequence 840 BP; 263 A; 182 C; 181 G; 214 T; 0 other;
 Query Match 92.8%; Score 726.8; DB 16; Length 840;
 Best Local Similarity 96.2%; Pred. No. 3,5e-191;
 Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;
 QY 1 ATGATCGAAACATACCAACCACTTCTCCCGATCTGCGGCACCTGAGTCCCATCAGC 60
 DB 22 ATGATCGAAACATACCAACCACTTCTCCCGATCTGCGGCACCTGAGTCCCATCAGC 81

Qy 61 ATGAAATTTTATGATTTACTTCTTTCTTATGACCCAGATGATGGGTGACGA 120
 Db 82 ATGAAATTTTATGATTTACTTCTTTCTTATGACCCAGATGATGGGTGACGA 141
 Qy 121 CTTTTCCTGTGATCTTCTTATGAAAGATTTGATGAAAGATGAAAGATTTCTCAT 180
 Db 142 CTTTTCCTGTGATCTTCTTATGAAAGATTTGATGAAAGATGAAAGATTTCTCAT 201
 Qy 181 GAAATTTTGTATCTTATGAAAGATTTGATGAAAGATGAAAGATTTCTCAT 240
 Db 202 GAAATTTTGTATCTTATGAAAGATTTGATGAAAGATGAAAGATTTCTCAT 261
 Qy 241 TTGCTGAATCTGTGAGAGATGAAAGATTTGATGAAAGATTTCTCAT 300
 Db 262 TTGCTGAATCTGTGAGAGATTTGAAAGATTTGATGAAAGATTTCTCAT 321
 Qy 301 AACAAAGAGA---GAAAAAGAAAAAGCTTTGAAATGCAAAAAGGTGATGCAATCTCT 357
 Db 322 AACAAAG 381
 Qy 358 CAAATTCGGGACATGTCATTAAGTGGCCAGAGTAAACAAATCTGTGTTACAGTGG 417
 Db 382 CAAATTCGGGACATGTCATTAAGTGGCCAGAGTAAACAAATCTGTGTTACAGTGG 441
 Qy 418 GCTGAAAAAGATCTACACCAATGAGCAACAATGCTGTAACCTGGAAGAGAGAGAG 477
 Db 442 GCTGAAAAAGATCTACACCAATGAGCAACAATGCTGTAACCTGGAAGAGAGAGAG 501
 Qy 478 CTGACCGTTTAAAG 537
 Db 502 CTGACCGTTTAAAG 561
 Qy 538 CGGAAAGCTTGAAGTCAAGTCCATTTATGACCAAGCTGCTGCTGCTGCTGCTGCTG 597
 Db 562 CGGAAAGCTTGAAGTCAAGTCCATTTATGACCAAGCTGCTGCTGCTGCTGCTGCTG 621
 Qy 598 TTGAGAGAAATCTTACTCAGAGCTGCAAAATCCCAAGTTCGCGCAAACTTGGGGGCA 657
 Db 622 TTGAGAGAAATCTTACTCAGAGCTGCAAAATCCCAAGTTCGCGCAAACTTGGGGGCA 681
 Qy 658 CAATCCATTCCTTGGGAGAGAGATTTGATGAAAGAGAGAGAGAGAGAGAGAGAGAG 717
 Db 682 CAATCCATTCCTTGGGAGAGAGATTTGATGAAAGAGAGAGAGAGAGAGAGAGAGAG 741
 Qy 718 GTGACTGATCCAG 777
 Db 742 GTGACTGATCCAG 801
 Qy 778 CTCTGA 783
 Db 802 CTCTGA 807

RESULT 8
 AAT93782
 ID AAT93782 standard; cDNA; 840 BP.
 XX
 AC AAT93782;
 XX
 DT 16-FEB-1998 (first entry)
 XX
 DE cDNA of CD40L, a novel cytokine ligand for CD40.
 XX
 KW Cytokine; activated CD4+ T cell; CD40; CD40L; monoclonal antibody;
 KM neoplastic cell proliferation; B-cell lymphoma; immune deficiency; AIDS;
 KM melanoma; carcinoma; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key
 CDS Location/Qualifiers
 FT 46..831
 FT /*tag= a

XX US5674492-A.
 XX 07-OCT-1997.
 XX
 XX 21-DEC-1994; 94US-0360923.
 XX
 XX 23-DEC-1993; 93US-0172664.
 XX
 PA (IMMUNEX CORP.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PI Armistage RJ, Fanslow WC, Longo DL, Murphy WJ;
 DR WPI; 1997-502273/46.
 DR P-Psdb; AAW34669.
 PT Treating or preventing neoplastic disease associated with
 PT CD40-expressing cells - particularly B-cell lymphoma, by
 PT administration of CD40-binding protein, preferably antibody or
 PT soluble CD40-ligand
 PS Claim 3; Columns 19-22; 21pp; English.
 CC The present sequence represents the cDNA sequence of a novel cytokine
 CC ligand for CD40 called CD40L. CD40L is a type II membrane polypeptide,
 CC which is expressed by activated CD4+ T cells, and causes B cell
 CC proliferation and induction of antibody secretion. The protein can be
 CC used to produce monoclonal antibodies, which in turn bind to
 CC CD40-expressing cells. This inhibits binding of soluble CD40 to its
 CC ligand CD40L. The monoclonal antibody against CD40L is used to inhibit
 CC proliferation of neoplastic cells, and is particularly useful in treating
 CC B-cell lymphoma (e.g. where induced after transplants or in other cases
 CC of immune deficiency such as AIDS), and also melanoma or carcinoma. Since
 CC the monoclonal antibodies inhibit neoplastic cells directly, they may not
 CC need to be coupled to a toxin or radioisotope, avoiding toxic effects on
 CC normal B cells.
 XX
 SQ Sequence 840 BP; 266 A; 185 C; 175 G; 214 T; 0 other;
 Query Match 92.8%; Score 726.8; DB 18; Length 840;
 Best Local Similarity 96.2%; Pred. No. 3.5e-191;
 Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;
 Qy 1 ATGATGAAACATACCAACCAATCTTCCCGATCTGCGGCACTGAGTCCCATCAGC 60
 Db 46 ATGATGAAACATACCAACCAATCTTCCCGATCTGCGGCACTGAGTCCCATCAGC 105
 Qy 61 ATGAAATTTTATGATTTACTTCTTATGAAAGATTTGATGAAAGATTTCTCAT 120
 Db 106 ATGAAATTTTATGATTTACTTCTTATGAAAGATTTGATGAAAGATTTCTCAT 165
 Qy 121 CTTTTCCTGTGATCTTCTTATGAAAGATTTGATGAAAGATTTCTCAT 180
 Db 166 CTTTTCCTGTGATCTTCTTATGAAAGATTTGATGAAAGATTTCTCAT 225
 Qy 181 GAAATTTTGTATCTTATGAAAGATTTGATGAAAGATTTGATGAAAGATTTCTCAT 240
 Db 226 GAAATTTTGTATCTTATGAAAGATTTGATGAAAGATTTGATGAAAGATTTCTCAT 285
 Qy 241 TTGCTGAATCTGTGAGAGATGAAAGATTTGATGAAAGATTTCTCAT 300
 Db 286 TTGCTGAATCTGTGAGAGATTTGAAAGATTTGATGAAAGATTTCTCAT 345
 Qy 301 AACAAAGAGA---GAAAAAGAAAAAGCTTTGAAATGCAAAAAGGTGATGCAATCTCT 357
 Db 346 AACAAAG 405
 Qy 358 CAAATTCGGGACATGTCATTAAGTGGCCAGAGTAAACAAATCTGTGTTACAGTGG 417
 Db 406 CAAATTCGGGACATGTCATTAAGTGGCCAGAGTAAACAAATCTGTGTTACAGTGG 465
 Qy 418 GCTGAAAAAGATCTACACCAATGAGCAACAATGCTGTAACCTGGAAGAGAGAGAG 477

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Db 466 GCTGAAAAGATCTACACCATGAGCAACACTTGTAACCTCGAAGAAATGGAAAACAG 525
Qy 478 CTGACCGTTAAAGACAAAGACTCTATTATATCTATGCCAAGTACCTTGTTCAT 537
Db 526 CTGACCGTTAAAGACAAAGACTCTATTATATCTATGCCAAGTACCTTGTTCAT 585
Qy 538 CGGGAAGCTTGAATCAAGCTCATTATATAGCCAGCTCTGCTTAAGTCCCGGTAGA 597
Db 586 CGGGAAGCTTGAATCAAGCTCATTATATAGCCAGCTCTGCTTAAGTCCCGGTAGA 645
Qy 598 TTGAGAGAACTTACTGAGAGTCCGAAATACCAAGTCCGCAAACTTGGCGGCA 657
Db 646 TTGAGAGAACTTACTGAGAGTCCGAAATACCAAGTCCGCAAACTTGGCGGCA 705
Qy 658 CAATCATTCACTTGGAGAGATTTGAATTCACACAGTGTCTGCTTGTTCAT 717
Db 706 CAATCATTCACTTGGAGAGATTTGAATTCACACAGTGTCTGCTTGTTCAT 765
Qy 718 GTGACTGATCCAGCCAAATGAGCACTGGCTTCACTGCTTGTTCAT 777
Db 766 GTGACTGATCCAGCCAAATGAGCACTGGCTTCACTGCTTGTTCAT 825
Qy 778 CTCTGA 783
Db 826 CTCTGA 831

RESULT 9
ID AAV61063 standard; DNA, 840 BP.
AC AAV61063;
XX
DT 08-DEC-1998 (first entry)
XX
DE Human CD40 ligand encoding DNA sequence.
XX
KW Human; CD40 ligand; TNF receptor family; activated T cell;
KW type 2 membrane glycoprotein; cell proliferation; differentiation;
KW B cell; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 22..807
FT /tag= a
FT /product= "CD40 ligand"
XX
PN US5817516-A.
XX
PD 06-OCT-1998.
XX
PF 28-APR-1995; 95US-0431055.
XX
PR 28-APR-1995; 95US-0431055.
XX
PR 28-APR-1994; 94US-0234580.
XX
PA (BOH ) BOEHRINGER INGELHEIM PHARM INC.
XX
PI Castle B, Kehrly M;
XX
DR MPI, 1998-556393/47.
DR P-FSDB; AAM71751.
XX
PT Increased proliferation of B cells in culture - by incubating them
PT in the presence of membrane-bound CD40 ligand
XX
PS Example 1; Fig 1; 37pp; English.
CC The present sequence encodes human CD40 ligand which is used in the
CC method of the invention. The method has been developed for proliferating
CC B cells to increase their number at least 100-fold. The method

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CC comprises: (a) providing high density, membrane bound CD40 ligand; and
CC (b) culturing one or more B cells in the presence of this ligand. The
CC culture results in a proliferation in the number of B cells of at least
CC 100 fold. Also described is a method as above where the B cells are
CC induced to differentiate into antibody-producing cells in the presence
CC of one or more cytokines. The method can be used for stimulating B-cell
CC proliferation in vitro or in vivo, e.g. for treating conditions in which
CC B-cell proliferation and activation is suppressed. Eight rounds of
CC division over six days can be achieved, corresponding to a 256-fold
CC increase in cell numbers, which is a vast increase compared to previous
CC culturing methods.
XX
SQ Sequence 840 BP; 263 A; 182 C; 181 G; 214 T; 0 other;
Qy 1 ATGATGAAACATACACCAAACTTCCCGGATCTCCGCGCATGCACTGCCATAGC 60
Db 22 ATGATGAAACATACACCAAACTTCCCGGATCTCCGCGCATGCACTGCCATAGC 81
Qy 61 ATGAAATTTTATGATTTTACTTACTGTTTTCCTATCCACCAGATTTGGTACGA 120
Db 82 ATGAAATTTTATGATTTTACTTACTGTTTTCCTATCCACCAGATTTGGTACGA 141
Qy 121 CTTTGGCTGCTGATCTTCAATGAAATGATGATGATGATGATGATGATGATGATGAT 180
Db 142 CTTTGGCTGCTGATCTTCAATGAAATGATGATGATGATGATGATGATGATGATGAT 201
Qy 181 GAAATTTTGTATTTATGAAATGATGATGATGATGATGATGATGATGATGATGAT 240
Db 202 GAAATTTTGTATTTATGAAATGATGATGATGATGATGATGATGATGATGATGAT 261
Qy 241 TTGCTGATCTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
Db 262 TTGCTGATCTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 321
Qy 301 AACAAAGAGA---GAAAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGATCCT 357
Db 322 AACAAAGAGAGACGAGAAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGATCCT 381
Qy 358 CAATTTGGGCACTGATCATAGTACGAGCAAGTAAACAACTGTGTACATGAG 417
Db 382 CAATTTGGGCACTGATCATAGTACGAGCAAGTAAACAACTGTGTACATGAG 441
Qy 418 GCTGAAAAGATACATACCATGAGCAACATTTGGTAACTCTGAAAATGGGAAACAG 477
Db 442 GCTGAAAAGATACATACCATGAGCAACATTTGGTAACTCTGAAAATGGGAAACAG 501
Qy 478 CTGACCGTTAAAGACAAAGACTCTATTATATCTATGCCAAGTACCTTGTTCAT 537
Db 502 CTGACCGTTAAAGACAAAGACTCTATTATATCTATGCCAAGTACCTTGTTCAT 561
Qy 538 CGGGAAGCTTGAATCAAGCTCATTATATAGCCAGCTCTGCTTAAGTCCCGGTAGA 597
Db 562 CGGGAAGCTTGAATCAAGCTCATTATATAGCCAGCTCTGCTTAAGTCCCGGTAGA 621
Qy 598 TTGAGAGAACTTACTGAGAGTCCGAAATACCAAGTCCGCAAACTTGGCGGCA 657
Db 622 TTGAGAGAACTTACTGAGAGTCCGAAATACCAAGTCCGCAAACTTGGCGGCA 681
Qy 658 CAATCATTCACTTGGAGAGATTTGAATTCACACAGTGTCTGCTTGTTCAT 717
Db 682 CAATCATTCACTTGGAGAGATTTGAATTCACACAGTGTCTGCTTGTTCAT 741
Qy 718 GTGACTGATCCAGCCAAATGAGCACTGGCTTCACTGCTTGTTCAT 777
Db 742 GTGACTGATCCAGCCAAATGAGCACTGGCTTCACTGCTTGTTCAT 801
Qy 778 CTCTGA 783
Db 802 CTCTGA 807

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RESULT 10

AAZ27525 ID AAZ27525 standard; cDNA; 840 BP.

AAZ27525;

13-DEC-1999 (first entry)

Human CD40-L coding sequence.

CD40-L; CD40 receptor ligand; anti-human CD40-L monoclonal antibody;

binding inhibitor; c1emeric CD40-L; anti-immunoglobulin M;

peripheral blood B cell; proliferation inhibitor; ss.

Homo sapiens.

US5961974-A.

24-MAY-1994; 94US-0249189.

25-OCT-1991; 91US-0783707.

23-OCT-1992; 92US-0969703.

(IMMV) IMMUNEX CORP.

Spriggs MK, Fanslow WC, Armitage RJ;

WPI; 1999-579604/49.

P-PSDB; AAY39338.

Anti-human CD40-Ligand monoclonal antibodies -

disclosure; Fig 2; 59pp; English.

This sequence encodes the human CD40 receptor ligand (CD40-L). The

invention relates to anti-human CD40-L monoclonal antibodies M90 secreted

by hybridoma hCD40L-M90 (ATCC HB-12055) and M91 secreted by hybridoma

hCD40L-M91 (ATCC HB-12056). M90 and M91 inhibit CD40-L binding to CD40

and the ability of trimeric CD40-L and anti-immunoglobulin M to induce

proliferation of peripheral blood B cells.

Sequence 840 BP; 266 A; 185 C; 175 G; 214 T; 0 other;

Query Match 92.8%; Score 726.8; DB 20; Length 840;

Best Local Similarity 96.2%; Pred. No. 3.5e-191;

Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

QY 1 ATGATCGAAACATACACAACTTCTCCCGATCTGCGGCACTGAGCTGCCATCAGC 60
 DB 46 ATGATCGAAACATACACAACTTCTCCCGATCTGCGGCACTGAGCTGCCATCAGC 105
 QY 61 ATGAAATTTTATGATTTTATCTGCTGTTTCTTATCACCAGATGATTGGGTCAAGA 120
 DB 106 ATGAAATTTTATGATTTTATCTGCTGTTTCTTATCACCAGATGATTGGGTCAAGA 165
 QY 121 CTTTGTCTGTATCTTCATAGAGATTGATGAGTGCAGAGAAAGTAACTTCAAT 180
 DB 166 CTTTGTCTGTATCTTCATAGAGATTGATGAGTGCAGAGAAAGTAACTTCAAT 225
 QY 181 GAAGATTTTGTATTCATTAATAAGCTAAAGAGTCAACAAAGAGAGATCTTTATCC 240
 DB 226 GAAGATTTTGTATTCATTAATAAGCTAAAGAGTCAACAAAGAGAGATCTTTATCC 285
 QY 241 TTGCTGAAGTGTGAGAGATGAGAGGCAATTTGAAGACTTGTCAAGATATACGTTA 300
 DB 286 TTACTGAAGTGTGAGAGATGAGAGGCAATTTGAAGACTTGTCAAGATATACGTTA 345
 QY 301 AACAAAGAGA---GAAAAAGAAAAAGCTTTGAATGCAAAAAAGTGATCAGAACTCT 357

DB 346 AACAAAGAGAGACAGAAAGAAAAAGCTTTGAAATGCAAAAAAGTGATCAGAACTCT 405
 QY 358 CAAATTCGGCAGCATGTCTATAGTAGGCCAGAGTAAACACATCTGTGTACAGTGG 417
 DB 406 CAAATTCGGCAGCATGTCTATAGTAGGCCAGAGTAAACACATCTGTGTACAGTGG 465
 QY 418 GCTGAAAAAGATCTACACATGAGCAACACTTGTGTAACTCGAAAAATGGAACAG 477
 DB 466 GCTGAAAAAGATCTACACATGAGCAACACTTGTGTAACTCGAAAAATGGAACAG 525
 QY 478 CTGACCTTTAAAGACAGAGCTATTTATATCTATGCCAAGTCACTTCTGTTCAT 537
 DB 526 CTGACCTTTAAAGACAGAGCTATTTATATCTATGCCAAGTCACTTCTGTTCAT 585
 QY 538 CGGAGACTTCGAGTCAAGCTCCATTTATATGACAGCTCTGCTAAAGTCCCGGTAGA 597
 DB 586 CGGAGACTTCGAGTCAAGCTCCATTTATATGACAGCTCTGCTAAAGTCCCGGTAGA 645
 QY 598 TTGAGAGAAATCTTACTCAGAGCTGCAATATCCACAGTTCCGCAACCTTGGCGGCA 657
 DB 646 TTGAGAGAAATCTTACTCAGAGCTGCAATATCCACAGTTCCGCAACCTTGGCGGCA 705
 QY 658 CAATCATTCATCTTGGAGAGATATTGAATTGCAACAGAGTGTGGTTGTCAAT 717
 DB 706 CAATCATTCATCTTGGAGAGATATTGAATTGCAACAGAGTGTGGTTGTCAAT 765
 QY 718 GTGACTATTCAAAGCCAGATGAGCCATGCGACTTCACATCTTGTGCTTACTCAA 777
 DB 766 GTGACTATTCAAAGCCAGATGAGCCATGCGACTTCACATCTTGTGCTTACTCAA 825
 QY 778 CTCTGA 783
 DB 826 CTCTGA 831

RESULT 11

AAFS5539 ID AAF55539 standard; DNA; 879 BP.

AAFS5539;

29-MAY-2001 (first entry)

Nucleotide sequence of human gp39 protein, a CD40 ligand.

gp39; CD40 ligand; osteoblast cell death; apoptosis; bone loss;

osteoporosis; osteonecrosis; inflammatory arthritis; estrogen loss;

ovariectomy; histiocytoma; lupus nephritis; Takayasu's arteritis;

Wegener's granulomatosis; nephritis; myositis; scleroderma;

thrombocytopenia; asthma; lung disease; cancer; ss.

Homo sapiens.

WO200116180-A2.

24-AUG-2000; 2000WO-US23276.

27-AUG-1999; 99US-0151250.

(TEXA) UNIV TEXAS SYSTEM.

Ahuja SS, Bonewald LF;

WPI; 2001-169007/17.

P-PSDB; AAB67612.

XX CD40 agonist containing composition, used to reduce bone cell death or
 PT apoptosis associated with osteoporosis, osteonecrosis and inflammatory
 PT arthritis -
 XX
 PS Disclosure; Page 113; 118pp; English.
 XX
 CC The present sequence encodes a gp39 protein. It is a CD40 ligand.
 CC CD40 ligands are used for reducing osteoblast cell death or apoptosis,
 CC and for treating or preventing bone loss in animals, preferably humans,
 CC at risk of, or undergoing, bone loss. The bone loss is associated with
 CC osteoporosis, osteonecrosis, inflammatory arthritis, post-menopausal
 CC oestrogen loss, oestrogen loss due to ovariectomy, total hysterectomy,
 CC lupus nephritis, Takayasu's arteritis, Wegener's granulomatosis,
 CC anti-glomerular basement membrane nephritis, myositis, scleroderma,
 CC idiopathic autoimmune thrombocytopenia, asthma, a chronic obstructive
 CC lung disease, nephrotic/nephritic syndrome, or cancer. They may also be
 CC used to treat or prevent bone loss in a subject undergoing, or scheduled
 CC for, an organ or bone marrow transplant.
 XX
 SQ Sequence 879 BP; 274 A; 193 C; 190 G; 222 T; 0 other;
 Query Match 92.8%; Score 726.8; DB 22; Length 879;
 Best Local Similarity 96.2%; Pred. No. 3.5e-191;
 Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;
 QY 1 ATGATCGAAGACATACACCAAACTTCTCCCGATCGCGCACTGAGTCCCATCAGC 60
 DB 22 ATGATCGAAGACATACACCAAACTTCTCCCGATCGCGCACTGAGTCCCATCAGC 81
 QY 61 ATGAAAATTTTATGATTTTATCTACTGTTTCTTATCACCAGATGATGGGTACCA 120
 DB 82 ATGAAAATTTTATGATTTTATCTACTGTTTCTTATCACCAGATGATGGGTACCA 141
 QY 121 CTTTTCGTGTATCTTCATAGAAATGATGATGATGATGATGATGATGATGATGAT 180
 DB 142 CTTTTCGTGTATCTTCATAGAAATGATGATGATGATGATGATGATGATGATGAT 201
 QY 181 GAAATTTTGTATCTTATGAAAAGCTTAAAGATGATGATGATGATGATGATGATGAT 240
 DB 202 GAAATTTTGTATCTTATGAAAAGCTTAAAGATGATGATGATGATGATGATGATGAT 261
 QY 241 TTGCTGAAGTGTGAGAGATGAGAGCAATTTGAGACCTTGTCAAGATATTAAGTTA 300
 DB 262 TTACTGAAGTGTGAGAGATGAGAGCAATTTGAGACCTTGTCAAGATATTAAGTTA 321
 QY 301 AACAAG 357
 DB 322 AACAAG 381
 QY 358 CAAATTCGCGCAATGTCATTAAGTGAAGCCAGCAAGTAAAGCAATCTGTGTACAGTGG 417
 DB 382 CAAATTCGCGCAATGTCATTAAGTGAAGCCAGCAAGTAAAGCAATCTGTGTACAGTGG 441
 QY 418 GCTGAAAAGATATACACCAATGAGCAAACTTGTAAACCTTGTAAAGTAAAGTAAAG 477
 DB 442 GCTGAAAAGATATACACCAATGAGCAAACTTGTAAACCTTGTAAAGTAAAGTAAAG 501
 QY 478 CTGACCGTTAAAGACAGAGAGCTGATTAATATATATGCTGCAAGTCACTTGTTCAT 537
 DB 502 CTGACCGTTAAAGACAGAGAGCTGATTAATATATATGCTGCAAGTCACTTGTTCAT 561
 QY 538 CGGGAAGCTTCGAGTCAAGCTCCATTTATGAGAGAGCTTCCCTTAAAGTCCCGCGTGA 597
 DB 562 CGGGAAGCTTCGAGTCAAGCTCCATTTATGAGAGAGCTTCCCTTAAAGTCCCGCGTGA 621
 QY 598 TTGAGAGAGATCTTACTGAGAGCTGCAAAATACCAAGTCCCGCAAACTTGGCGGCA 657
 DB 622 TTGAGAGAGATCTTACTGAGAGCTGCAAAATACCAAGTCCCGCAAACTTGGCGGCA 681
 QY 658 CAATCCATTCAGTTGGAGAGATTTTGAATGCAACAGAGTCTTGGTGTTCAT 717
 DB 682 CAATCCATTCAGTTGGAGAGATTTTGAATGCAACAGAGTCTTGGTGTTCAT 741

QY 718 GTGACGATCGAAGCAAGTGAAGCACTGAGCTTACGCTCTTGGCTTACTCAAA 777
 DB 742 GTGACGATCGAAGCAAGTGAAGCACTGAGCTTACGCTCTTGGCTTACTCAAA 801
 QY 778 CTCTGA 783
 DB 802 CTCTGA 807
 RESULT 12
 ID AAA51745
 AAA51745 standard; cDNA; 1816 BP.
 AC AAA51745;
 XX 31-OCT-2000 (first entry)
 DT 31-OCT-2000 (first entry)
 XX
 DE Human CD40 ligand cDNA.
 XX
 KW CD40 ligand; CD40; T cell; T cell receptor; rearrangement; maturation;
 KW cell death inhibition; stress-induced; immunosuppressive; anti-thyroid;
 KW anti-inflammatory; anti-diabetic; anti-rheumatic; anti-anaemic;
 KW ophthalmological; anti-psoriatic; nephrotrophic; hepatotropic; virucide;
 KW dermatological; cytostatic; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 40..825
 FT /*tag= a
 FT /product= Human_CD40_ligand
 PN W0200039283-A1.
 XX
 PD 06-JUL-2000.
 XX
 PF 22-DEC-1999; 99WO-US30930.
 PR 29-DEC-1998; 98US-0114106.
 XX
 PA (UVE-) UNIV VERMONT & STATE AGRIC COLLEGE.
 PI
 PI Newell MK, Wagner D, Newell E;
 PI WPI: 2000-452387/39.
 DR P-PSDB; AAY96993.
 XX
 PT Inducing T cell receptor gene rearrangement for treating autoimmune
 PT diseases comprises contacting T cells with a CD40-binding agent
 PS
 PS Disclosure; Page 46; 50pp; English.
 CC CD40 engagement on T cells can be used to induce T cell receptor
 CC rearrangement and enhance T cell affinity for a particular antigen. CD40
 CC engagement can be brought about by contacting CD40 with a CD40-binding
 CC agent, e.g. human CD40 ligand. The CD40-binding agents can also be used
 CC in methods for promoting T cell maturation, inhibiting T cell receptor
 CC rearrangement, inhibiting environmental stress-induced cell death,
 CC altering the specificity of a T cell towards an antigen, inducing T cell
 CC reactivity towards an antigen or enhancing environmental stress-induced
 CC cell death (all claimed). T cell affinity maturation towards a specific
 CC antigen can be inhibited, especially for a self-antigen in an autoimmune
 CC disease, which includes rheumatoid arthritis, uveitis, insulin-dependent
 CC diabetes mellitus, haemolytic anaemia, rheumatic fever, Crohn's disease,
 CC Guillain-Barre syndrome, psoriasis, thyroiditis, Grave's disease,
 CC myasthenia gravis, glomerulonephritis, autoimmune hepatitis or systemic
 CC lupus erythematosus. Inducing environmental stress-induced T cell death
 CC is carried out in a cancerous T cell or a self-reactive T cell where the
 CC environmental stress is a chemotherapeutic agent (claimed).
 XX
 SQ Sequence 1816 BP; 520 A; 461 C; 343 G; 492 T; 0 other;

Query Match 92.8%; Score 726.8; Db 21; Length 1816;
 Best Local Similarity 96.2%; Pred. No. 4,7e-191;
 Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

Qy 1 ATGATCGAAACATACCAACCAATCTCCCGCATCTGCGGCACTGAGCTGCCATCAGC 60
 Db 40 ATGATCGAAACATACCAACCAATCTCCCGCATCTGCGGCACTGAGCTGCCATCAGC 99

Qy 61 ATGAAATTTTATGATTTACTTACTGTTTTTTCTTATCCACCAATGATGGGTGAGA 120
 Db 100 ATGAAATTTTATGATTTACTTACTGTTTTTTCTTATCCACCAATGATGGGTGAGA 159

Qy 121 CTTTGGCTGTATCTTCTATAGAAATTTGAAAGGTCGAGAGAAATTAACCTTCA 180
 Db 160 CTTTGGCTGTATCTTCTATAGAAATTTGAAAGGTCGAGAGAAATTAACCTTCA 219

Qy 181 GAAGATTTTGTATTCATATAAAAGCTTAAAGATGCAACAAAGAGAAAGATCTTTATCC 240
 Db 220 GAAGATTTTGTATTCATATAAAAGCTTAAAGATGCAACAAAGAGAAAGATCTTTATCC 279

Qy 241 TTGCTGAATCTGAGAGATGAGAAAGCAATTTGAAAGCTTGTCAAGATATTAACGTTA 300
 Db 280 TTACTGAATCTGAGAGATGAGAAAGCAATTTGAAAGCTTGTGTGAAGATATTAAGTTA 339

Qy 301 AACAAAGAGA---GAAAAAGAAAAAGCTTGAATGCAAAAGGTGATCAGAACTCT 357
 Db 340 AACAAAGAGAGACAAAGAAAGAAAGCTTGAATGCAAAAGGTGATCAGAACTCT 399

Qy 358 CAATTTGCGGCACTGTCTATTAAGTGGCGAGCAAGTAAACCAATCTGTGTTCAGTGA 417
 Db 400 CAATTTGCGGCACTGTCTATTAAGTGGCGAGCAAGTAAACCAATCTGTGTTCAGTGA 459

Qy 418 GCTGAAAAAGATCTACACATGAGCAACAACTTGTATCCCTGGAAGATGGGAAACAG 477
 Db 460 GCTGAAAAAGATCTACACATGAGCAACAACTTGTATCCCTGGAAGATGGGAAACAG 519

Qy 478 CTGACCGTTAAAGACAAAGACTCTATTAATCTAATGCCCAAGTCACTCTGTTCAT 537
 Db 520 CTGACCGTTAAAGACAAAGACTCTATTAATCTAATGCCCAAGTCACTCTGTTCAT 579

Qy 538 CGGAAAGCTTGAGTCAAGCTCCATTTATAGCAAGCTCTGCTTAAAGTCCCGGTTGA 597
 Db 580 CGGAAAGCTTGAGTCAAGCTCCATTTATAGCAAGCTCTGCTTAAAGTCCCGGTTGA 639

Qy 598 TTGAGAGATCTTATCTCAGAGCTGCAAAATCCACAGTTCCGCAACCTTGGCGGCA 657
 Db 640 TTGAGAGATCTTATCTCAGAGCTGCAAAATCCACAGTTCCGCAACCTTGGCGGCA 699

Qy 658 CAATCATTCCTTGGAGAGATTTTGAATTTGCAACAGAGTCTTGGTGTTCAT 717
 Db 700 CAATCATTCCTTGGAGAGATTTTGAATTTGCAACAGAGTCTTGGTGTTCAT 759

Qy 718 GTGACTGATCGAAGCAAGTGAAGTCACTGCGCTTCAAGTCTTGGCTTACTCAAA 777
 Db 760 GTGACTGATCGAAGCAAGTGAAGTCACTGCGCTTCAAGTCTTGGCTTACTCAAA 819

Qy 778 CTCTGA 783
 Db 820 CTCTGA 825

XX OS Homo sapiens.
 XX PN WO200175067-A2.
 XX PD 11-OCT-2001.
 XX PF 30-MAR-2001; 2001WO-US08631.
 XX PR 31-MAR-2000; 2000US-0540217.
 XX PR 23-AUG-2000; 2000US-0649167.
 XX PA (HYSE-) HYSBQ INC.
 XX PI Drmanac RT, Liu C, Tang YT;
 XX DR WPI: 2001-639362/73.
 XX DR P-PSDB; ABG22384.
 XX PT New isolated polynucleotide and encoded polypeptides, useful in
 XX PT diagnostics, forensics, gene mapping, identification of mutations
 XX PT responsible for genetic disorders or other traits and to assess
 XX PT biodiversity -
 XX PS Claim 1; SEQ ID NO 22375; 103bp; English.

CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 1816 BP; 520 A; 461 C; 343 G; 492 T; 0 other;

Query Match 92.8%; Score 726.8; Db 23; Length 1816;
 Best Local Similarity 96.2%; Pred. No. 4,7e-191;
 Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

Qy 1 ATGATCGAAACATACCAACCAATCTCCCGCATCTGCGGCACTGAGCTGCCATCAGC 60
 Db 40 ATGATCGAAACATACCAACCAATCTCCCGCATCTGCGGCACTGAGCTGCCATCAGC 99

Qy 61 ATGAAATTTTATGATTTACTTACTGTTTTTTCTTATCCACCAATGATGGGTGAGA 120
 Db 100 ATGAAATTTTATGATTTACTTACTGTTTTTTCTTATCCACCAATGATGGGTGAGA 159

Qy 121 CTTTGGCTGTATCTTCTATAGAAATTTGAAAGGTCGAGAGAAATTAACCTTCA 180
 Db 160 CTTTGGCTGTATCTTCTATAGAAATTTGAAAGGTCGAGAGAAATTAACCTTCA 219

Qy 181 GAAGATTTTGTATTCATATAAAAGCTTAAAGATGCAACAAAGAGAAAGATCTTTATCC 240
 Db 220 GAAGATTTTGTATTCATATAAAAGCTTAAAGATGCAACAAAGAGAAAGATCTTTATCC 279

Qy 241 TTGCTGAATCTGAGAGATGAGAAAGCAATTTGAAAGCTTGTCAAGATATTAACGTTA 300
 Db 280 TTACTGAATCTGAGAGATGAGAAAGCAATTTGAAAGCTTGTGTGAAGATATTAAGTTA 339

Qy	301	AACAAAGAAG- - - GAATAAAGAAAACAGCTTGAATCAAAAAGGTGACGAATCT	357
Db	340	AACAAAGGAGAGAGAAAGAAAACAGCTTGAATGCAAAAAGGTGATCAGAACTCT	399
Qy	358	CAAAATGGGGCAATGTCATTAAGTGAAGCCACGACGTAAACACATCTGTGTTACATGG	417
.Db	400	CAAAATGGGGCAATGTCATTAAGTGAAGCCACGACGTAAACACATCTGTGTTACATGG	459
Qy	418	GCTGAAAAAGGANTCTACACATAGACAAACAATTGTAACCTGGAATAATGGAAAAAG	477
Db	460	GCTGAAAAAGGANTCTACACATAGACAAACAATTGTAACCTGGAATAATGGAAAAAG	519
Qy	478	CTGACCGCTTAAACACAGAAGCTCATATTATCTGATGCCAAGTCACTTGTGTCGAA	537
Db	520	CTGACCGCTTAAACACAGAAGCTCATATTATCTGATGCCAAGTCACTTGTGTCGAA	579
Qy	538	CGGGAAGCTTGAGTCAAGCTCCATTATTAAGCCAGCTCTGCTTAAAGTCCCGGTGAG	597
Db	580	CGGGAAGCTTGAGTCAAGCTCCATTATTAAGCCAGCTCTGCTTAAAGTCCCGGTGAG	639
Qy	598	TTGCGAGAGATCTTACACAGAGCTCAATATCCACAGTTCGCGCAAACTTGCGGGCA	657
Db	640	TTGCGAGAGATCTTACACAGAGCTCAATATCCACAGTTCGCGCAAACTTGCGGGCA	699
Qy	658	CAATCATCTTCACTTGGGAGAGATTTGAATGCAACAAGTCTGCTGATTTGTCAAT	717
Db	700	CAATCATCTTCACTTGGGAGAGATTTGAATGCAACAAGTCTGCTGATTTGTCAAT	759
Qy	718	GTGACTGATCCAGCCAAAGAGAGCAGTGCAGCTTCGCTTGGCTTACTCAAA	777
Db	760	GTGACTGATCCAGCCAAAGAGAGCAGTGCAGCTTCGCTTGGCTTACTCAAA	819
Qy	778	CTCTGA 783	
Db	820	CTCTGA 825	
RESULT 14			
AA	AA	AAT58122 standard; CDWA; 840 BP.	
XX	XX	AAT58122;	
DT	DT	19-SEP-1997 (first entry)	
XX	XX		
XX	XX		
DE	DE	Human CD40L mutein coding sequence, with substitution at codon 194.	
KM	KM	CD40 ligand; membrane bound glycoprotein; B cell proliferation;	
KW	KW	antibody secretion; immunoglobulin E; cytokine; mutein; ss.	
XX	XX		
OS	OS	Homo sapiens.	
XX	XX	Synthetic.	
XX	XX		
FT	FT	Key	Location/Qualifiers
FT	FT	CD5	46..831
FT	FT		/*tag= a
FT	FT		/product= CD40L mutein
FT	FT		/note= "Encodes CD40L in which the Cys residue at position 194 is replaced by Trp, Ser, Asp or Lys"
FT	FT	mutation	625..627
FT	FT		/*tag= b
FT	FT		/*note= "Wild-type TGC (Cys) codon is mutated to a codon for Trp, Ser, Asp or Lys"
XX	XX		
XX	XX		
XX	XX	WO9640918-A2.	
XX	XX		
XX	XX	19-DEC-1996.	
XX	XX		
XX	XX	06-JUN-1996;	96WO-US09632.
XX	XX		
XX	XX	07-JUN-1995;	95US-0484624.
XX	XX		

Db 586 CGGGAAGCTTGAAGTCAAGCTCATTTATACGAGCCTGNNCTAAGTCCCGGCTAGA 645
 QY 598 TTGAGAGAAATCTTACTCAGAGCTGCAATATCCAGATCTCCGCAAACTTCCGGGCAA 657
 Db 646 TTGAGAGAAATCTTACTCAGAGCTGCAATATCCAGATCTCCGCAAACTTCCGGGCAA 705
 QY 658 CAATCATTCACTTGGAGAGATTTGATTTGCAACGAGTGTCTTGGTGTTCAT 717
 Db 706 CAATCATTCACTTGGAGAGATTTGATTTGCAACGAGTGTCTTGGTGTTCAT 765
 QY 718 GTGACTGATCCAGCCAGTGAAGCCATGGCTTCACTCTTGGTGTTCAT 777
 Db 766 GTGACTGATCCAGCCAGTGAAGCCATGGCTTCACTCTTGGTGTTCAT 825
 QY 778 CTCTGA 783
 Db 826 CTCTGA 831

RESULT 15

AA057984
 ID AA057984 standard; DNA; 840 BP.

AC AA057984;

DT 20-AUG-1994 (first entry)

DE Genomic sequence of human gp39.

KM gp39; T-cell antigen; CD40 ligand; B-cell proliferation;
 B-cell differentiation; ss.

OS Homo sapiens.

FT Key Location/Qualifiers

FT CDS 22..807

FT /'tag= a

PN EF585943-A.

PD 09-MAR-1994.

PF 03-SEP-1993; 93BP-0114153.

PR 04-SEP-1992; 92US-0940605.

PA (BRIM) BRISTOL-MYERS SQUIBB CO.

PI Aruffo AA, Hollenbaugh D, Ledbetter JA, Aruffo A;

DR WPI: 1994-076264/10.

DR P-PSDB; AAR59548.

XX New nucleic acid encoding human gp39 T cell antigen - which is a

XX ligand for the CD40 receptor, causing proliferation and

XX differentiation of B cells and some cancer cells

XX Claim 1; Fig 1; 39pp; English.

XX The complete nucleic acid sequence of human gp39 (hgp39) protein

XX (corresp. to CDNA) and the complete AA sequence of hgp39 are

XX presented in AA057984 and AAR59548 respectively and contd. in plasmid

XX CDNA-hgp39, deposited with the ATCC as E. coli, CDNA MC1061/P3-hgp39

XX and assigned accession No. 69050. The human T cell antigen gp39 is a

XX ligand for the CD40 receptor. Soluble gp39 may be produced using the

XX expression vector CD8-gp39.

SO Sequence 840 BP; 263 A; 180 C; 183 G; 214 T; 0 other;

Query Match 92.4%; Score 723.6; DB 15; Length 840;

Best Local Similarity 95.9%; Pred. No. 2.7e-190;

Matches 754; Conservative 0; Mismatches 29; Indels 3; Gaps 1;

QY 1 ATGATGAAACATACACCAACCTTCCCGCATCTGGGCACTGACCTGCCATCAGC 60
 Db 22 ATGATGAAACATACACCAACCTTCCCGCATCTGGGCACTGACCTGCCATCAGC 81
 QY 61 ATGAAATTTTATGATTTTACTTATGTTTCTTATACCCAGATGATGGGTCA 120
 Db 82 ATGAAATTTTATGATTTTACTTATGTTTCTTATACCCAGATGATGGGTCA 141
 QY 121 CTTTCTCTGATCTTATGAAAGTGTGATGATGATGATGATGATGATGATGAT 180
 Db 142 CTTTCTCTGATCTTATGAAAGTGTGATGATGATGATGATGATGATGATGAT 201
 QY 181 GAAATTTTATGATTTTATGAAAGTGTGATGATGATGATGATGATGATGATGAT 240
 Db 202 GAAATTTTATGATTTTATGAAAGTGTGATGATGATGATGATGATGATGATGAT 261
 QY 241 TTGCTGAACTGTGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGATGAT 300
 Db 262 TTGCTGAACTGTGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGATGAT 321
 QY 301 AACAAAGAGA--GAAAAAGAAAAACGCTTGAATGCAAAAAGGTATGATGATCT 357
 Db 322 AACAAAGAGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATGATGATCT 381
 QY 358 CAAATTTGCGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 417
 Db 382 CAAATTTGCGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 441
 QY 418 GCTGAAAAAGATATCTACACCATGAGCAAACTTGTATCCCTGAAAAATGGAAACAG 477
 Db 442 GCTGAAAAAGATATCTACACCATGAGCAAACTTGTATCCCTGAAAAATGGAAACAG 501
 QY 478 CTGACGCTTAAAGACAGAGACTGATATATCTATGCGCAAGCACTTCTGTTCAAT 537
 Db 502 CTGACGCTTAAAGACAGAGACTGATATATCTATGCGCAAGCACTTCTGTTCAAT 561
 QY 538 CGGGAAGCTTCAAGTCAAGCTTCAATTTATAGCCAGCTCTGCTAAAGTCCCGGTAGA 597
 Db 562 CGGGAAGCTTCAAGTCAAGCTTCAATTTATAGCCAGCTCTGCTAAAGTCCCGGTAGA 621
 QY 598 TTGAGAGAAATCTTACTGAGAGCTGCAAAATACCACTTCCGCAAACTTGGGGCAA 657
 Db 622 TTGAGAGAAATCTTACTGAGAGCTGCAAAATACCACTTCCGCAAACTTGGGGCAA 681
 QY 658 CAATCATTCACTTGGAGAGATTTGAAATTTGCAACAGGTGCTTGGTGTTCAT 717
 Db 682 CAATCATTCACTTGGAGAGATTTGAAATTTGCAACAGGTGCTTGGTGTTCAT 741
 QY 718 GTGACTGATCCAGCCAGTGAAGCCATGGCTTCACTCTTGGTGTTCAT 777
 Db 742 GTGACTGATCCAGCCAGTGAAGCCATGGCTTCACTCTTGGTGTTCAT 801
 QY 778 CTCTGA 783
 Db 802 CTCTGA 807

Search completed: March 8, 2003, 22:12:58
 Job time : 166.589 secs

4.

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: March 9, 2003, 02:11:48 ; Search time 54.0541 Seconds

(without alignments)
9675.146 Million cell updates/sec

Title: US-08-982-272-20

Perfect score: 1 ATGATCGAATACACCA.....TTGCTTACTCAACTCTGA 783

Scoring table:
Gapop 10.0 , Gapext 1.0

Searched: 478924 seqs, 33395956 residues

Total number of hits satisfying chosen parameters: 957848

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA.*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/2/pubpna/PTC_NEW_PUB.seq.*
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13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	616.6	78.7	1250	US-10-182-093-1	Sequence 1, Appl1
2	155.8	19.9	2395	US-09-875-453-9	Sequence 9, Appl1
3	46	5.9	9121	US-09-070-927A-221	Sequence 221, Appl
4	37.4	4.8	431	US-09-960-352-5558	Sequence 5558, Ap
5	37.2	4.8	736	US-09-772-134B-11	Sequence 31, Appl
6	37.2	4.8	24768	US-09-764-887-602	Sequence 602, App
7	36.8	4.7	127197	US-09-754-853A-1	Sequence 1, Appl1
8	36.4	4.6	337	US-09-960-352-14232	Sequence 14232, A
9	36.4	4.6	399	US-09-960-352-14574	Sequence 14574, A
10	36.4	4.6	404	US-09-960-352-9259	Sequence 9259, Ap
11	36.4	4.6	420	US-09-960-352-7144	Sequence 7144, Ap
12	36.4	4.6	433	US-09-960-352-3058	Sequence 3058, Ap
13	36.2	4.6	262	US-09-919-580-896	Sequence 896, App
14	36.2	4.6	2430	US-10-105-695-1	Sequence 1, Appl1
15	36.2	4.6	2430	US-10-105-695-1	Sequence 1, Appl1
16	36.2	4.6	2430	US-10-106-014-1	Sequence 1, Appl1
17	36.2	4.6	544	US-09-864-761-7124	Sequence 7124, Ap
18	36	4.6	341	US-09-960-352-12302	Sequence 12302, A
19	35.8	4.6			

20	35.6	4.5	335913	9	US-09-754-853A-2	Sequence 2, Appl1
21	35.6	4.5	335913	9	US-09-754-853A-3	Sequence 3, Appl1
22	35.4	4.5	424	10	US-09-960-352-11218	Sequence 11218, A
23	35.4	4.5	1352	9	US-09-938-842A-3149	Sequence 3149, Ap
24	35.4	4.5	1352	9	US-09-938-842A-5264	Sequence 5264, Ap
25	35	4.5	23632	10	US-09-764-878-262	Sequence 262, App
26	35	4.5	23632	10	US-09-764-860-941	Sequence 941, App
27	34.8	4.4	312	10	US-09-960-352-8414	Sequence 8414, Ap
28	34.8	4.4	344	10	US-09-960-352-1036	Sequence 1036, Ap
29	34.8	4.4	391	10	US-09-813-358-196	Sequence 196, App
30	34.8	4.4	326014	10	US-09-731-231A-3	Sequence 3, Appl1
31	34.8	4.4	465237	10	US-09-933-267A-1	Sequence 1, Appl1
32	34.2	4.4	422	10	US-09-764-864-675	Sequence 675, App
33	34.2	4.4	20561	9	US-10-001-857-100	Sequence 100, App
34	34.2	4.4	176373	9	US-09-070-927A-292	Sequence 292, App
35	34.2	4.4	176373	9	US-10-095-407-17	Sequence 17, Appl
36	34	4.3	1354	10	US-09-925-301-315	Sequence 315, App
37	34	4.3	1919	9	US-09-822-846-56	Sequence 56, Appl
38	34	4.3	1919	9	US-09-822-846-57	Sequence 57, Appl
39	34	4.3	4237	10	US-09-745-763-20	Sequence 20, Appl
40	34	4.3	9717	10	US-09-764-847-1581	Sequence 1581, Ap
41	33.6	4.3	170	10	US-09-867-701-9094	Sequence 9094, Ap
42	33.6	4.3	25377	9	US-10-061-119-4	Sequence 4, Appl1
43	33.6	4.3	32185	10	US-09-764-877-3171	Sequence 3171, Ap
44	33.4	4.3	327	10	US-09-960-352-4630	Sequence 4630, Ap
45	33.4	4.3	375	10	US-09-960-352-15014	Sequence 15014, A

ALIGNMENTS

RESULT 1
US-10-182-093-1
; Sequence 1, Application US/10182093
; Publication No. US20030021808A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as represented by
; APPLICANT: the Secretary, Department of Health and Human Services,
; APPLICANT: C/O Center for Disease Control and Prevention
; APPLICANT: Tzipi, Ralph
; APPLICANT: Jones, Les
; APPLICANT: Anderson, Larry
; APPLICANT: Brown, Michael
; TITLE OF INVENTION: CD40 Ligand Adjuvant for Respiratory
; TITLE OF INVENTION: Syncytial Virus
; FILE REFERENCE: 14114.030102
; CURRENT APPLICATION NUMBER: US/10/182.093
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/179,905
; PRIOR FILING DATE: 2000-02-02
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1250
; TYPE: DNA
; ORGANISM: Murine
US-10-182-093-1

Query Match 78.7%; Score 616.6; DB 9; Length 1250;
Best Local Similarity 86.7%; Pred. No. 8.6e-155;
Matches 679; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

Qy	1	ATGATCGAATACCACTTCCCGATCTGCGGACGACGATGCGCCATCAGC	60
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Qy	61	ATGATCGAATACCACTTCCCGATCTGCGGACGACGATGCGCCATCAGC	120
Db	73	ATGATCGAATACCACTTCCCGATCTGCGGACGACGATGCGCCATCAGC	132
Qy	121	CTTTTGGCTGCTATCTTCAATGATGATGATGATGATGATGATGATGATG	180
Db	133	CTTTTGGCTGCTATCTTCAATGATGATGATGATGATGATGATGATGATG	192

Qy	181	GAAGATTTTGTTATTCATATAAAAAAGCTTAAAGAGATGCAACAAAGAGAAAGATCTTTATCC	240
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Qy	301	AACAAAGAAAGAAAAAAGAAAAAGCTTTGAAATGCAAAAAAGGTGATCGAATCCTCA	3600
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Qy	361	ATTGCGGCACTGTATCATTAAGTAGGGCCAGACAGTAAACAACATCGTGTTCACGTGGGCT	4200
Db	373	ATTGCGGCACTGTATCATTAAGTAGGGCCAGACAGTAAACAACATCGTGTTCACGTGGGCT	4322
Qy	421	GAAAAAGATACACACCATAGCAACAACCTTGGTAACTTGAAAAATGGGAAAAAGAGCTG	4800
Db	433	AACAAAGGATTTATATACATGAAAAAGCAACTGGTATCTTGAAAAATGGGAAAAAGAGCTG	4922
Qy	481	ACCGTTAAAAAGCAAGAGACTTATATATCTAATGCCAAGTACACTTGTTCCAAATGG	5400
Db	493	ACCGTTAAAAAGAGAGACTTATATATCTAATGCCAAGTACACTTGTTCCAAATGG	5522
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Db	553	GAAAGCTTGAGTCAAGTCCATTTATAGCCAGCCTTGCTCTTAAAGTCCCCGGTAGATTC	6121
Qy	601	GAGAGATCTTATACAGAGTCCAAATACCCACAGTTCGGCCAAACCTTGGCGGCACTA	6600
Db	613	GAGAGATCTTATACAGAGTCCAAATACCCACAGTTCGGCCCTTGGCTGAAAGCCACAGATTCGATCT	6722
Qy	661	TCATATCCTTGGGAGAGATTTTAAATGTGCAACAGTGTCTTGCGTTTGTCAATGTG	7200
Db	673	TCGTTCTACTGGGCGGAGTGTATTAATTAACAAGCTGTGGTCTTGCTGTTGTCAACGTG	7322
Qy	721	ACTGATCCAAAGCCAAAGTGAGCCATGGCACTGGCTTCAGCTCTTTGGCTTACTCAATCC	7800
Db	733	ACTGAAAGCAACCAAGTGATTCACAGAGATGGCTTCTCATCTTTTGGCTTACTCAATCC	7922
Qy	781	TGA 783	
Db	793	TGA 795	
RESULT 2			
US-09-875-453-9			
Sequence 9, Application US/09875453			
Publication No. US20030027320A1			
GENERAL INFORMATION:			
APPLICANT: Kim, Jungshuk P.			
APPLICANT: Starr, Douglas B.			
APPLICANT: Tam, Albert W.			
APPLICANT: Laurance, Megan E.			
APPLICANT: Michelotti, Emil F.			
APPLICANT: Veiligan, Mark D.			
APPLICANT: Latour, Derek R.			
APPLICANT: Thomas, Rita L.			
APPLICANT: Kongsachitth, Ana			
APPLICANT: Sheppard, Liana T.			
APPLICANT: Lim, Moon Young			
APPLICANT: Brice, Thomas W.			
TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION			
FILE REFERENCE: 4600-0135.30			
CURRENT APPLICATION NUMBER: US/09/875,453			
CURRENT FILING DATE: 2001-06-06			
PRIOR APPLICATION NUMBER: US 60/209,549			
PRIOR FILING DATE: 2000-06-06			
NUMBER OF SEQ. ID NOS: 78			
SOFTWARE: FastSeq for Windows Version 4.0			
SEQ. ID NO. 9			
LENGTH: 2395			

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/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-875-453-9

Query Match      19.9%; Score 155.8; DB 9, Length 2395;
Best Local Similarity 90.7%; Pred. No. 9e-32;
Matches 166; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY      1  ATATGCAAAATACACAACTTCCTCCCGATCGCGGCACATGSGATGCCCATAGC 60
Db      1999 ATATGCAAAATACACAACTTCCTCCCGATCGCGGCACATGSGATGCCCATAGC 1998

QY      61  ATGAAATTTTATGATTTACTTACTGTTTTTTCTTATCACCCAGATGTTGGTCA 120
Db      1999 ATGAAATTTTATGATTTACTTACTGTTTTTTCTTATCACCCAGATGTTGGTCA 2058

QY      121 CTTTTCGTGTGATCTTCATAGAAATGATGATCGAAGGAGGAAATTAACCTTCAT 180
Db      2059 CTTTTCGTGTGATCTTCATAGAAAGGCTGAGCAAGATGAATGAGGTCAGCA 2118

QY      181 GAA 183
Db      2119 TAA 2121

RESULT 3
US-09-070-927A-221
/ Sequence 221, Application US/09070927A
/ Patent No. US2002012016A1
/ GENERAL INFORMATION:
/ APPLICANT: Charles A. Kunsch
/           Patrick J. Dillon
/           Steven Barash
/ TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
/ NUMBER OF SEQUENCES: 992
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Human Genome Sciences, Inc.
/ STREET: 9410 Key West Avenue
/ CITY: Rockville
/ STATE: Maryland
/ COUNTRY: USA
/ ZIP: 20850
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
/ COMPUTER: HP Vectra 486/33
/ OPERATING SYSTEM: MSDOS version 6.2
/ SOFTWARE: ASCII Text
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/070,927A
/ FILING DATE: 04-May-2000
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/046,655
/ FILING DATE: 1997-05-16
/ APPLICATION NUMBER: 60/044,031
/ FILING DATE: 1997-05-06
/ APPLICATION NUMBER: 60/066,009
/ FILING DATE: 1997-11-14
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Kenley K. Hoover
/ REGISTRATION NUMBER: 40,302
/ REFERENCE/DOCKET NUMBER: PB369
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (301) 309-8504
/ TELEFAX: (301) 309-8512
/ INFORMATION FOR SEQ ID NO: 221:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 9121 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ SEQUENCE DESCRIPTION: SEQ ID NO: 221:
US-09-070-927A-221

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Query Match 5.9%; Score 46; DB 10; Length 9121;
Best Local Similarity 52.6%; Pred. No. 0.031; Mismatches 90; Indels 0; Gaps 0;
Matches 100; Conservative 0;

Qy 161 AAGAGAAATTAACCTTCATGAATTTTGTATTCATTAATAAGTAAAGATGCAACA 220
Db 8754 AAGAAAAAGCAAAAAATTTCTAGCTATTTTGAAGAGAAAAACAATGAAATTTTATA 8813
Qy 221 AAGAGAAAGATCTTATCTGCTGAAGCTGTGAGAGATGAGAGCAATTTGAAGACC 280
Db 8814 AATGAAAGAACTTATTTTGCATTAATCGCTGCTAAAGATGAAACATGTTTAAAC 8873
Qy 281 TTGTCAAGATATTAAGCTTAAACAAAGAGAAAAAGAAAAACGTTGAAATGCAAA 340
Db 8874 TTTCAGAGATATTTGTTTGGAGATGAGAGCAAAAAAATTTTGCATGATATGAAAA 8933
Qy 341 AAGGTATCA 350
Db 8934 CAATTGATTA 8943

RESULT 4
US-09-960-352-5558/c
; Sequence 5558, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Mengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21 (10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 5558
; LENGTH: 431
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 24-LIB3057-024-Q1-X1-F7
US-09-960-352-5558

Query Match 4.8%; Score 37.4; DB 10; Length 431;
Best Local Similarity 43.0%; Pred. No. 1.6; Mismatches 241; Indels 0; Gaps 0;
Matches 182; Conservative 0;

Qy 142 AGAAGATTGATAGTCGAGAGAGAACTTCATGAAGATTTTGTATTCATTAATA 201
Db 430 AAAAAAATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 371
Qy 202 AAGCTAAAGATGCAACAAAGAGAGATCTTTATCTCTGCTGAATGTGAGAGATG 261
Db 370 AATAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 311
Qy 262 AGAAGCAATTTGAAGCTTGTCAAGATTAAGCTTAAACAAAGAGAGAAAAAGAA 321
Db 310 TAATAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 251
Qy 322 AACGCTTGAATGCAAAAGATGATCAAGATCTCAATTCGCGCATGTCATTAAT 381
Db 250 AAAAAAATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 191
Qy 382 GAGGCGAGAGATTAACAATCTGTGTTCAAGTGGCTGAAGAAAGATGACACATG 441
Db 190 AAAAAAATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 131
Qy 442 AGCAACAATCTGTGATCCCTGGAAGAAAGAGATGACCTTAAAGCAAGATC 501
Db 130 TAAAAAATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 71
Qy 502 TATTATATCTATGCCAAGTCACTTCTGTTCAATGGGAAAGCTTGAGTCAAGCTCA 561

Db 70 CCAATTAATAATAATAACCAACAGCTAGCTAGCTGACAGAAACCAAGCTCCCAACA 11
Qy 562 TTT 564
Db 10 GTT 8

RESULT 5
US-09-772-134B-31/c
; Sequence 31, Application US/09772134B
; Patent No. US20020144310A1
; GENERAL INFORMATION:
; APPLICANT: Southern Illinois University
; APPLICANT: Lightfoot, David
; APPLICANT: Meksem, Khalid
; TITLE OF INVENTION: ISOLATED POLYNUCLEOTIDES AND POLYPEPTIDES RELATING TO LOCI UN
; TITLE OF INVENTION: RESISTANCE TO SOYBEAN CYST NEMATODE AND SOYBEAN SUDDEN DEATH
; FILE REFERENCE: 1268/4/2
; CURRENT APPLICATION NUMBER: US/09/772,134B
; CURRENT FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: 60/178, 811
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31
; LENGTH: 736
; TYPE: DNA
; ORGANISM: soybean
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(736)
; OTHER INFORMATION: n is an undetermined nucleotide (dATP, dCTP, dGTP, or dTTP)
US-09-772-134B-31

Query Match 4.8%; Score 37.2; DB 10; Length 736;
Best Local Similarity 50.9%; Pred. No. 2.3; Mismatches 84; Indels 0; Gaps 0;
Matches 87; Conservative 0;

Qy 192 ATTCAATAAAGAGCTTAAGAGATGCAACAAAGAGAGATCTTATCTTCTGAACTG 251
Db 184 ATGAAATAATAATGATGAAATAATAATAATAATAATAATAATAATAATAATAATA 125
Qy 252 TGAGAGATGAGAGCAATTTGAAAGCTTGTCAAGATTAAGCTTAAACAAAGAGA 311
Db 124 TTTACCATCTTAAATGAAATGAAATTAATTAATGCAAGATTAATGAAAAAATGA 65
Qy 312 GAAAAAGAAACAGCTTTGAATGCAAAAAAGGTATGAGATCTCAAT 362
Db 64 ATCAAGAGCAAAAAATTAATAATGTTAAATTTGAAATTCGAAATCTATATGT 14

RESULT 6
US-09-764-887-602/c
; Sequence 602, Application US/09764887
; Patent No. US20020042096A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA113
; CURRENT APPLICATION NUMBER: US/09/764,887
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 658
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 602
; LENGTH: 24768
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-887-602

Query Match 4.8%; Score 37.2; DB 10; Length 24768;

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: March 8, 2003, 21:49:58 ; Search time 33.5164 Seconds
(without alignments)
7164.491 Million cell updates/sec

Title: US-08-982-272-20
783

Sequence: 1 ATGATCGAAGCTCAACCA.....TTGGCTTACTCAACTCGA 783

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/prodata/2/ina/5B_COMB.seq.*
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6: /cgn2_6/prodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	726.8	92.8	786	1	US-08-446-922-3
2	726.8	92.8	786	5	PCR-US93-10034-3
3	726.8	92.8	840	1	US-07-940-605A-1
4	726.8	92.8	840	1	US-08-184-422-7
5	726.8	92.8	840	1	US-08-360-823A-1
6	726.8	92.8	840	1	US-08-431-053-3
7	726.8	92.8	840	2	US-08-690-096-1
8	726.8	92.8	840	2	US-08-249-189-11
9	726.8	92.8	840	2	US-08-484-624A-11
10	726.8	92.8	840	2	US-08-477-733B-11
11	726.8	92.8	840	3	US-08-763-995-1
12	726.8	92.8	840	3	US-09-088-913A-11
13	726.8	92.8	840	3	US-08-589-771B-7
14	726.8	92.8	840	4	US-08-759-819-11
15	726.8	92.8	840	4	US-08-770-974-11
16	726.8	92.8	840	4	US-08-858-197-3
17	726.8	92.8	840	4	US-08-770-981-11
18	726.8	92.8	840	4	US-09-399-106-11
19	618.2	79.0	783	1	US-08-446-922-5
20	618.2	79.0	783	2	US-08-249-189-11
21	618.2	79.0	783	2	US-08-484-624A-11
22	618.2	79.0	783	2	US-08-477-733B-11
23	618.2	79.0	783	3	US-09-088-913A-11
24	618.2	79.0	783	4	US-08-769-819-11
25	618.2	79.0	783	4	US-08-770-974-11
26	618.2	79.0	783	4	US-08-770-981-11
27	618.2	79.0	783	4	US-09-399-106-11

28	618.2	79.0	783	5	PCR-US93-10034-5
29	616.6	78.7	818	1	US-08-431-055-1
30	616.6	78.7	818	4	US-08-858-197-1
31	580.6	74.2	1425	2	US-08-249-189-15
32	580.6	74.2	1425	2	US-08-484-624A-15
33	580.6	74.2	1425	2	US-08-477-733B-15
34	580.6	74.2	1425	3	US-09-088-913A-15
35	580.6	74.2	1425	4	US-08-770-974-15
36	580.6	74.2	1425	4	US-08-770-981-15
37	580.6	74.2	1425	4	US-09-399-106-15
38	580.6	74.2	1425	4	US-08-446-922-10
39	579.6	74.0	929	1	US-08-249-189-20
40	579.6	74.0	929	2	US-08-484-624A-20
41	579.6	74.0	929	2	US-08-477-733B-20
42	579.6	74.0	929	3	US-09-088-913A-20
43	579.6	74.0	929	4	US-08-769-819-20
44	579.6	74.0	929	4	US-08-770-974-20
45	579.6	74.0	929	4	US-08-770-974-20

ALIGNMENTS

RESULT 1
US-08-446-922-3
; Sequence 3, Application US/08446922
; Patent No. 5716805
; GENERAL INFORMATION:
; APPLICANT: Spriggs, Melanie
; APPLICANT: Srivivasan, Subhashini
; TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.1
; SOFTWARE: Microsoft Word for Apple, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,922
; FILING DATE: 08-13-93
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/107,353
; FILING DATE: 08-13-93
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 1003-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO. 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 786 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Human
; STRAIN: CD40-L
; FEATURE:

NAME/KEY: CDS
LOCATION: 1..783
US-08-446-922-3

Query Match 92.8%; Score 726.8; DB 1; Length 786;
Best Local Similarity 96.2%; Pred. No. 2.7e-197;
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

QY 1 ATGATCGAAACATACACCAACTCTCCCGATCGGCGGCACTGGACCTCCATCAGC 60
DB 1 ATGATCGAAACATACACCAACTCTCCCGATCGGCGGCACTGGACCTCCATCAGC 60
QY 61 ATGAAATTTTATGATTTACTTACTGTTTTCTTATCACCAGATGGTGACGA 120
DB 61 ATGAAATTTTATGATTTACTTACTGTTTTCTTATCACCAGATGGTGACGA 120
QY 121 CTTTTCGTGTATCTTCTATGAAAGATTGATTAAGTGAAGAGAACTTTCAT 180
DB 121 CTTTTCGTGTATCTTCTATGAAAGATTGATTAAGTGAAGAGAACTTTCAT 180
QY 181 GAAGATTTTGTATCTTAAAGAGATGACAAAGAGAGAGAGATCTTTATCC 240
DB 181 GAAGATTTTGTATCTTAAAGAGATGACAAAGAGAGAGAGATCTTTATCC 240
QY 241 TTGCTGAATCTGTAGAGAGATGAGAGCAATTTGAAGACTTGTCAAGATATTAAGTTA 300
DB 241 TTGCTGAATCTGTAGAGAGATGAGAGCAATTTGAAGACTTGTCAAGATATTAAGTTA 300
QY 301 AACAAAGAGA---GAAAAAGAAAAACGCTTTGAAATGCAAAAAAGGTATCAAGATCT 357
DB 301 AACAAAG 360
QY 358 CAAATTCGGGACATGTCATTAAGTGAAGGCGAGCAAGTAAAGACATCTGTATCAAGTGG 417
DB 358 CAAATTCGGGACATGTCATTAAGTGAAGGCGAGCAAGTAAAGACATCTGTATCAAGTGG 417
QY 418 GGTGAAAAAGATACACCAATGAGCAAACTGGTAAACCTGGAAATGGGAAACAG 477
DB 421 GGTGAAAAAGATACACCAATGAGCAAACTGGTAAACCTGGAAATGGGAAACAG 480
QY 478 CTGACCGTTAAAGAGACAGAGCTCTATTATATATGACCAAGTCACTTGTTCAT 537
DB 481 CTGACCGTTAAAG 540
QY 538 CGGAGAGCTTGAAGAGCTGCAATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 597
DB 541 CGGAGAGCTTGAAGAGCTGCAATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
QY 598 TTGAGAGAAATCTTACTGAGAGCTGCAATTAATGAGAGAGAGAGAGAGAGAGAGAGAG 657
DB 601 TTGAGAGAAATCTTACTGAGAGCTGCAATTAATGAGAGAGAGAGAGAGAGAGAGAGAG 660
QY 658 CAATTCATCTGAGAGAGAGATTTGAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 717
DB 661 CAATTCATCTGAGAGAGAGATTTGAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY 718 GTGACTGATCAAG 777
DB 721 GTGACTGATCAAG 780
QY 778 CTCTGA 783
DB 781 CTCTGA 786

RESULT 2
PCT-US93-10034-3
Sequence 3, Application PC/TUS9310034
GENERAL INFORMATION:
APPLICANT: Spriggs, Melanie
APPLICANT: Srinivasan, Subhashini
TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric
Proteins

NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10034
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 1003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 786 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Human
STRAIN: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 1..783
PCT-US93-10034-3
Query Match 92.8%; Score 726.8; DB 5; Length 786;
Best Local Similarity 96.2%; Pred. No. 2.7e-197;
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

QY 1 ATGATCGAAACATACACCAACTCTCCCGATCGGCGGCACTGGACCTCCATCAGC 60
DB 1 ATGATCGAAACATACACCAACTCTCCCGATCGGCGGCACTGGACCTCCATCAGC 60
QY 61 ATGAAATTTTATGATTTACTTACTGTTTTCTTATCACCAGATGGTGACGA 120
DB 61 ATGAAATTTTATGATTTACTTACTGTTTTCTTATCACCAGATGGTGACGA 120
QY 121 CTTTTCGTGTATCTTCTATGAAAGATTGATTAAGTGAAGAGAGAACTTTCAT 180
DB 121 CTTTTCGTGTATCTTCTATGAAAGATTGATTAAGTGAAGAGAGAACTTTCAT 180
QY 181 GAAGATTTTGTATCTTAAAGAGATGACAAAGAGAGAGAGAGATCTTTATCC 240
DB 181 GAAGATTTTGTATCTTAAAGAGATGACAAAGAGAGAGAGAGATCTTTATCC 240
QY 241 TTGCTGAATCTGTAGAGAGATGAGAGCAATTTGAAGACTTGTCAAGATATTAAGTTA 300
DB 241 TTGCTGAATCTGTAGAGAGATGAGAGCAATTTGAAGACTTGTCAAGATATTAAGTTA 300
QY 301 AACAAAGAGA---GAAAAAGAAAAACGCTTTGAAATGCAAAAAAGGTATCAAGATCT 357
DB 301 AACAAAG 360
QY 358 CAAATTCGGGACATGTCATTAAGTGAAGGCGAGCAAGTAAAGACATCTGTATCAAGTGG 417
DB 361 CAAATTCGGGACATGTCATTAAGTGAAGGCGAGCAAGTAAAGACATCTGTATCAAGTGG 420

Qy	418	GCTGAAAAGGATACACACATGAGCAAACTTGTAACCTTGAAAATGGAAACAG	4777
Db	421	GCTGAAAAGGATACACACATGAGCAAACTTGTAACCTTGAAAATGGAAACAG	4800
Qy	478	CTGACCGTTAAAGACAGAGACTATATATATCTATATGCCCAAGTCACTCTGTTCCAT	5377
Db	481	CTGACCGTTAAAGACAGAGACTATATATATCTATATGCCCAAGTCACTCTGTTCCAT	5400
Qy	538	CGGGAAGCTTGAGATCAAGCTCATTTATATAGCCAGCGCTTGCTTAAAGTCCCGGGTAGA	5977
Db	541	CGGGAAGCTTGAGATCAAGCTCATTTATATAGCCAGCGCTTGCTTAAAGTCCCGGGTAGA	6000
Qy	598	TTGCGAGAACTTACTCTGAGAGCTGCAATATCCACAGTTCGGCAAACTTGCGGGACA	6577
Db	601	TTGCGAGAACTTACTCTGAGAGCTGCAATATCCACAGTTCGGCAAACTTGCGGGACA	6600
Qy	658	CAATCATTCACCTTGAGGAGAGATTTGAATGGACAACAGGTGCTTCGGTGTGTCAT	7177
Db	661	CAATCATTCACCTTGAGGAGAGATTTGAATGGACAACAGGTGCTTCGGTGTGTCAT	7200
Qy	718	GTAACATGATCAAGCCAAAGTGAGCATTGGACCTTCAGCTGCTTTGGCTTACTCAA	7777
Db	721	GTAACATGATCAAGCCAAAGTGAGCATTGGACCTTCAGCTGCTTTGGCTTACTCAA	7800
Qy	778	CTCTGA 783	
Db	781	CTCTGA 786	

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1      RESULT 3
2      US-07-940-605A-1
3      Sequence 1, Application US/07940605A
4      Patent No 5540926
5      GENERAL INFORMATION:
6      APPLICANT: ARIUPO, ALEJANDRO
7      APPLICANT: HOLLENBACH, DIANE
8      APPLICANT: LEDBETTER, JEFFREY A.
9      TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40
10     NUMBER OF SEQUENCES: 15
11     CORRESPONDENCE ADDRESS:
12     ADDRESSEE: Pennie & Edmonds
13     STREET: 1155 Avenue of the Americas
14     City: New York
15     STATE: New York
16     COUNTRY: U S A
17     ZIP: 10036-2711
18
19     COMPUTER READABLE FORM:
20     MEDIUM TYPE: floppy disk
21     COMPUTER: IBM PC compatible
22     OPERATING SYSTEM: PC-DOS/MS-DOS
23     SOFTWARE: PatentIn Release #1.0, Version #1.25
24     CURRENT APPLICATION DATA:
25     APPLICATION NUMBER: US/07/940,605A
26     FILING DATE: 04-SEP-1992
27     CLASSIFICATION: 530
28
29     ATTORNEY/AGENT INFORMATION:
30     NAME: Mistock, S. Leslie
31     REGISTRATION NUMBER: 18,872
32     REFERENCE/DOCKET NUMBER: 5624-184
33     TELECOMMUNICATION INFORMATION:
34     TELEPHONE: 212 790-9090
35     TELEFAX: 212 869-8864/9741
36     TELEX: 66141 PENNIE
37
38     INFORMATION FOR SEQ ID NO: 1:
39     SEQUENCE CHARACTERISTICS:
40     LENGTH: 840 base pairs
41     TYPE: nucleic acid
42     STRANDEDNESS: single
43     TOPOLOGY: linear
44
45     MOLECULE TYPE: DNA (genomic)
46
47     FEATURE:
48     NAME/KEY: CDS
49     LOCATION: 22..807

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US-07-940-605A-1

Query Match	92.8%;	Score 726.8;	DB 1;	Length 840;
Best Local Similarity	96.2%;	Pred. No. 2.7e-197;		
Matches 756; Conservative	0;	Mismatches 27;	Indels 3;	Gaps 1;

Oy	1	ATGATCGAAACATACAAACAAATCTTCCCGCATCTGGGCACTGACATGCGCATAGC	60
Db	22	ATGATCGAAACATACAAACAAATCTTCCCGCATCTGGGCACTGACATGCGCATAGC	81
Oy	61	ATGAAATTTTATATGATTTACTTACTGTTTTTTCTTATCACCAGATATTGGGTCAGCA	120
Db	82	ATGAAATTTTATATGATTTACTTACTGTTTTTTCTTATCACCAGATATGTTGGTCAGCA	141
Oy	121	CTTTTGTGCTGATATCTTATGAGAAATTGATTAAGGTGCAAGAGAAATTAACCTTCAT	180
Db	142	CTTTTGTGCTGATATCTTATGAGAAAGTTGCAAGATATGAAGATTAAGAAATCTTCAT	201
Oy	181	GAAATTTTGTATTCATTAATAAGCTTAAGATGCAACAAAGAGAAAGATCTTATCC	240
Db	202	GAAATTTTGTATTCATTAATAAGCATATCAGATGCAACAGAGAAAGATCTTATCC	261
Oy	241	TTGCTGAACTGTGAGAGATGAGAGCAATTTGAAGACTTTGCAAGATTAACGTTA	300
Db	262	TTATCGATCTGTAGAGATTAATAAGCATTTGAAGGCTTTGTGAAGATTAATGTTA	321
Oy	301	AACAAAGAGA---GAAAAAGAAAAACGCTTTGAAATGCAAAAAGTATCAGAAATCCT	357
Db	322	AACAAAGAGAGACGAAAGAAAGAAAAACGCTTTGAAATGCAAAAAGTATCAGAAATCCT	381
Oy	358	CAATTTGGGACATGTCATATGAGGCGACGATAAACACATCTGTATCAGTGG	417
Db	382	CAATTTGGGACATGTCATATGAGGCGACGATAAACACATCTGTATCAGTGG	441
Oy	418	GCTGAAAGGATATCTACCACTGAGCAACAATTGTATCCCTGGAAATATGGGAAAG	477
Db	442	GCTGAAAGGATATCTACCACTGAGCAACAATTGTATCCCTGGAAATATGGGAAAG	501
Oy	478	CTGACCGTTAAAGAACAGAGACTCTATATATCTATGCCAAGTCACTTGTTCAT	537
Db	502	CTGACCGTTAAAGAACAGAGACTCTATATATCTATGCCAAGTCACTTGTTCAT	561
Oy	538	CGGAAAGCTTGAAGTCAAGTCCATTTATAGCAAGCGCTGCTCTAAAGTCCCGGTTGA	597
Db	562	CGGAAAGCTTGAAGTCAAGTCCATTTATAGCAAGCGCTGCTCTAAAGTCCCGGTTGA	621
Oy	598	TTGAGAGAAATCTTACTCAGAGCTGCAGATACCAACGTTCCGCAACCTTGGCGGCA	657
Db	622	TTGAGAGAAATCTTACTCAGAGCTGCAGATATCCCAACGTTCCGCAACCTTGGCGGCA	681
Oy	658	CAATCCATTCCTTGGAGAGATTTTGAATAGCAACAGAGGCTGCGGTTTGTCAAT	711
Db	682	CAATCCATTCCTTGGAGAGATTTTGAATAGCAACAGAGTCTGCGTTTGTCAAT	741
Oy	718	GTCATGATTCMAACCAAGTGAGCCATGGCACTGGCTTACGCTCTTGGCTTACTCAA	777
Db	742	GTCATGATTCMAACCAAGTGAGCATGGCACTGGCTTACGCTCTTGGCTTACTCAA	801
Oy	778	CTCTGA 783	
Db	802	CTCTGA 807	

RESULT 4
 US-06-184-422-7
 Sequence 7, Application US/06184422
 Patent No. 555321
 GENERAL INFORMATION:
 APPLICANT: ARMITAGE, RICHARD
 APPLICANT: DAVISON, BARRY
 APPLICANT: FANLON, WILLIAM
 APPLICANT: RENSHAW, BLAIR
 APPLICANT: SPRIGGS, MELANIE

APPLICANT: MIDWER, MICHAEL
TITLE OF INVENTION: DETECTION AND TREATMENT OF MUTATIONS
TITLE OF INVENTION: IN A CD40 LIGAND GENE
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.1
SOFTWARE: MS Word for Apple 5.1, Version a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/184,422
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/009,258
FILING DATE: 01/22/93
ATTORNEY/AGENT INFORMATION:
NAME: PERKINS, PATRICIA ANNE
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2810-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHEetical: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46..831
US-08-184-422-7
Query Match 92.8%; Score 726.8; DB 1; Length 840;
Best Local Similarity 96.2%; Pred. No. 2.7e-197;
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

QY 1 ATGATCGAACAATCAACAACTTCTCCCGATCTGGGGGCACTGGAGCCCAATCAGC 60
DB 46 ATGATCGAACAATCAACAACTTCTCCCGATCTGGGGGCACTGGAGCCCAATCAGC 105
QY 61 ATGAAAATTTTATGATTAATCTTACTGTTTTTTCTTATCACCAGATGATGGTCACCA 120
DB 106 ATGAAAATTTTATGATTAATCTTACTGTTTTTTCTTATCACCAGATGATGGTCACCA 165
QY 121 CTTTTCGTGATCTTCATAGAAAGTGGATGAGTGAAGGTGAGAGGAAGTAACCTTAT 180
DB 166 CTTTTCGTGATCTTCATAGAAAGTGGATGAGTGAAGGTGAGAGGAAGTAACCTTAT 225
QY 181 GAAATTTTGTATTCATAAAAGCTTAAGAGTCAACAAAGAGAGATCTTATCC 240
DB 226 GAAATTTTGTATTCATAAAAGCTTAAGAGTCAACAAAGAGAGATCTTATCC 285
QY 241 TTGCTGAACGTGAGAGAGTGAAGCAATTTGAAGACCTTGCAAGATTAACGTA 300
DB 286 TTACTGAACGTGAGAGAGATTAAGGCACTTTGAAGGCTTTGAGAGATTAAGGTA 345
QY 301 AACAAAGAGA--GAAAAAGAAAAACGCTTGAATGCMAAAAGGTGATCAGATCCT 357

DB 346 AACAAAGAGACGACAGAAAGAAACAGTTTGAAATGCAAAAGGTATAGATCT 405
QY 358 CAATTCGCGCAATGTCATTAAGTGAAGCCAGACAGTAACAAATCTGTGTTACAGTGG 417
DB 406 CAAATTCGCGCAATGTCATTAAGTGAAGCCAGACAGTAACAAATCTGTGTTACAGTGG 465
QY 418 GCTGAAAAGAGATCTACACATGAGCAACATTTGGTAAACCTGGAAAAATGGAAAAAG 477
DB 466 GCTGAAAAGAGATCTACACATGAGCAACATTTGGTAAACCTGGAAAAATGGAAAAAG 525
QY 478 CTGACGCTTAAAGCAAGACCTCTATTAATCTATATGCCCAGTCACTTCTGTTCAAT 537
DB 526 CTGACGCTTAAAGCAAGACCTCTATTAATCTATATGCCCAGTCACTTCTGTTCAAT 585
QY 538 CGGAAAGCTTCAGAGTCAAGCTCCCATTTATAGCAGCCCTGCTTAAAGTCCCGGTAGA 597
DB 586 CGGAAAGCTTCAGAGTCAAGCTCCCATTTATAGCAGCCCTGCTTAAAGTCCCGGTAGA 645
QY 598 TTGAGAGATCTTATCAGAGCTGCAAAATACCAAGTTCGCGCAACCTTGGGCGCA 657
DB 646 TTGAGAGATCTTATCAGAGCTGCAAAATACCAAGTTCGCGCAACCTTGGGCGCA 705
QY 658 CAATTCATTCAGTGGAGAGATTTGAAATGCAACAGATGCTTGGTGTGCAAT 717
DB 706 CAATTCATTCAGTGGAGAGATTTGAAATGCAACAGATGCTTGGTGTGCAAT 765
QY 718 GTGACTGATTCAGAGCAAGTGAAGCCTGAGCTGCTTCAAGCTTGTGCTTACTAA 777
DB 766 GTGACTGATTCAGAGCAAGTGAAGCCTGAGCTGCTTCAAGCTTGTGCTTACTAA 825
QY 778 CTCTGA 783
DB 826 CTCTGA 831

RESULT 5
US-08-360-923A-1
Sequence 1, Application US/08360923A
Patent No. 5674492
GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: FANSLAW, WILLIAM
APPLICANT: LONGO, DAN L.
APPLICANT: KORETH, WILLIAM
TITLE OF INVENTION: METHOD OF PREVENTING OR TREATING
TITLE OF INVENTION: DISEASE CHARACTERIZED BY NEOPLASTIC CELLS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: Apple Macintosh System 7.1
SOFTWARE: Microsoft Word for Macintosh, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,923A
FILING DATE: December 21, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/172,664
FILING DATE: December 23, 1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2818-A

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206)597-0430
 TELEFAX: (206)233-0644
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 840 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHEICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 IMMEDIATE SOURCE:
 CLONE: CD40-L
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 46..831
 US-08-360-923A-1

Query Match 92.8%; Score 726.8; DB 1; Length 840;
 Best Local Similarity 96.2%; Pred. No. 2.7e-197;
 Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

Qy 1 ATGATCGAAACATACCAACCACTTCGCCGATCGCGGCACTGAGCTGCCCATCAGC 60
 Db 46 ATGATCGAAACATACCAACCACTTCGCCGATCGCGGCACTGAGCTGCCCATCAGC 105
 Qy 61 ATGAAATTTTATGATTTTACTTACTCTTTTCTTATCATCCAGATGATGGTGCAGCA 120
 Db 106 ATGAAATTTTATGATTTTACTTACTCTTTTCTTATCATCCAGATGATGGTGCAGCA 165
 Qy 121 CTTTTCGCTGATCTTCTTCAATGAAGATTGATGAAGTGAAGAGAGATGAAGTAACTTCAT 180
 Db 166 CTTTTCGCTGATCTTCTTCAATGAAGATTGATGAAGTGAAGAGATGAAGTAACTTCAT 225
 Qy 181 GAAGATTTTGTATTCATTAAGAAAGCTAAAGATGCAACAAAGAGAGATCTTTATCC 240
 Db 226 GAAGATTTTGTATTCATTAAGAAAGCTAAAGATGCAACAAAGAGAGATCTTTATCC 285
 Qy 241 TTGCTGAAGTGAAGAGATGAGAGAGCAATTTGAAGACCTTGTCAGAGATATACGTTA 300
 Db 286 TTGCTGAAGTGAAGAGATGAGAGAGCAATTTGAAGACCTTGTCAGAGATATACGTTA 345
 Qy 301 AACAAAGAGA--GAAAAAGAAAAAGCTTTGAATGCAAAAAGTGAATCAGATCCT 357
 Db 346 AACAAAGAGA--GAAAAAGAAAAAGCTTTGAATGCAAAAAGTGAATCAGATCCT 405
 Qy 358 CAAATGGGGGACATGTCATTAAGTGGGCGACAGTAAACAAATCTGTATCAGTGG 417
 Db 406 CAAATGGGGGACATGTCATTAAGTGGGCGACAGTAAACAAATCTGTATCAGTGG 465
 Qy 418 GCTGAAAAAGATCTACACCATGAGCAACATTTGGTAACTCTGAAATGGGAAACAG 477
 Db 466 GCTGAAAAAGATCTACACCATGAGCAACATTTGGTAACTCTGAAATGGGAAACAG 525
 Qy 478 CTGACCGTTAAAGCAAGAGCTTATTAATCATGCCCCAAGCTGCTGTTCCAAAT 537
 Db 526 CTGACCGTTAAAGCAAGAGCTTATTAATCATGCCCCAAGCTGCTGTTCCAAAT 585
 Qy 538 CGGAAAGCTTGAAGTCAAGCTCATTTATAGCCAGCTCTGCTTAAAGTCCCCGGGTGA 597
 Db 586 CGGAAAGCTTGAAGTCAAGCTCATTTATAGCCAGCTCTGCTTAAAGTCCCCGGGTGA 645
 Qy 598 TTGAGAGAACTTACTCAGAGCTGCAATACCAAGTTCCGCGCAAACTTGGCGGCAA 657
 Db 646 TTGAGAGAACTTACTCAGAGCTGCAATACCAAGTTCCGCGCAAACTTGGCGGCAA 705
 Qy 658 CAATCAATTCATTGGGAGAGATTTGAATTCGAACCAAGTCTTCGGTGTGTTGCAAT 717
 Db 706 CAATCAATTCATTGGGAGAGATTTGAATTCGAACCAAGTCTTCGGTGTGTTGCAAT 765

Qy 718 GTGACTATCAAGCCAGATGAGGCAATGAGCACTGAGCTTCAAGTCTTTGGTTACTGAAA 777
 Db 766 GTGACTATCAAGCCAGATGAGGCAATGAGCACTGAGCTTCAAGTCTTTGGTTACTGAAA 825
 Qy 778 CTCTGA 783
 Db 826 CTCTGA 831

RESULT 6

US-08-431-055-3

Sequence 3, Application US/08431055
 Patent No. 5817516

GENERAL INFORMATION:

APPLICANT: KERRY, MERILYN R

APPLICANT: CASTLE, BRIAN E

TITLE OF INVENTION: METHODS FOR PROLIFERATING AND

TITLE OF INVENTION: DIFFERENTIATING B CELLS, AND USES THEREOF

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX

STREET: 100 NEW YORK AVE. N.W. SUITE 600

CITY: WASHINGTON

STATE: D.C.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/431,055

FILING DATE: 28-APR-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/234,580

FILING DATE: 28-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: MULLMAN, ROBERT A

REGISTRATION NUMBER: 36,217

REFERENCE/DOCKET NUMBER: 1011.1030000/RM

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 840 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: linear

MOLECULE TYPE: DNA

FEATURE:

NAME/KEY: CDS

LOCATION: 22..807

US-08-431-055-3

Query Match

Best Local Similarity 92.8%; Score 726.8; DB 1; Length 840;

Best Local Similarity 96.2%; Pred. No. 2.7e-197;
 Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

Qy 1 ATGATCGAAACATACCAACCACTTCGCCGATCGCGGCACTGAGCTGCCCATCAGC 60
 Db 22 ATGATCGAAACATACCAACCACTTCGCCGATCGCGGCACTGAGCTGCCCATCAGC 81
 Qy 61 ATGAAATTTTATGATTTTACTTACTCTTTTCTTATCATCCAGATGATGGTGCAGCA 120
 Db 82 ATGAAATTTTATGATTTTACTTACTCTTTTCTTATCATCCAGATGATGGTGCAGCA 141
 Qy 121 CTTTTCGCTGATCTTCTTCAATGAAGATTGATGAAGTGAAGAGATGAAGTAACTTCAT 180
 Db 142 CTTTTCGCTGATCTTCTTCAATGAAGATTGATGAAGTGAAGAGATGAAGTAACTTCAT 201
 Qy 181 GAAGATTTTGTATTCATTAAGAAAGCTAAAGATGCAACAAAGAGAGATCTTTATCC 240

Db 202 GAAAGTTTGTATTCATGAAACGATACAGATGCAACAGAGAAATCTTATTC 261
 Qy 241 TTGCTGAACCTGTGAGAGATGAGAGCAATTTGAAGCTTGTCAAGATATACCTTA 300
 Db 262 TTACTGAACCTGTGAGAGATGAGAGCAATTTGAAGCTTGTCAAGATATACCTTA 321
 Qy 301 AACAAAG 357
 Db 322 AACAAAG 381
 Qy 358 CAAATTGGGAGACATCTCTTAAGTGGAGCCAGCAAGTAAACATCTGTGTACAGTGG 417
 Db 382 CAAATTGGGAGACATCTCTTAAGTGGAGCCAGCAAGTAAACATCTGTGTACAGTGG 441
 Qy 418 GCTGAAAAGAGATACATACATGAGCAACATCTGTGTAACCTGGAAGAGAGAGAGAG 477
 Db 442 GCTGAAAAGAGATACATACATGAGCAACATCTGTGTAACCTGGAAGAGAGAGAGAG 501
 Qy 478 CTGACCGTTAAAG 537
 Db 502 CTGACCGTTAAAG 561
 Qy 538 CGGAGAGCTTGAAGTCAAGCTCATTATAGCCAGCTGTGCTAAAGTCCCGGTAGA 597
 Db 562 CGGAGAGCTTGAAGTCAAGCTCATTATAGCCAGCTGTGCTAAAGTCCCGGTAGA 621
 Qy 598 TTGAGAGAGATCTTACTGAGCTGCAAAATCCCAAGTCCGCAAACTTGGGAGCA 657
 Db 622 TTGAGAGAGATCTTACTGAGCTGCAAAATCCCAAGTCCGCAAACTTGGGAGCA 681
 Qy 658 CAATCATTCACCTTGGAGAGATTTGAATGCAACAGTGGCTGGATTTGTCAT 717
 Db 682 CAATCATTCACCTTGGAGAGATTTGAATGCAACAGTGGCTGGATTTGTCAT 741
 Qy 718 GTGAGTATCCAGAGCAAGTGGAGCCAGTGGCTTCAAGCTTGGCTTACCTCAA 777
 Db 742 GTGAGTATCCAGAGCAAGTGGAGCCAGTGGCTTCAAGCTTGGCTTACCTCAA 801
 Qy 778 CTCTGA 783
 Db 802 CTCTGA 807

RESULT 7
 US-08-690-096-1
 Sequence 1, Application US/08690096
 Patent No. 5945513
 GENERAL INFORMATION:
 APPLICANT: ARUPFO, ALEJANDRO
 APPLICANT: HOLLENBAUGH, DIANE
 APPLICANT: LEDBETTER, JEFFREY A.
 TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036-2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/690,096
 FILING DATE: 31-JUL-1996
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/940,605
 FILING DATE: 04-SEP-1992

ATTORNEY/AGENT INFORMATION:
 NAME: Mastrock, S. Leslie
 REGISTRATION NUMBER: 18,872
 REFERENCE/DOCKET NUMBER: 5624-184
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212 790-9090
 TELEFAX: 212 869-8864/9741
 TELE: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 840 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 22..807
 US-08-690-096-1

Query Match 92.8%; Score 726.8; DB 2; Length 840;
 Best Local Similarity 96.2%; Pred. No. 2.7e-197;
 Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

1 ATGATGAAACATACAAACCTCTCCCGATCTGGGCACTGGAGCTGCCATAGC 60
 22 ATGATGAAACATACAAACCTCTCCCGATCTGGGCACTGGAGCTGCCATAGC 81
 Qy 61 ATGAAATTTTATGATTTTACTTACTGTTTTCTTATCAACCAAGATGATGGTACGA 120
 Db 82 ATGAAATTTTATGATTTTACTTACTGTTTTCTTATCAACCAAGATGATGGTACGA 141
 Qy 121 CTTTGTGCTGATCTTATCATAGAGATGATGATGATGATGATGATGATGATGATGAT 180
 Db 142 CTTTGTGCTGATCTTATCATAGAGATGATGATGATGATGATGATGATGATGATGAT 201
 Qy 181 GAAATTTTGTATCATTAATAAAGCTAAAGATGCAACAAGAGAGATCTTTATTC 240
 Db 202 GAAATTTTGTATCATTAATAAAGCTAAAGATGCAACAAGAGAGATCTTTATTC 261
 Qy 241 TTGCTGAACCTGTGAGAGATGAGAGCAATTTGAAGCTTGTCAAGATATACCTTA 300
 Db 262 TTACTGAACCTGTGAGAGATGAGAGCAATTTGAAGCTTGTCAAGATATACCTTA 321
 Qy 301 AACAAAG 357
 Db 322 AACAAAG 381
 Qy 358 CAAATTGGGAGACATCTCTTAAGTGGAGCCAGCAAGTAAACATCTGTGTACAGTGG 417
 Db 382 CAAATTGGGAGACATCTCTTAAGTGGAGCCAGCAAGTAAACATCTGTGTACAGTGG 441
 Qy 418 GCTGAAAAGAGATACATACATGAGCAACATCTGTGTAACCTGGAAGAGAGAGAGAG 477
 Db 442 GCTGAAAAGAGATACATACATGAGCAACATCTGTGTAACCTGGAAGAGAGAGAGAG 501
 Qy 478 CTGACCGTTAAAG 537
 Db 502 CTGACCGTTAAAG 561
 Qy 538 CGGAGAGCTTGAAGTCAAGCTCATTATAGCCAGCTGTGCTAAAGTCCCGGTAGA 597
 Db 562 CGGAGAGCTTGAAGTCAAGCTCATTATAGCCAGCTGTGCTAAAGTCCCGGTAGA 621
 Qy 598 TTGAGAGAGATCTTACTGAGCTGCAAAATCCCAAGTCCGCAAACTTGGGAGCA 657
 Db 622 TTGAGAGAGATCTTACTGAGCTGCAAAATCCCAAGTCCGCAAACTTGGGAGCA 681
 Qy 658 CAATCATTCACCTTGGAGAGATTTGAATGCAACAGTGGCTGGATTTGTCAT 717
 Db 682 CAATCATTCACCTTGGAGAGATTTGAATGCAACAGTGGCTGGATTTGTCAT 741
 Qy 718 GTGAGTATCCAGAGCAAGTGGAGCCAGTGGCTTCAAGCTTGGCTTACCTCAA 777

1 TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
2 NUMBER OF SEQUENCES: 26
3 CORRESPONDENCE ADDRESS:
4 ADDRESSEE: IMDEX CORPORATION
5 STREET: 51 UNIVERSITY STREET
6 CITY: SEATTLE
7 STATE: WASHINGTON
8 COUNTRY: USA
9 ZIP: 98101
10 COMPUTER READABLE FORM:
11 MEDIUM TYPE: Floppy disk
12 COMPUTER: Apple Macintosh
13 OPERATING SYSTEM: Apple Operating System 7.5.5
14 SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1
15 CURRENT APPLICATION DATA:
16 APPLICATION NUMBER: US/08/484,624A
17 FILING DATE:
18 CLASSIFICATION:
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER: 08/477,733
21 FILING DATE: June 07, 1995
22 CLASSIFICATION:
23 PRIOR APPLICATION DATA:
24 APPLICATION NUMBER: 07/969,703
25 FILING DATE: October 23, 1992
26 CLASSIFICATION:
27 PRIOR APPLICATION DATA:
28 APPLICATION NUMBER: 07/805,723
29 FILING DATE: December 5, 1991
30 CLASSIFICATION:
31 PRIOR APPLICATION DATA:
32 APPLICATION NUMBER: 07/783,707
33 FILING DATE: October 25, 1991
34 CLASSIFICATION:
35 ATTORNEY/AGENT INFORMATION:
36 NAME: Perkins, Patricia A.
37 REGISTRATION NUMBER: 34,693
38 REFERENCE/DOCKET NUMBER: 2802-D
39 TELECOMMUNICATION INFORMATION:
40 TELEPHONE: 2065870430
41 TELEFAX: 2065870606
42 INFORMATION FOR SEQ ID NO: 11:
43 SEQUENCE CHARACTERISTICS:
44 LENGTH: 840 base pairs
45 TYPE: nucleic acid
46 STRANDEDNESS: single
47 TOPOLOGY: linear
48 MOLECULE TYPE: cDNA
49 HYPOTHEICAL: NO
50 ANTI-SENSE: NO
51 ORIGINAL SOURCE:
52 ORGANISM: Homo sapiens
53 IMMEDIATE SOURCE:
54 CLONE: CD40-L
55 FEATURE:
56 NAME/KEY: CDS
57 LOCATION: 46..831
58 US-08-484-624A-11
59
60 Query Match 92.8%; Score 726.8; DB 2; Length 840;
61 Best Local Similarity 96.2%; Pred. No. 2.7e-197;
62 Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

166 CTTTTCCTGTGTATCTTCAATAGAGTTGCAAGAGATGAGAAAGATCTTCAT 225
181 GAAATTTTGTATTTATTAATAAAAGCTAAAGATGCAACAAAGAGAGATCTTATCC 240
226 GAAATTTTGTATTTATTAATAAAAGCTAAAGATGCAACAAAGAGAGATCTTATCC 285
241 TTGCTGAATGTGAGAGATGAGAGCAATTTGAAGCTTGTCAAGATTTAACTGA 300
286 TTACTGACCTGTGAGAGATTTAAAGCCAGTTTGAAGCTTGTGAGAGATTTAACTGA 345
301 AACAAAGAGA---GAAAAAGAAACAGCTTTGAATGCAAAAAGGTATGAAATCT 357
346 AACAAAG 405
358 CAATTCGCGCAATGTATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 417
406 CAATTCGCGCAATGTATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 465
418 GCTGAAAAAGATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 477
466 GCTGAAAAAGATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 525
478 CTGACGCTTAAAG 537
526 CTGACGCTTAAAG 585
538 CCGGAGAGCTTGAAG 597
586 CCGGAGAGCTTGAAG 645
598 TTGAGAGAGATTTTACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 657
646 TTGAGAGAGATTTTACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 705
658 CAATTCCTTCACTGAG 717
706 CAATTCCTTCACTGAG 765
718 GTGAGATGATCAAG 777
766 GTGAGATGATCAAG 825
QY 778 CTCTGA 783
DB 826 CTCTGA 831
RESULT 10
US-08-477-733B-11
Sequence 11, Application US/08477733B
Patent No. 5981724
GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: FANSLON, WILLIAM
APPLICANT: SPRIGGS, MELANIE
APPLICANT: SRINIVASAN, SUBHASHINI
APPLICANT: GIBSON, MARYLOU
APPLICANT: MORRIS, ARVIA E.
APPLICANT: MCGREW, JEFFERY
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMDEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1

```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,733B
FILING DATE: June 07, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,189
FILING DATE: May 24, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,703
FILING DATE: October 23, 1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/805,723
FILING DATE: December 5, 1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/783,707
FILING DATE: October 25, 1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46..831
US-08-477-733B-11

Query Match          92.8%; Score 726.8; DB 2; Length 840;
Best Local Similarity 96.2%; Pred. No. 2,7e-197;
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

QY 1 ATGATCGAAACATCAACCAAACTCTCCCGATCTGCGGCGCACTGGAATGCCATCAGC 60
DB 46 ATGATCGAAACATCAACCAAACTCTCTCCGATCTGCGGCGCACTGGAATGCCATCAGC 105
QY 61 ATGAAATTTTATGATTTTACTTACTCTGTTTCTTATCAACCAAGATGATGGTCAGCA 120
DB 106 ATGAAATTTTATGATTTTACTTACTCTGTTTCTTATCAACCAAGATGATGGTCAGCA 165
QY 121 CTTTTCGTGATCTTCTTATGAAGATTGATTAAGTGAAGAGAGAAAGTAACTTCAT 180
DB 166 CTTTTCGTGATCTTCTTATGAAGATTGATTAAGTGAAGAGAGAAAGTAACTTCAT 225
QY 181 GAAGATTTTATTCATTAATAAAGCTAAAGATGCAACAAAGAGAGAGATCTTTATCC 240
DB 226 GAAGATTTTATTCATTAATAAAGCTAAAGATGCAACAAAGAGAGAGATCTTTATCC 285
QY 241 TTGCTGAACCTGAGAGATGAGAAAGCAATTTGAAGACCTTGTCAAGATATTAACCTTA 300
DB 286 TTACTGAACCTGAGAGATGAGAAAGCAATTTGAAGACCTTGTGTGAAGATATTAACCTTA 345
QY 301 AACAAAGAGA---GAAAAAGAAAAACAGCTTTGAATGCAAAAAGCTGATCAAAATCCT 357
DB 346 AACAAAGAGAGAGAGAAAGAAAAACAGCTTTGAATGCAAAAAGCTGATCAAAATCCT 405

QY 358 CAATTCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 417
DB 406 CAATTCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 465
QY 418 GCTGAAAAAGATATCAACCAATGAGCAACCACTTGTAACTCGAAAAAGAGAGAGAG 477
DB 466 GCTGAAAAAGATATCAACCAATGAGCAACCACTTGTAACTCGAAAAAGAGAGAGAG 525
QY 478 CTGACCTTTAAAGCAAGGAGCTCTATTTATCTATGCGCAAGTACCTTGTGTCAT 537
DB 526 CTGACCTTTAAAGCAAGGAGCTCTATTTATCTATGCGCAAGTACCTTGTGTCAT 585
QY 538 CGGGAAGCTTGAAGTCAAGCTTCAATTAAGCAAGCTTGTGTCAT 597
DB 586 CGGGAAGCTTGAAGTCAAGCTTCAATTAAGCAAGCTTGTGTCAT 645
QY 598 TTGAGAGAGATCTTATCTGAGAGCTGCAAAATACCAAGTTCGCGCAAACTTGCAGG 657
DB 646 TTGAGAGAGATCTTATCTGAGAGCTGCAAAATACCAAGTTCGCGCAAACTTGCAGG 705
QY 658 CAATTCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 717
DB 706 CAATTCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 765
QY 718 GTGACTATTCAGAGCAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 777
DB 766 GTGACTATTCAGAGCAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 825
QY 778 CTCTGA 783
DB 826 CTCTGA 831

RESULT 11
US-08-763-995-1
Sequence 1, Application US/08763995
Patent No. 6017527
GENERAL INFORMATION:
APPLICANT: MARASKOVSKY, EUGENE
TITLE OF INVENTION: METHOD OF ACTIVATING DENDRITIC CELLS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Power Macintosh 7200/90
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Macintosh, Version #6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/763,995
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/677,762
FILING DATE: 10 JUL 1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2845-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
```

TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46..831
US-08-763-995-1

Query Match 92.8%; Score 726.8; DB 3; Length 840;
Best Local Similarity 96.2%; Pred. No. 2.7e-197;
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

QY 1 ATGATCGAAACATACCAACCACTCTCCCGATCTGGCGGCACTGGACCTGACCATCAGC 60
DB 46 ATGATCGAAACATACCAACCACTCTCCCGATCTGGCGGCACTGGACCTGACCATCAGC 105
QY 61 ATGAAATTTTATGATTTTACTTCTTTTCTTATCACCAGATGATGGGTGACA 120
DB 106 ATGAAATTTTATGATTTTACTTCTTTTCTTATCACCAGATGATGGGTGACA 165
QY 121 CTTTGGCTGTATCTTATGAAAGTGGATAAGTGAAGAGAAAGTAACTTCTAT 180
DB 166 CTTTGGCTGTATCTTATGAAAGTGGATAAGTGAAGAGAAAGTAACTTCTAT 225
QY 181 GAAGTTTGTATCTTAAAGCTTAAAGATGCAAGAAAGAAAGATTTTATCC 240
DB 226 GAAGTTTGTATCTTAAAGCTTAAAGATGCAAGAAAGAAAGATTTTATCC 285
QY 241 TTGCTGAACGTGAGAGATGAGAGCAATTTGAAGCTTGTCAAGATATTAAGTTA 300
DB 286 TTGCTGAACGTGAGAGATGAGAGCAATTTGAAGCTTGTCAAGATATTAAGTTA 345
QY 301 AACAAAGAGA---GAAAAAGAAAAAGCTTTGAAGTCAAAAAAGTATCAAGATCT 357
DB 346 AACAAAGAGAAGAGAAAGAAAAAGCTTTGAAGTCAAAAAAGTATCAAGATCT 405
QY 358 CAAATTCGGGACATGTCATTAAGTGGAGCCAGCAAGTAAACAGATCTGTATCAGTGG 417
DB 406 CAAATTCGGGACATGTCATTAAGTGGAGCCAGCAAGTAAACAGATCTGTATCAGTGG 465
QY 418 GGTGAAAAAGATCTACACCACTGAGCAACAAGTGGTAACTGGGAAAAAGGAAAAAG 477
DB 466 GGTGAAAAAGATCTACACCACTGAGCAACAAGTGGTAACTGGGAAAAAGGAAAAAG 525
QY 478 CTGACCGTTAAAGACAGAGCTCTATTATATCTATGCCAAGTCACTTCTGTCCAT 537
DB 526 CTGACCGTTAAAGACAGAGCTCTATTATATCTATGCCAAGTCACTTCTGTCCAT 585
QY 538 CGGGAGGCTTGGAGTCAAGCTCATTATAGCCAGCTCTCCAAAGTCCCGCGTGA 597
DB 586 CGGGAGGCTTGGAGTCAAGCTCATTATAGCCAGCTCTCCAAAGTCCCGCGTGA 645
QY 598 TTGAGAGAAATCTTACTGAGCTGCAAAATACCAAGTTCGCGCAAACTTGGCGGCA 657
DB 646 TTGAGAGAAATCTTACTGAGCTGCAAAATACCAAGTTCGCGCAAACTTGGCGGCA 705
QY 658 CAATTCATCTTGGAGAGATTTTGAATGCAACAGGCTTGGGTTGTTGTCAT 717
DB 706 CAATTCATCTTGGAGAGATTTTGAATGCAACAGGCTTGGGTTGTTGTCAT 765
QY 718 GTGACTGATCCAAAGCCAGTGGCATGAGCTGAGCTTCAAGTCTTGGCTTACTCAA 777
DB 766 GTGACTGATCCAAAGCCAGTGGCATGAGCTGAGCTTCAAGTCTTGGCTTACTCAA 825
QY 778 CTCTGA 783
DB 826 CTCTGA 831

RESULT 12

US-09-088-913A-11
Sequence 11, Application US/09088913A
Patent No. 6087329
GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: FANSLAW, WILLIAM
APPLICANT: SPRIGGS, MELANIE
APPLICANT: SRINIVASAN, SUBHASHINI
APPLICANT: GIBSON, MARYLOU
APPLICANT: MORRIS, ARVIA E.
APPLICANT: MCGREW, JEFFERY
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/088, 913A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484, 624
FILING DATE:
APPLICATION NUMBER: 06/477, 733
FILING DATE: June 07, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969, 703
FILING DATE: October 23, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/805, 723
FILING DATE: December 5, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/783, 707
FILING DATE: October 25, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46..831
US-09-088-913A-11
Query Match 92.8%; Score 726.8; DB 3; Length 840;
Best Local Similarity 96.2%; Pred. No. 2.7e-197;
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

QY 1 ATGATCGAAGATACCAACCACTTCTCCCGATTCGCGCCACATGATGCCATCAGC 60
 DB 46 ATGATCGAAGATACCAACCACTTCTCCCGATTCGCGCCACATGATGCCATCAGC 105
 QY 61 ATGAAATTTTATGATTTTACTTACTCTGTTTTCTTATCACCAGATGTTGGTCAGCA 120
 DB 106 ATGAAATTTTATGATTTTACTTACTCTGTTTTCTTATCACCAGATGATTTGGTCAGCA 165
 QY 121 CTTTTCGCTGTATCTTCTCAAGATTTGATTAAGTGTGAAGATGATTAAGTTCAT 180
 DB 166 CTTTTCGCTGTATCTTCTCAAGATTTGATTAAGTGTGAAGATGATTAAGTTCAT 225
 QY 181 GAAGATTTTGTATTCATTAAGATTAAGATGATTAAGATGATTAAGATGATTAAGTTCAT 240
 DB 226 GAAGATTTTGTATTCATTAAGATTAAGATGATTAAGATGATTAAGATGATTAAGTTCAT 285
 QY 241 TTGCTGAATCTGTGAGAGATGAGATTAAGATGATTAAGATGATTAAGATGATTAAGTTCAT 300
 DB 286 TTGCTGAATCTGTGAGAGATGAGATTAAGATGATTAAGATGATTAAGATGATTAAGTTCAT 345
 QY 301 AACAAAGAGA---GAAAAAGAAAAAGCTTTGAAATGCAAAAAAGTATCAGATTCCT 357
 DB 346 AACAAAGATCCT 405
 QY 358 CAAATTTGGGCGACATGTCATTAAGTGGCGACAGTAAACAAATCTGTGTTACAGTGG 417
 DB 406 CAAATTTGGGCGACATGTCATTAAGTGGCGACAGTAAACAAATCTGTGTTACAGTGG 465
 QY 418 GCTGAAAAAGATACCTACCATGAGCAACATTTGTTAACTCTGAGAAATGGGAAACAG 477
 DB 466 GCTGAAAAAGATACCTACCATGAGCAACATTTGTTAACTCTGAGAAATGGGAAACAG 525
 QY 478 CTGACCGTTTAAAG 537
 DB 526 CTGACCGTTTAAAG 585
 QY 538 CGGAAAGCTTGAAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCCGGATGA 597
 DB 586 CGGAAAGCTTGAAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCCGGATGA 645
 QY 598 TTGAGAGAGATCTTACTCAGAGCTGCAAAATCCAGTTCGCGCAAACTTTGGGAGCA 657
 DB 646 TTGAGAGAGATCTTACTCAGAGCTGCAAAATCCAGTTCGCGCAAACTTTGGGAGCA 705
 QY 658 CAATTCATCTGAGAGAGAGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 717
 DB 706 CAATTCATCTGAGAGAGAGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 765
 QY 718 GTGACTGATCCAGAGCAAGTGAAGCACTGGCTTCAAGTCTTTGGGCTTACTCAAA 777
 DB 766 GTGACTGATCCAGAGCAAGTGAAGCACTGGCTTCAAGTCTTTGGGCTTACTCAAA 825
 QY 778 CTCTGA 783
 DB 826 CTCTGA 831

RESULT 13

US-08-589-771B-7

Sequence 7, Application US/08589771B

Patent No. 6106832

GENERAL INFORMATION:

APPLICANT: ARMITAGE, RICHARD

APPLICANT: DAVISON, BARRY

APPLICANT: FANSLON, WILLIAM

APPLICANT: RENSLOW, BLAIR

APPLICANT: SPRIGGS, MELANIE

APPLICANT: WIDMER, MICHAEL

TITLE OF INVENTION: TREATMENT OF INDIVIDUALS EXHIBITING

DEFECTIVE CD40L (as amended)

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESS: IMMUNEX CORPORATION
 STREET: 51 UNIVERSITY STREET
 CITY: SEATTLE
 STATE: WASHINGTON
 COUNTRY: USA
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: MS-DOS/Windows 95
 SOFTWARE: Word for Windows 95, 7.04
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/589,771B
 FILING DATE: January 22, 1996
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/009,258
 FILING DATE: 01/22/93
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: HENRY, JANIS C.
 REGISTRATION NUMBER: 34,347
 REFERENCE/DOCKET NUMBER: 2810-C
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 2065870430
 TELEFAX: 2065870606
 INFORMATION FOR SEQ. ID NO. 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 840 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHEICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 IMMEDIATE SOURCE:
 CLONE: CD40-L
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 46..831
 US-08-589-771B-7

Query Match 92.8%; Score 726.8; DB 3; Length 840;
 Best Local Similarity 96.2%; Pred. No. 2,7e-197;
 Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

QY 1 ATGATCGAAGATACCAACCACTTCTCCCGATTCGCGCCACATGATGCCATCAGC 60
 DB 46 ATGATCGAAGATACCAACCACTTCTCCCGATTCGCGCCACATGATGCCATCAGC 105
 QY 61 ATGAAATTTTATGATTTTACTTACTCTGTTTTCTTATCACCAGATGTTGGTCAGCA 120
 DB 106 ATGAAATTTTATGATTTTACTTACTCTGTTTTCTTATCACCAGATGATTTGGTCAGCA 165
 QY 121 CTTTTCGCTGTATCTTCTCAAGATTTGATTAAGTGTGAAGATGATTAAGTTCAT 180
 DB 166 CTTTTCGCTGTATCTTCTCAAGATTTGATTAAGTGTGAAGATGATTAAGTTCAT 225
 QY 181 GAAGATTTTGTATTCATTAAGATTAAGATGATTAAGATGATTAAGATGATTAAGTTCAT 240
 DB 226 GAAGATTTTGTATTCATTAAGATTAAGATGATTAAGATGATTAAGATGATTAAGTTCAT 285
 QY 241 TTGCTGAATCTGTGAGAGATGAGATTAAGATGATTAAGATGATTAAGATGATTAAGTTCAT 300
 DB 286 TTGCTGAATCTGTGAGAGATGAGATTAAGATGATTAAGATGATTAAGATGATTAAGTTCAT 345
 QY 301 AACAAAGAGA---GAAAAAGAAAAAGCTTTGAAATGCAAAAAAGTATCAGATTCCT 357
 DB 346 AACAAAGATCCT 405
 QY 358 CAAATTTGGGCGACATGTCATTAAGTGGCGACAGTAAACAAATCTGTGTTACAGTGG 417

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Db 406 CAAATTGGCGCAGATGTCATTAAGTGAAGCCGACGTAAGAAACAGTCGTGTTACAGTGG 465
Qy 418 GCTGAAAAAGATCTACACCTAGCAACACTTGGTAACCTGGAAAAATGGAAAAACAG 477
Db 466 GCTGAAAAAGATCTACACCTAGCAACACTTGGTAACCTGGAAAAATGGAAAAACAG 525
Qy 478 CTGACCGTTAAAGACAGAGCTATTATATCTATATGAGCCCAAGTCACTCTGTCCAAAT 537
Db 526 CTGACCGTTAAAGACAGAGCTATTATATCTATATGAGCCCAAGTCACTCTGTCCAAAT 585
Qy 538 CGGGAAGCTTGAGTCAAGCTCAATTTATAGCAAGCTCTGCTTAAAGTCCCGGTAGA 597
Db 586 CGGGAAGCTTGAGTCAAGCTCAATTTATAGCAAGCTCTGCTTAAAGTCCCGGTAGA 645
Qy 598 TTGAGAGATCTTACTAGAGCTGCAATATCCACAGTTCCGCAAACTCTGCGGCA 657
Db 646 TTGAGAGATCTTACTAGAGCTGCAATATCCACAGTTCCGCAAACTCTGCGGCA 705
Qy 658 CAATCATCTTCTGGAGAGATATTGAATTGCAACGAGTCTGCTGCTTGTTCAT 717
Db 706 CAATCATCTTCTGGAGAGATATTGAATTGCAACGAGTCTGCTGCTTGTTCAT 765
Qy 718 GTGACTGATCCAGCCAGTGAAGCCAGTGGCTGCTGCTTGTTCAT 777
Db 766 GTGACTGATCCAGCCAGTGAAGCCAGTGGCTGCTGCTTGTTCAT 825
Qy 778 CTCTGA 783
Db 826 CTCTGA 831

RESULT 14
US-08-769-819-11
; Sequence 11, Application US/08769819
; Patent No. 6264951
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: FANSLON, WILLIAM
; APPLICANT: SPRIGGS, MELANIE
; APPLICANT: SRINIVASAN, SUBHASHINI
; APPLICANT: GIBSON, MARYLOU
; TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESS: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.1
; SOFTWARE: Microsoft Word for Apple, version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/769,819
; FILING DATE: 19-DEC-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/484,624
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: 08/249,189
; FILING DATE: May 24, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/969,703
; FILING DATE: October 23, 1992
; APPLICATION NUMBER: 07/805,723
; FILING DATE: December 5, 1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/783,707

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; FILING DATE: October 25, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2802-E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 2065870430
; TELEFAX: 2065870606
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 840 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: CD40-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 46..831
; US-08-769-819-11

Query Match 92.8%; Score 726.8; DB 4; Length 840;
Best Local Similarity 96.2%; Pred. No. 2.7e-197;
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

Qy 1 ATGATGAAACATACACCAACTCTCCCGATCTGGGCGCATGAGCCATCGCAGC 60
Db 46 ATGATGAAACATACACCAACTCTCCCGATCTGGGCGCATGAGCCATCGCAGC 105
Qy 61 ATGAAATTTTATATATTTACTACTGTTTCTTATACCAAGATGATGGGCGCA 120
Db 106 ATGAAATTTTATATATTTACTACTGTTTCTTATACCAAGATGATGGGCGCA 165
Qy 121 CTTTGTCTGTATCTTCATAGAGATTGATAGTTCGAGAGAGAGTAACTTCAT 180
Db 166 CTTTGTCTGTATCTTCATAGAGATTGATAGTTCGAGAGAGAGTAACTTCAT 225
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Db 286 TTGCTAGCTGTAGAGATGAGAGGCAATTTGAAGCCTTGTCAAGATATACTTA 345
Qy 301 AACAAAGAGA---GAAAAAAGAAACAGCTTGAATGCAAAAAGGATCAAAATCCT 357
Db 346 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 405
Qy 358 CAAATTCGCGCATGTATAGTGAAGGCGCAGAGTAAACAAATCTGTGTATACAGTGG 417
Db 406 CAAATTCGCGCATGTATAGTGAAGGCGCAGAGTAAACAAATCTGTGTATACAGTGG 465
Qy 418 GCTGAAAAAGATCTACACCTAGCAACACTTGGTAACCTGGAAAAATGGAAAAACAG 477
Db 466 GCTGAAAAAGATCTACACCTAGCAACACTTGGTAACCTGGAAAAATGGAAAAACAG 525
Qy 478 CTGACCGTTAAAGACAGAGCTATTATATCTATATGAGCCCAAGTCACTCTGTCCAAAT 537
Db 526 CTGACCGTTAAAGACAGAGCTATTATATCTATATGAGCCCAAGTCACTCTGTCCAAAT 585
Qy 538 CGGGAAGCTTGAGTCAAGCTCAATTTATAGCAAGCTCTGCTTAAAGTCCCGGTAGA 597
Db 586 CGGGAAGCTTGAGTCAAGCTCAATTTATAGCAAGCTCTGCTTAAAGTCCCGGTAGA 645
Qy 598 TTGAGAGATCTTACTAGAGCTGCAATATCCACAGTTCCGCAAACTCTGCGGCA 657
Db 646 TTGAGAGATCTTACTAGAGCTGCAATATCCACAGTTCCGCAAACTCTGCGGCA 705

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